ICEID
2015
International Conference
on Emerging Infectious Diseases

August 24-26, 2015
Hyatt Regency Atlanta
Atlanta, Georgia

2015 International Conference on Emerging Infectious Diseases

Program and Abstracts Book

Organized by

Centers for Disease Control and Prevention

Council of State and Territorial Epidemiologists

Association of Public Health Laboratories

World Health Organization

American Society for Microbiology

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ICEID 2015 Conference

Schedule-at-a-Glance*

Registration 6:00 AM - 8:00 PM

Monday, August 24, 2015

Poster Set-up
7:00 AM - 8:00 AM

Plenary Sessions
8:00 AM - 9:00 AM

A1. Climate Change
A2. Hemorrhagic Fevers
A3. Antimicrobial Resistance— Global Issues
A4. Malaria

Plenary Sessions
9:10 AM - 10:10 AM

B1. Science and the Media
B2. New Opportunities in TB Control
B3. Healthcare-Associated Infections
B4. Intersection of Chronic and Infectious Diseases

Coffee Break
10:10 AM - 10:30 AM

Panel Sessions
10:30 AM - 12:00 PM

C1. Infections from Contaminated Pharmaceuticals
C2. Coronaviruses
C3. Advanced Molecular Detection
C4. Disease Elimination and Eradiction
C5. *Clostridium difficile*
C6. Global Tour of EIDs

Lunch 12:00 PM - 12:30 PM
(on your own)

Poster Sessions

Directors' Tour of Posters

Panel Sessions
1:45 PM - 3:15 PM

D1. Advancing Antibiotic Stewardship in Healthcare Settings
D2. Communicating Infectious Disease Risks
D3. Ebola
D4. Bioinformatics
D5. Emerging Influenza Viruses
D6. New Vector Control Strategies

Coffee Break
3:15 PM - 3:30 PM

Poster Sessions
3:30 PM - 4:45 PM

Directors' Tour of Posters

Keynote Session
5:00 PM - 7:30 PM

Reception
7:30 PM - 9:30 PM

Registration 7:00 AM - 5:00 PM	Tuesday, August 25, 2015	Registration 7:00 AM - 12:00 PM	Wednesday, August 26, 2015
	Poster Set-up 7:00 AM - 8:00 AM		Poster Set-up 7:00 AM - 8:00 AM
	Plenary Sessions 8:00 AM - 9:00 AM		Plenary Sessions 8:00 AM - 9:00 AM
	E1. Reemergence of Vaccine-Preventable Diseases E2. Ebola E3. Dengue E4. The Microbiome		J1. Control of HIV/AIDS and Ebola J2. Infectious Diseases in Popular Culture (Cinema) J3. Global Water and Sanitation J4. Middle East Respiratory Syndrome (MERS)
	Plenary Sessions 9:10 AM - 10:10 AM		Plenary Sessions 9:10 AM - 10:10 AM
	F1. Global Trade and EIDs F2. Influenza F3. The Global Health Security Agenda F4. Bioinformatics		K1. Chikungunya K2. Advanced Molecular Detection K3. 20 Years of the Emerging Infections Program K4. Polio
	Coffee Break 10:10 AM - 10:30 AM		Coffee Break 10:10 AM - 10:30 AM
	Panel Sessions 10:30 AM - 12:00 PM		Panel Sessions 10:30 AM - 12:00 PM
	G1. Integration of Public Health and Infectious Disease Clinicians G2. Emerging Fungal Diseases G3. Emerging Tickborne Diseases G4. Culture-Independent Diagnostics G5. Vaccine-Preventable Diseases: Global Issues G6. Global Water and Sanitation		L1. Emerging Infections in Immunologically Unique Hosts L2. Public Policy and Infectious Diseases L3. Early Detection and Prediction of Outbreaks L4. Emerging Respiratory Infections in the Eastern Mediterranean Region L5. One Health L6. Controlling Bloodborne Pathogens
	Lunch 12:00 PM - 12:30 PM (on your own)		Lunch 12:00 PM - 12:30 PM (on your own)
	Poster Sessions 12:30 PM - 1:45 PM		Poster Sessions 12:30 PM - 1:45 PM 12:30 PM - 1:45 PM
	Directors' Tour of Posters		Directors' Tour of Posters
	Panel Sessions 1:45 PM - 3:15 PM		Panel Sessions 1:45 PM - 3:15 PM
	H1. Healthcare-Associated Infections H2. Infectious Diseases in Humanitarian (Disaster) Settings H3. Emerging Mosquito-Borne Diseases H4. The Ethics of Research During Infectious Disease Epidemics H5. Foodborne Diseases H6. Rabies		M1. Social Determinants of EIDs M2. Sexually Transmitted Diseases M3. Pathogen Discovery and New Syndromes M4. New Data Systems and Platforms for Surveillance M5. Respiratory Diseases M6. Tropical and Zoonotic Infections
	Coffee Break 3:15 PM - 3:30 PM		Coffee Break 3:15 PM - 3:30 PM
	Oral Presentations 3:30 PM - 5:00 PM		Oral Presentations 3:30 PM - 5:00 PM
	I1. Vector-Borne Diseases I2. Vaccine-Preventable Diseases I3. Surveillance I I4. Antimicrobial Resistance I5. Foodborne Diseases I I6. Late Breakers I		N1. Healthcare-Associated Infections N2. Respiratory Diseases N3. Advances in Microbial Detection and Characterization N4. Surveillance II N5. Foodborne Diseases II N6. Late Breakers II
	Poster Sessions 5:00 PM - 6:15 PM		
	Directors' Tour of Posters		

***Note: Registration will also be open on Sunday, August 23, 2015 from 5:00 PM - 7:00 PM**

Committees

Steering Committee

Duane Kilgus, *Chair*

National Center for Immunization and Respiratory Diseases
Centers for Disease Control and Prevention

Scientific Program Committee Co-chairs

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Office of Infectious Diseases

Ermias Belay
National Center for Emerging and Zoonotic Infectious Diseases

Kashef Ijaz
Center for Global Health

Taraz Samandari
National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention

Cynthia Whitney
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Emerging Infectious Diseases

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ICEID 2015 Conference
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Council of State and Territorial Epidemiologists
Association of Public Health Laboratories
World Health Organization
American Society for Microbiology

Sponsors

American Academy of Pediatrics
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American Society of Tropical Medicine and Hygiene
American Veterinary Medical Association
Association for Professionals in Infection Control and Epidemiology
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Pediatric Infectious Diseases Society
Society for Healthcare Epidemiology of America
US Agency for International Development
US Department of Agriculture, Animal and Plant Health Inspection Service
US Department of Agriculture, Food Safety Inspection Service
US Department of Defense, Global Emerging Infections Surveillance and Response System
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US Geological Survey, National Wildlife Health Center
US National Institutes of Health, Fogarty International Center
US National Institutes of Health, National Institute of Allergy and Infectious Diseases
World Organization for Animal Health

ICEID 2015 Leaders Program

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Ministry of Health, Jordan

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International Centre for Diarrhoeal Diseases Research, Bangladesh

Mohamed Samai
University of Sierra Leone, Sierra Leone

Maman Zaneidou
Ministry of Public Health, Niger

Rima F. Khabbaz, M.D.

Welcome to Atlanta

Dear Colleagues,

On behalf of the Centers for Disease Control and Prevention (CDC), I would like to welcome you to the 2015 International Conference on Emerging Infectious Diseases. ICEID 2015 marks the ninth occurrence of this global public health event, organized by CDC in collaboration with the American Society for Microbiology, the Association of Public Health Laboratories, the Council of State and Territorial Epidemiologists, and the World Health Organization, with additional support from more than 25 multidisciplinary public health partners.

Since the last ICEID, we have witnessed the largest outbreak of Ebola virus disease on record, the emergence of a new severe respiratory disease—Middle East Respiratory Syndrome (MERS), global increases in antimicrobial resistance, and the continued expansion of infectious diseases into new geographic areas. While substantial barriers persist, we have also seen remarkable progress in controlling these threats through new tools, technologies, and partnerships. With its expansive list of distinguished speakers and experts, ICEID 2015 provides an exceptional venue for exchanging the latest information on these and other critically important public health issues. I would like to especially thank this year's scientific program and steering committees for their hard work in making this possible.

I hope that you will enjoy ICEID 2015 and find opportunities for enhancing your work and building public health partnerships.

Thank you for attending the conference.

Rima F. Khabbaz, M.D.
Deputy Director for Infectious Diseases
Director, Office of Infectious Diseases
Centers for Disease Control and Prevention

General Information

Affiliated Events

A complete list of Affiliated Events is available in the Addendum provided separately.

Americans with Disabilities Act Compliance

The Hyatt Regency Atlanta is in compliance with the Americans with Disabilities Act to the extent of the law. If special accommodations would enhance your enjoyment of the conference, please visit the ICEID/ASM Headquarters Office in Executive Conference Suite 219 located on the second floor of the Atrium Tower. We will make all reasonable accommodations to ensure your comfort at the meeting.

Business Center

The Hyatt Regency Atlanta business center is located on the lobby level.

Hours:

- Monday – Friday ..... 7:00 a.m. – 7:00 p.m.
- Saturday ..... 8:00 a.m. – 1:00 p.m.
- Sunday ..... Closed

Cameras and Recording

Digital recorders, cameras (including camera phones), and video cameras (including video phones) are prohibited in the poster hall and session rooms. Anyone found photographing, videotaping, or recording in the prohibited areas will be asked to surrender their badge immediately and leave the conference. No refund will be provided. This rule is strictly enforced.

Child Safety

Children are not permitted into session rooms. Children under the age of 16 are not permitted on the Exhibit Hall Floor.

Continuing Education Credit

Continuing Education will be offered. See page 10 for details.

E-Central

Located on the ballroom level and exhibit level, E-Central stations will be available for attendees during the hours listed below.

Hours:

- Sunday, August 23 ..... 5:00 p.m. – 7:00 p.m.
- Monday, August 24 ..... 6:00 a.m. – 9:30 p.m.
- Tuesday, August 25 ..... 7:00 a.m. – 6:15 p.m.
- Wednesday, August 26 ..... 7:00 a.m. – 5:00 p.m.

The following services and information are available:

- **Continuing Education Information**
- **E-mail Access**: E-mail access provides attendees access to their corporate or personal e-mail accounts. E-mail access provides hotlinks to the most popular e-mail programs as a prompt that allows users of other web-driven e-mail programs to enter their provider's URL. Users without e-mail accounts or with non-driven accounts may utilize the "Send Only" option to send messages to an e-mail address.

Exhibits

Exhibits will be held in the Grand Hall on the exhibit level of the Hyatt Regency Atlanta.

Hours:

- Monday, August 24 ..... 10:10 a.m. – 4:45 p.m. *and* 7:30 p.m. – 9:30 p.m.
- Tuesday, August 25 ..... 10:10 a.m. – 6:15 p.m.
- Wednesday, August 26..... 10:10 a.m. – 1:45 p.m.

A complete list of exhibitors is available in the Addendum provided separately.

Food and Beverage

There are many dining options within walking distance of the Hyatt Regency Atlanta. Peachtree Center is located at the corner of Peachtree Street and International Boulevard and has a large variety of food choices.

Headquarters Office

The ICEID/ASM Headquarters Office is located in Executive Conference Suite 219 located on the second floor of the Atrium Tower. Feel free to come to us with questions or concerns.

Hours:

- Sunday, August 23 . . . . . 12:00 p.m. – 7:00 p.m.
- Monday, August 24 . . . . . 6:00 a.m. – 5:00 p.m.
- Tuesday, August 25 . . . . . 7:00 a.m. – 6:15 p.m.
- Wednesday, August 26. . . 7:00 a.m. – 5:00 p.m.

Opening Reception

Be sure to attend the Opening Reception with food, drink and camaraderie on Monday, August 24, from 7:30 p.m. – 9:30 p.m. Tickets are required and can be purchased at Registration.

Poster Presenters

Poster set-up is from 7:00 a.m. – 8:00 a.m. on the day of your presentation. Posters are located in the Exhibit Hall (Grand Hall on the exhibit level). You must set up your poster during this time regardless of your presentation time.

Press Room

Press representatives are welcome at the conference. Please check in at the Press Room, located in the Executive Conference Suite 222 on the second floor of the Atrium Tower.

Registration

Registration is located in front of Grand Hall on the exhibit level and will be open during the times listed below.

Hours:

- Sunday, August 23 ..... 5:00 p.m. – 7:00 p.m.
- Monday, August 24 ..... 6:00 a.m. – 8:00 p.m.
- Tuesday, August 25 ..... 7:00 a.m. – 5:00 p.m.
- Wednesday, August 26..... 7:00 a.m. – 12:00 p.m.

Speaker Ready Room

Speakers may preview their electronic presentations in the Speaker Ready Room, located in the Learning Center (ballroom level). The room is equipped with PCs loaded with PowerPoint and other software so that you may view and make changes to your electronic files. Please submit your presentation to the speaker ready room at least 2 hours before the start of the session in which you will be speaking.

Hours:

- Sunday, August 23 ..... 5:00 p.m. – 7:00 p.m.
- Monday, August 24 ..... 6:00 a.m. – 5:00 p.m.
- Tuesday, August 25 ..... 7:00 a.m. – 6:00 p.m.
- Wednesday, August 26..... 7:00 a.m. – 3:30 p.m.

Verification of Attendance

Conference attendees requiring a certificate verifying their attendance should visit the ASM/ICEID Headquarters Office in Executive Conference Suite 219 located on the second floor of the Atrium Tower or Registration on the exhibit level beginning Tuesday, August 25. We will be happy to provide you with the needed documentation.

Continuing Education Credit

Continuing Education credit will be offered. Our target audience includes physicians, nurses, and health educators. Additional continuing education details will be provided at the conference.

Accreditation Statements

CME: The Centers for Disease Control and Prevention is accredited by the Accreditation Council for Continuing Medical Education (ACCME®) to provide continuing medical education for physicians.

The Centers for Disease Control and Prevention designates this **Live material** for a maximum of **17.5** *AMA PRA Category 1 Credits™*. Physicians s*hould claim only the credit commensurate with the extent* of their participation in the activity.

CNE: The Centers for Disease Control and Prevention is accredited as a provider of Continuing Nursing Education by the American Nurses Credentialing Center's Commission on Accreditation. This activity provides **17.5** contact hours.

CEU: The Centers for Disease Control and Prevention is authorized by the International Association for Continuing Education and Training (IACET) to offer **2.1** CEU's for this program.

CECH: Sponsored by the Centers for Disease Control and Prevention, a designated provider of continuing education contact hours (CECH) in health education by the National Commission for Health Education Credentialing, Inc. This program is designated for Certified Health Education Specialists (CHES) and/or Master Certified Health Education Specialists (MCHES) to receive up to **17.5** total Category I continuing education contact hours. Maximum advanced level continuing education contact hours available are **0**. CDC provider number **98614**.

CPH (Certified Public Health Professionals): CDC is an approved provider of CPH Recertification Credits by the National Board of Public Health Examiners. Effective October 1, 2013, the National Board of Public Health Examiners (NBPHE) accepts continuing education units (CEU) for CPH recertification credits from CDC. Please select CEU as your choice for continuing education when registering for a course on TCEOnline. Learners seeking CPH should use the guidelines provided by the NBPHE for calculating recertification credits. For assistance please contact NBPHE at http://www.NBPHE.org.

Disclosure

In compliance with continuing education requirements, all presenters must disclose any financial or other associations with the manufacturers of commercial products, suppliers of commercial services, or commercial supporters as well as any use of unlabeled product(s) or product(s) under investigational use.

CDC, our planners, content experts, and their spouses/partners wish to disclose they have no financial interests or other relationships with the manufacturers of commercial products, suppliers of commercial services, or commercial supporters with the exception of those disclosures listed in the Addendum provided at the conference and online at www.iceid.org.

Content will not include any discussion of the unlabeled use of a product or a product under investigational use with the exception of those disclosures listed in the Addendum provided at the conference and online at www.iceid.org.

CDC does not accept commercial support.

Monday, August 24

Poster Set-up for the Day
7:00 AM – 8:00 AM

All posters presented on Monday will be available for viewing in the Grand Hall from 10:10 AM to 4:45 PM. Authors will be present at posters for one hour and fifteen minutes as noted under the Scientific Sessions schedule for the day.

Scientific Sessions

A. Concurrent Plenary Sessions
8:00 AM - 9:00 AM

A1. Climate Change
Centennial Ballroom I

Moderator:
Ruth Berkelman: Emory University, Atlanta, GA

Speaker:
Impact of Climate Variability on Vector-borne Disease Transmission
Kenneth Linthicum; US Department of Agriculture, Agricultural Research Service, Gainesville, FL

A2. Update on Hemorrhagic Fevers
Centennial Ballroom II

Moderator:
Dianna Blau; Centers for Disease Control and Prevention, Atlanta, GA

Speaker:
Hemorrhagic Fever in West Africa: Never Forget Lassa Fever!
Pierre Rollin; Centers for Disease Control and Prevention, Atlanta, GA

A3. Antimicrobial Resistance (Global Issues)
Centennial Ballroom III

Moderator:
Scott Fridkin; Centers for Disease Control and Prevention, Atlanta, GA

Speakers:
Global Leadership to Address Antimicrobial Resistance: The Global Health Security Agenda and AR Global Action Plan
Beth P. Bell; Centers for Disease Control and Prevention, Atlanta, GA

Cross-cultural Challenges and Cross-border Collaborations on Combating Antimicrobial Resistance: Lessons Learned from Europe
Dominique Monnet; European Centre for Disease Prevention and Control, Stockholm, Sweden

A4. Malaria
Centennial Ballroom IV

Moderator:
Larry Madoff; International Society for Infectious Diseases, Boston, MA

Speaker:
Harnessing Genomics for Global Health: Evolving Infectious Diseases and Lessons for the Science of Malaria Eradication
Dyann Wirth; Harvard T.H. Chan School of Public Health, Boston, MA

B. Concurrent Plenary Sessions
9:10 AM - 10:10 AM

B1. Science and the Media
Centennial Ballroom I

Moderator:
Dave Daigle; Centers for Disease Control and Prevention, Atlanta, GA

Speaker:
Field Notes from a Medical Correspondent
Elizabeth Cohen; Cable News Network, Turner Broadcasting Systems, Inc., Atlanta, GA

B2. New Opportunities for Tuberculosis Control: New Genes and New Treatments
Centennial Ballroom II

Moderator:
Peter Cegielski; Centers for Disease Control and Prevention, Atlanta, GA

Speaker:
Molecular Testing for Drug Resistance in Tuberculosis
James Posey; Centers for Disease Control and Prevention, Atlanta, GA

B3. Challenges in Prevention of Healthcare-Associated Infections
Centennial Ballroom III

Moderator:
Kavita Trivedi; Society for Healthcare Epidemiology of America, Berkeley, CA

Speaker:
Carbapenem Resistance: The Political and Scientific Perspective from India
Abdul Ghafur; Apollo Specialty Hospital, Chennai, India

B4. Intersection of Chronic Diseases and Infectious Diseases
Centennial Ballroom IV

Moderator:

Samira Asma; Centers for Disease Control and Prevention, Atlanta, GA

Speaker:

Halving Premature Death
Richard Peto; University of Oxford, Oxford, United Kingdom

Break
10:10 AM – 10:30 AM | Grand Hall

C. Concurrent Panel Sessions
10:30 AM - 12:00 PM

C1. Infections from Contaminated Pharmaceuticals or Counterfeit Medications
International Ballroom South

Moderators:

Tom Chiller
Scott Fridkin
Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Lessons Learned from Recent Investigations of Pharmaceutical Products Contaminated with Fungi
Rachel Smith; Centers for Disease Control and Prevention, Atlanta, GA

Current US Requirements for Compounding Medications: Advances and Gaps
Eric Kastango; Clinical IQ, LLC and CriticalPoint, LLC, Madison, NJ

Regulating US Pharmacies to Improve Patient Safety from Contaminated Products: A View from a State Board of Pharmacy
Virginia Herold; California State Board of Pharmacy, Sacramento, CA

C2. Emergence and Pathogenesis of Coronaviruses
Centennial Ballroom I

Moderators:

Dianna Blau; Centers for Disease Control and Prevention, Atlanta, GA

Sam Dominguez; Pediatric Infectious Diseases Society, Aurora, CO

Speakers:

Can Coronavirus Host-Jumping Events Be Predicted?
Kathryn Holmes; University of Colorado School of Medicine, Aurora, CO

Mechanisms of Zoonotic Coronavirus Emergence
Ralph S. Baric; University of North Carolina at Chapel Hill, Chapel Hill, NC

Animal Coronaviruses: Historical Perspectives for Emerging Human Coronaviruses
Linda J. Saif; Food Animal Health Research Program, The Ohio State University, Wooster, OH

C3. Advanced Molecular Detection
Centennial Ballroom II

Moderators:

Greg Armstrong
Scott Sammons
Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Retrospective and Real-time Molecular Epidemiology of the 2014-2015 Ebola Outbreak: A European Perspective
Miles Carroll; Public Health England, Salisbury, United Kingdom

Genomic Epidemiology of Bacterial Pathogens—the Potential and Possible Pitfalls
William Hanage; Harvard University, Cambridge, MA

Transforming Public Health Response through Innovation and Partnership
Jill Taylor; Wadsworth Center, New York State Department of Health, Albany, NY

C4. Disease Elimination and Eradication
International Ballroom North

Moderators:

Eric Mast
Monica Parise
Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Polio's Last Mile: Implementing Eradication Efforts in Hard-to-reach, Insecure, and Conflict Areas
John Vertefeuille; Centers for Disease Control and Prevention, Atlanta, GA

Malaria Eradication v2.0: Historical Lessons and Historic Opportunities
Justin Cohen; Clinton Health Access Initiative, Boston, MA

Guinea Worm Eradication—Challenges Winding Up the Final Inch
Sharon Roy; Centers for Disease Control and Prevention, Atlanta, GA

Update on Measles Elimination
Katrina Kretsinger, Centers for Disease Control and Prevention, Atlanta, GA

C5. *Clostridium difficile* Infection
Centennial Ballroom III

Moderators:

Richard Danila; Council of State and Territorial Epidemiologists, St. Paul, MN

Clifford McDonald; Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Update on *Clostridium difficile* Infection in Europe and Other Non-U.S. Settings
Tim Peto; John Radcliffe Hospital, Oxford, United Kingdom

Controversies in the Diagnosis of *Clostridium difficile* Infection in the United States
Dale Gerding; Loyola University Chicago Stritch School of Medicine, Chicago, IL

Paradigm Changes in Fecal Microbiota Transplant for *Clostridium difficile*
Colleen Kraft; Emory University, Atlanta, GA

C6. Global Tour of EIDs
Centennial Ballroom IV

Moderators:

Peter Drotman; Centers for Disease Control and Prevention, Atlanta, GA

Larry Madoff; International Society for Infectious Diseases, Boston, MA

Speakers:

Africa
Nina Marano; CDC Kenya, Nairobi, Kenya

Asia
Shua Chai; Centers for Disease Control and Prevention, Field Epidemiology Training Programme, Dhaka, Bangladesh

Australia
Paul Effler; Western Australia Department of Health, Perth, Australia

Europe
Ines Steffens; European Centre for Disease Prevention and Control, Stockholm, Sweden

North America
David Freedman; University of Alabama at Birmingham, Birmingham, AL

South America
Jaime Torres, Tropical Medicine Institute of Caracas, Caracas, Venezuela

Lunch
12:00 PM – 12:30 PM | On your own

Poster Session with Authors – I
12:30 PM - 1:45 PM | Grand Hall

Director's Tour of Posters
Nancy Messonnier
Deputy Director, National Center for Immunization and Respiratory Diseases

Molecular Epidemiology

Board 1: Surveillance System in Guangdong, China: Serovar Distribution, Antimicrobial Resistance Profiles, and PFGE Typing of *Salmonella enterica* Strains

Board 2: The Molecular Epidemiology Characteristics and Genetic Diversity of *Salmonella* Typhimurium in Guangdong, China

Board 3: Examination of PulseNet Data to Assess the Utility of Pulsed-field Gel Electrophoresis (PFGE) for *Campylobacter* Outbreak Investigations

Board 4: Distribution of Hepatitis C Virus Genotypes in the United Arab Emirates

Board 5: Multi-locus VNTR-based Diversity of Emerging Monophasic Variant of Serovar Typhimurium for French Outbreak Investigation

Board 6: Interspecies Transfer of Plasmids Harboring Resistance Genes in a Patient with *Klebsiella pneumoniae* Carbapenemase (KPC)-producing Carbapenem-resistant *Enterobacteriaceae* (CRE)

Board 7: Optical Mapping and Genome Sequences of Isolates of *Bartonella bacilliformis*

Board 8: Detection of Human Bocavirus Types 1 and 3 in Egyptian Children with Acute Gastroenteritis

Board 9: Emergence of Norovirus GI.3 Outbreaks in the United States, 2013-2014

Board 10: Molecular Epidemiology of Human Adenoviruses in South West India

Board 11: Molecular Genetic Monitoring in Influenza Sentinel Surveillance Among Patients with Influenza-like Illnesses (ILI) and Severe Acute Respiratory Infections (SARI) in the Republic of Kazakhstan

Board 12: Identification of a *Janibacter* Species from a Patient with Endocarditis Based on Ultra-deep Sequencing of Bacterial Genomes

Board 13: Molecular Epidemiology of Pathogenic and Non-pathogenic Hantaviruses in Slovenia

Board 14: A Simple Genotyping Method for Differentiation of *Blastocystis* Subtypes and Genetic Variation of *Blastocystis* sp. in Thailand

Advanced Molecular Detection (AMD)

Board 15: Detection of Single and Mixed Subtype Influenza Viruses with Next-Generation Sequencing Platform

Board 16: Development of a Flexible, Rapid, High-capacity Sequencing Method for MERS-CoV

Board 17: Transforming Public Health Microbiology in the United States with Whole Genome Sequencing (WGS)—PulseNet and Beyond

Board 18: Transforming Public Health Microbiology for *Campylobacteraceae* with Whole Genome Sequencing

Board 19: Metagenomic Pathogen Detection and Gut Microbiome Response to Foodborne Illness

Board 20: A Bioinformatic Pipeline to Genotype and Compare Hundreds of *Bacillus anthracis* Genomes

Board 21: Implementation of Whole Genome Sequencing (WGS) for Surveillance of Shiga Toxin-producing *Escherichia coli* (STEC) in the United States

Board 22: Rapid Molecular Detection and Characterization of *Legionella* for Outbreak Response

Board 23: The Application of Whole Genome Multi-locus Sequence Typing to Characterize *Listeria monocytogenes*

Board 24: Rapid Identification of *Burkholderia pseudomallei* by Using a Pyrosequencing Based Algorithm

Board 25: Describing Meaningful Starting and Ending Points for a Dynamic Change Process: Advanced Molecular Detection in Public Health

Board 26: Targeted Re-sequencing and Metagenomics Analysis to Identify and Characterize Pathogens in Respiratory Specimens from Unexplained Respiratory Disease Outbreak (URDO) Responses

Board 27: Point-of-care Multiplex Detection and Differentiation of Chikungunya and Dengue Viruses in Whole Blood

Laboratory Support for Strengthening Infectious Disease Surveillance and Monitoring Infections

Board 28: Little Effect of Varying Specimen Storage Temperature on Influenza PCR Results

Board 29: PulseNet Promotes Global Health Security and Enhances Disease Surveillance in Mexico Through Laboratory Training

Board 30: Molecular Epidemiological Characterization of *Brucella canis* from Humans in Zhejiang, China

Board 31: Improving Laboratory Quality Management Systems in Selected Public Health Laboratories in Egypt

Board 32: Overview of FilmArray™ Respiratory Panel Results from the Department of Defense Global Laboratory-based Influenza Surveillance Program

Board 33: Assessment of Public Health Laboratory System in Cambodia

Board 34: Severe Acute Respiratory Infection (SARI) and Pandemic Influenza Preparedness Central Public Health Laboratories, Egypt (2007-2014)

Board 35: The Public Health Laboratory System Database: Developing a National Public Health Laboratory Test Directory

Board 36: Disparate Detection Outcomes for Anti-HCV IgG and HCV RNA in Dried Blood Spots

Board 37: Cluster of False-positive Influenza Rapid Antigen Tests, Denver, Colorado, 2013-14: Impact on Clinical Management and Public Health Surveillance

Board 38: Evaluation of the Microscopic Observation Drug Susceptibility (MODS) Assay for Direct Detection of MDR-TB and XDR-TB

Board 39: A TaqMan Array Card (TAC) for Detection of Pathogens Causing Acute Febrile Illness in East Africa

Board 40: Passive Hepatitis Delta Surveillance in the United States: 2012-2014

Board 41: Performance of a Hepatitis C Virus Core Antigen Assay for Identifying Persons in the United States with Current Hepatitis C Virus Infection

Board 42: Combined Anti-hepatitis E Virus IgG Serotesting for Resolving Hepatitis E Virus Epidemiology in the United States

Board 43: Investigation of Acute Neurological Disease Using a Simple Differential Diagnostic Tool for 29 Etiological Agents of Febrile Disease in South Africa

Board 44: The Detection of Anti-dengue Virus IgM in Urine as a Putative Marker for Severe Disease

Board 45: Differences in Viral Antigens Distribution Between Wild Type and Vaccine-associated Viscerotropic Yellow Fever Fatal Cases

Board 46: Reference Laboratory of Malaria as an Element of Vigilance in Armenia

Board 47: Laboratory Diagnostics of Equine Influenza

Board 48: Genetic Diversity of *Mycobacterium tuberculosis* and Mutation Profiles in Drug Resistance Associated Genes in Bagamoyo District, Tanzania

Board 49: Detection of *Bacillus anthracis* and Determining the Presence of Plasmid rX01 and rX02 in PCR

New or Rapid Diagnostics

Board 50: Performance of Quidel Sofia Rapid Diagnostic Influenza Test, 2012-2014

Board 51: Establishment of a National Influenza Centre (NIC) in a Post Conflict and Resource Limited Country (Afghanistan): Progress and Challenges

Board 52: Evaluation of the Performance of Rapid Diagnostic Tests for Rotavirus and Cholera in Dadaab Refugee Camp and the Kenya/Somali Border

Board 53: Assessment of Arbor Vita A/H7N9 Rapid Subtyping Test

Board 54: Immunodiagnostic Development for Lyme Disease Targeting *Borrelia burgdorferi* HtrA Protease

Board 55: Application of Genotypic Characterization for the Direct Detection of Drug Resistant Genes in *Mycobacterium tuberculosis* in Clinical Samples from Children

Board 56: Comparison of a Multipathogen Detection Platform to Singleplex qPCR Assays for Detection of Respiratory Infections Among Persons at Nine International Sites

Board 57: A Loop-mediated Isothermal Amplification Method for Rapid Detection of *Salmonella enterica* Serovar Typhi Infection

Board 58: Development and Characterization of Mouse Monoclonal Antibodies Against Monomeric Dengue Virus Non-structural Glycoprotein 1 (NS1)

Board 59: The Utility of a Rapid Dengue Diagnostic Test to Detect Outbreaks in Places Lacking Established Diagnostic Testing—Angola, Republic of the Marshall Islands, Federated States of Micronesia, and Fiji

Board 60: Biophysical Characterization of the *Plasmodium falciparum* Biomarker HRP2 Toward High-sensitivity Lateral Flow Immunoassay Infection Detection Tests for Malaria Elimination Campaigns

Laboratory Proficiency Testing/Quality Assurance

Board 61: Clinical Evaluation and Validation of Laboratory Methods for the Diagnosis of *Bordetella pertussis* Infection: Culture, Polymerase Chain Reaction (PCR), and Anti-pertussis Toxin IgG Serology (IgG-PT)

Board 62: The Investigation of Infectious Disease Laboratory Management of a Less-developed Province in China

Board 63: Quality of HIV Testing in Zambia (2009 - 2012): The Impact of National Quality Assurance Systems

Board 64: Evaluation of Data Analysis Software Programs for Quantitative Fluorescent Microsphere Immuno Array (FMIA) Validation

Host and Microbial Genetics

Board 65: Host Genetic Susceptibility to Enteric Viruses: A Systematic Review

Surveillance for Vaccine-Preventable Diseases

Board 66: Population-based Incidence of Childhood Pneumonia Associated with Viral Infections in a Tropical Developing Country

Board 67: Global Role and Burden of Influenza in Adult Respiratory Hospitalizations: A Systematic Analysis

Board 68: An Applied Comprehensive Surveillance System Using Human Antibody, Epidemiological, Entomological, and Veterinary Surveillance to Monitor Japanese Encephalitis in Beijing, China

Board 69: Measles Outbreak—Northern Lao PDR, January 2013

New Vaccines

Board 70: Global Age Distribution of Pediatric Norovirus Cases

Board 71: Estimating the Impact of Pediatric Non-typhoidal *Salmonella* Vaccination on the Number of Invasive Illnesses Prevented Among Children < 5 Years of Age in the United States

Board 72: Modeling Norovirus Transmission and Strategies for Vaccination in the United States

Board 73: Indirect Cohort Analysis of 10-valent Pneumococcal Conjugate Vaccine Effectiveness Against Vaccine-type and Vaccine-related Invasive Pneumococcal Disease

New Challenges for "Old" Vaccines and Vaccine-Preventable Diseases

Board 74: Seroprevalence to 2011 Swine Variant Influenza A (H3N2v) Among Three Age Groups of US Department of Defense Service Members

Vaccine-Preventable Diseases

Board 75: Seroepidemiology of Diphtheria and Pertussis in Beijing, China: A Cross-sectional Study

Board 76: Sub-optimal Vaccine Effectiveness for the Live Attenuated Influenza Vaccine Among Air Force Children, 2013-14 Season

Board 77: Estimated Tetanus Immunity by Multiplex Bead Assay and Double-antigen ELISA in a National Survey of Women Aged 15-39 Years, Cambodia, 2012

Board 78: Influenza Vaccine Effectiveness During 2010-2014: Maintained Protection Throughout Duration of Influenza Season Among US Department of Defense Beneficiaries

Board 79: Prevalence and Factors Associated with Rotavirus Gastroenteritis Among Hospitalized Children Less Than 5 Years of Age in Enugu Metropolis, Nigeria, 2012

Board 80: A Measles Outbreak in a Middle School with High Coverage of Prior Evidence of Immunity, Beijing

Board 81: Assessing the Cocooning Strategy for Preventing Infant Pertussis—United States, 2011

Board 82: Vaccine Coverage and Adherence to EPI Schedules in Eight Resource Poor Settings in the Malnutrition and Enteric Disease (MAL-ED) Cohort Study

Board 83: Time Trends in Diarrhea Mortality in Mexican Children Under 5 Over Three Decades: Impact of Various Interventions Including Clean Water, Sanitation, and the Rotavirus Vaccine

Board 84: Reminders, Recommendations and Offers for Adult Influenza Vaccination, 2011-2012 Season, United States

Polio Eradication: New Approaches

Board 85: The Effect of Diarrheal Disease on Bivalent Oral Polio Vaccine (bOPV) Seroconversion in Nepali Children

Global Vaccine Initiatives

Board 86: Early Findings from an Evaluation of Influenza Vaccination on Birth Outcomes in Lao PDR, 2014

Board 87: Introducing Seasonal Influenza Vaccine in Low Income Countries: An Adverse Events Following Immunization (AEFI) and Acceptability Survey in Lao People's Democratic Republic

Board 88: Seasonal Influenza Vaccine Recommendation: Northern or Southern Hemisphere Formulation? A Challenge in Adoption for Tropical Bangladesh

Late Breakers I

Board LB-1: Empiric Antibiotic Usage in Mild Respiratory Illness Among Outpatients in Bangladesh: National Hospital-based Influenza Surveillance Findings (2007–2014)

Board LB-2: A Prospective Clinicomicrobiological Study of Tuberculous Meningitis in a Neurocare Centre: An Indian Perspective

Board LB-3: Findings of the Disease-specific Surveillance Program

Board LB-4: Factors Influencing the Duration of Immunity in Poultry Vaccinated Against Highly Pathogenic Avian Influenza H5N1 in the Mekong River Delta of Vietnam, 2008–2010

Board LB-5: Prevalence of Middle East Respiratory Syndrome Coronavirus (MERS-CoV)-like Antibodies in Dromedary Camels in Israel

Board LB-6: Rates of Antimicrobial Resistant Organisms Under Surveillance in Canada: January 1, 2009, to December 31, 2014

Board LB-7: Enhanced Chikungunya Surveillance—Florida, 2014

Board LB-8: Analyzing Influenza Pandemic Preparedness in Nepal: Simulation Modeling and Surveillance Mapping

Board LB-9: Tuberculosis and Cryptococcosis Co-infection: A New Challenge for Global HIV/AIDS and TB Control

Board LB-10: Estimating the MERS-associated Risk of Death in the Republic of Korea, 2015

D. Concurrent Panel Sessions
1:45 PM - 3:15 PM

D1. New Advances to Optimize Antibiotic Stewardship in Healthcare Settings
Centennial Ballroom III

Moderators:

James Hughes; Emory University, Atlanta, GA

Kavita Trivedi; Society for Healthcare Epidemiology of America, Berkeley, CA

Speakers:

Advanced Ideas for Measurement in Antimicrobial Stewardship
Conan MacDougall; University of California, San Francisco, School of Pharmacy, San Francisco, CA

Advancing Diagnostic Testing to Improve Antibiotic Prescribing: What Is on the Horizon?
Romney Humphries; University of California, Los Angeles, Los Angeles, CA

New Solutions to an Old Problem: Making Real Progress in Reducing Unnecessary Antibiotic Use in the Outpatient Setting
Jeffrey Gerber; The Children's Hospital of Philadelphia, Philadelphia, PA

D2. Risky Business: Communicating Infectious Disease Risks
Centennial Ballroom I

Moderators:

Glen Nowak; The University of Georgia, Athens, GA

Dana Pitts; Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Communicating Effectively with Reporters during Breaking Health Crises
Jason Beaubien; National Public Radio, Washington, DC

Reporting on Ebola: Ensuring Accuracy for an Emerging Picture
Elizabeth Cohen; Cable News Network, Turner Broadcasting System, Inc., Atlanta, GA

Ebola: A Tale of Two Outbreaks—Conducting Risk Communications in West Africa and the United States
Dave Daigle; Centers for Disease Control and Prevention, Atlanta, GA

Bridging the Gap: Helping Scientists, Government, and Reporters Find the Story
Jana Telfer; Centers for Disease Control and Prevention, Atlanta, GA

D3. Ebola
Centennial Ballroom II

Moderators:

Ermias Belay
Joel Montgomery
Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Clinical Management and Therapeutic Options for Patients Infected with Ebola Virus
Bruce Ribner; Emory University, Atlanta, GA

Getting to Zero: Shoe Leather Epidemiology in an Ebola Epidemic
Barbara Marston; Centers for Disease Control and Prevention, Atlanta, GA

Ebola Vaccine Studies
Marc-Alain Widdowson, Centers for Disease Control and Prevention, Atlanta, GA

Mohamed Samai; University of Sierra Leone, Freetown, Sierra Leone

D4. Use of Bioinformatics and Big Data in Public Health
International Ballroom South

Moderators:

Chelsea Lane; National Institutes of Health, Bethesda, MD

Duncan MacCannell; Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Bioinformatics in Real-time Pathogen Surveillance
Nicholas Loman; University of Birmingham, Birmingham, United Kingdom

Approaches to Analysing 1000s of Bacterial Isolates
Torsten Seemann; University of Melbourne, Melbourne, Australia

Reconstructing Outbreaks with Genomics: Where Are We Now, Where Are We Going?
Jennifer Gardy; British Columbia Centre for Disease Control, Vancouver, Canada

D5. Monitoring for the Next Pandemic Threat: Updates on Emerging Influenza Viruses
Centennial Ballroom IV

Moderators:

Joseph Bresee; Centers for Disease Control and Prevention, Atlanta, GA

Thomas Gomez; U.S. Department of Agriculture, Animal and Plant Health Inspection Service, Atlanta, GA

Speakers:

From Influenza H7N9 in China to a Global Strategy of Monitoring Emerging Influenza Viruses
Wenqing Zhang; World Health Organization, Geneva, Switzerland

Influenza H5N1 in Egypt—Increasing Risk?
Samir Refaey Abu-Zid; Ministry of Health, Egypt, Cairo, Egypt

Emergence and Spread of Highly Pathogenic Influenza H5Nx Viruses in North America, 2014-2015
Mia Kim Torchetti; US Department of Agriculture, National Veterinary Services Laboratories, Ames, IA

D6. New Vector Control Strategies
International Ballroom North

Moderators:

Seth Irish; Centers for Disease Control and Prevention, Atlanta, GA

Mary Wilson; American Society of Tropical Medicine and Hygiene, San Francisco, CA

Speakers:

Genetic Control of Mosquitos
Luke Alphey; The Pirbright Institute, Surrey, United Kingdom

Less Is More: Advances in the Use of Baits to Control Tsetse Flies and Sleeping Sickness in Africa
Stephen Torr; Liverpool School of Tropical Medicine, Liverpool, United Kingdom

Mass Drug Administrations of Ivermectin for Malaria Transmission Control
Brian Foy; Colorado State University, Fort Collins, CO

Break
3:15 PM – 3:30 PM | Grand Hall

Poster Session with Authors – II
3:30 PM - 4:45 PM | Grand Hall

Director's Tour of Posters
Beth P. Bell
Director, National Center for Emerging and Zoonotic Infectious Diseases

Innovative Strategies to Control and Prevent Healthcare-Associated Infections

Board 89: Increasing the Efficiency and Yield of a Tuberculosis Contact Investigation Through Electronic Data Systems Matching—New York City, 2013

Board 90: A Hand Sanitizer Intervention to Improve Hand-hygiene Behavior in a Tertiary Care Public Hospital in Bangladesh

Board 91: Targeting Intervention for Healthcare-associated Infections in Tennessee: Methods for Identifying and Communicating Facility-specific Impact on Statewide Standardized Infection Ratios

Board 92: MicroRNAs Regulating Tulane Virus Replication in LLCMK2 Cells: New Targets with Therapeutic Potential

Healthcare Worker Safety/Infection Control

Board 93: T-Zone Teaching Moment for Healthcare Workers to Prevent Contraction of Virulent Organisms Using Positive Deviance

Board 94: Incidence of Latent Tuberculosis Infection Among Nursing Students in a Tertiary Care Hospital—Bangladesh, 2011-2013

Board 95: Epidemiological Analysis of Microbiological Results of Intrahospital Infections in General Hospital Veles, 2010-2014

Board 96: Biosafety Cabinets Testing, Calibration, and Certification Problems in the Armenian Ministry of Health Laboratories, 2013

Board 97: Ebola Virus Disease—Gaps in Knowledge and Practices of Health-care Workers in Lagos State, Nigeria, August 2014

Board 98: Barriers to Implementation of Optimal Laboratory Biosafety Practices in Pakistan

Board 99: Serological Monitoring of Leptospirosis Among Laboratory Animals

Tracking and Preventing Healthcare-Associated Infections

Board 100: 124 Acute Care Hospitals and Point-prevalence Survey of Health Care-associated Infections in a Certain Area of East China in 2014

Board 101: Role of Personal Clothing in Transmission of Respiratory Infection Within the Neonatal Intensive Care Unit (NICU)

Board 102: Forty Percent Attack Rate of Multi-strain *Staphylococcus aureus* Skin Infection Among Neonates in an International Private Hospital in Bangkok, July 2013

Board 103: Latent Tuberculosis Infection Among Health Care Workers in Tuberculosis Specialty Hospitals, Bangladesh, 2012-2013: Putting Infection Control Into Context

Board 104: Impact of Monthly Data Quality Checks for Facilities on Surgical Site Infection (SSI) Data

Board 105: Trends in the Incidence of *Clostridium difficile* Infection in Monroe County, New York, from 2010-2014

Board 106: Risk Factors of MDR Gram-negative Bacteremia Among Hospitalized Patients

Detecting Emerging Threats in Healthcare

Board 107: Surveillance for Recent Animal Contact Among Patients with Febrile Illness in Bangladesh Hospitals to Identify Emerging Zoonoses

Board 108: Chikungunya: First Time Identified in Dhaka City, Bangladesh

Board 109: An Outbreak of *Salmonella* Paratyphi A Infection in Shenzhen, China

Board 110: 12 Acute Measles Encephalitis Cases Without Rash

Board 111: Development of a 16-plex PCR Assay Based on the GeXP Principle for the Detection of Diarrhea Pathogens

Board 112: Middle East Respiratory Syndrome and Severe Acute Respiratory Syndrome—an Epidemiological Comparison

Board 113: Novel Technology Combats an Old Foe: WGST Utilized to Investigate the Origin of *Sarocladium kiliense* in a Multi-national Outbreak

Board 114: Human Parvovirus B19 Infections Have Emerged but Given a Back Seat: A Pioneer Work from a Single Centre in India Indicates a High Disease Burden

Board 115: Profile of *Candida* Infections in HIV Seropositive Patients from a Tertiary Care Hospital in New Delhi

Board 116: Japanese Encephalitis Virus Detected in Non-encephalitic Illnesses from West Java

Antimicrobial Use and Resistance

Board 117: *Staphylococcus aureus* Bacteremia and Methicillin Resistance in Two Rural Provinces in Thailand, 2006-2013

Board 118: Lessons Learned from an Annual Kids' Art Competition to Promote Antimicrobial Stewardship

Board 119: Antimicrobial Resistance Among Shigella Isolates from Rural Western Kenya: 2006-2014

Board 120: The Prevalence of MRSA and ESBL Producing *Escherichia coli* and *Klebsiella pneumonia*: Tawam Hospital, 2004-2013

Board 121: Antimicrobial Resistance in *Escherichia coli* O157 Isolates from Humans, United States, 1996-2012

Board 122: Molecular and Clinical Characteristics of Methicillin-resistant *Staphylococcus aureus* Infections in Nine Sentinel Hospitals Across Shenzhen City, China

Board 123: Ciprofloxacin-resistant *Salmonella enterica* ser. Kentucky from Imported Foods

Board 124: Surveillance of Antimicrobial Suceptibility in *Salmonella* in Tawam Hospital

Board 125: A Collaborative Approach to Promote Appropriate Antibiotic Use with Practical Considerations for Sick-child Exclusion Policies in Pennsylvania

Board 126: Antimicrobial Resistance in ICU, Tawam Hospital, Al Ain, UAE

Board 127: Improving Antibiotic Use in Tennessee: The Tennessee Department of Health's Collaborative Approach

Board 128: Detection and Molecular Characterization of Antibiotic Resistant *Staphylococcus aureus* from Milk in the North-West Province, South Africa

Board 129: A Significant Positive Correlation Between Antibiotic Resistance and Biofilm Forming Ability of *Salmonella* Typhimurium

Board 130: Antimicrobial Resistant Non-typhoidal *Salmonella* Among Human and Retail Food Isolates, Tennessee, 2010-2013

Board 131: Use of Carbapenems in an Intensive Care Unit and the Effect of Educational Intervention in Rationalizing Its Use at a Tertiary Hospital

Board 132: Detection of Genes Codifying for Metallo-beta-lactamase Among Imipenem Resistant *Pseudomonas aeruginosa* Isolated in Egypt

Board 133: A Novel Class of Chikungunya Virus Inhibitors Targets the Enzymatic Activity of the Viral Capping Enzyme NsP1

Board 134: Battling Antimicrobial Resistance: Antimicrobial Resistance Surveillance in the DoD Global Emerging Infections Surveillance and Response System (GEIS) Partner Network

Board 135: Comparative Study of the Antiviral Activity of Broad-spectrum and Enterovirus-specific Inhibitors Against Clinical Isolates of Enterovirus-D68

Board 136: When "Germs Don't Get Killed and They Attack Again and Again": Knowledge and Attitudes About Antibiotic Resistance Among Laypersons and Health Care Providers in Karachi, Pakistan

Board 137: Shared Antibiotic Stewardship and "One Health" Surveillance for Antibiotic Resistance: The Washington State Experience

Board 138: Improved Malaria SYBR Green I-based Fluorescence Assay Detection Limit in Field Samples with Varied Parasitemia and Hematocrit

Board 139: Temporal Trends in Prevalence of *Plasmodium falciparum* Molecular Markers Selected for by Artemether-lumefantrine Treatment in Pre-ACT and Post-ACT Parasites in Western Kenya

Board 140: Antimicrobial Resistance of Treated Wool Samples with Madder

Blood, Organ, and Other Tissue Safety

Board 141: *Babesia* Sero-epidemiology in Australian Blood Donors

Board 142: Emergence of Australian WNV_{KUN} Strains: What Does This Mean for Blood Safety?

Board 143: Blood Transfusion Safety Among Blood Donors and Recipients in Minna—North-Central Nigeria, 2014

Risk Assessment

Board 144: Ultrasonography-assisted Liposuction for an HIV Patient with Severe Respiratory Failure and Associated Cervical Lipohypertrophy

Board 145: The Assessment for Severe Fever with Thrombocytopenia Syndrome Surveillance in Hubei Province, China

Board 146: Pertussis Infection in US Pregnant Women, 2012-2014

Board 147: Clinical Case Definitions for Influenza-associated Outpatient Consultations in Rural North India

Board 148: *Mycobacterium bovis* Bacillus Calmette-Guérin (BCG) Osteomyelitis of the Fibular After Intravesical BCG Therapy for Bladder Cancer

Board 149: Relevance of Morbidity Markers in Community Diagnosis of Urinary Schistosomiasis in a Resource Constrained Environment, Nigeria, 2012

Board 150: Prevalence of Influenza Viruses in Asymptomatic Persons

Board 151: Case Definitions Used in Severe Respiratory Disease Surveillance. What Do They Mean? An Evaluation of Data from Western Kenya

Board 152: Increase in Vibriosis in New York State: How Can We Improve Surveillance and Outbreak Identification?

Board 153: Aetiology of Acute Febrile Illness (AFI) Cases in a Primary Care Hospital in the Western Ghat Region of India

Board 154: Study of Adverse Drug Reactions and Treatment Outcome in MDR-TB Patients Registered at DOTS-PLUS Site, in a Tertiary Care Teaching Hospital, Gujarat, India

Board 155: Factors Associated with Tuberculosis Treatment Outcomes in Bangladesh—Results from 2012 National Surveillance Data

Foodborne and Waterborne Infections

Board 156: Evidence for Non-foodborne Transmission in Some Cases of Neonatal Listeriosis

Board 157: Exposure Routes in Vibriosis in the United States, 1988-2013

Board 158: Increase of *Vibrio alginolyticus* in the United States, 1988-2012

Board 159: Incidence of Norovirus Among Kaiser Permanente Member Populations in the United States, 2012-2013

Board 160: Outbreaks Attributed to Fish—United States, 1998-2012

Board 161: Changes in Overall Incidence of Foodborne Illness in the United States, by Age Group, Foodborne Diseases Active Surveillance Network (FoodNet), 1996-2013

Board 162: Does the Distribution of *Campylobacter* Species in the United States Differ by Geographic Region?

Board 163: Phenotypic and Genotypic Characteristics of Clinical Enterotoxigenic *Escherichia coli* (ETEC) Isolates in Southern Coastal Region of China

Board 164: Are All Pediatric HUS Cases the Same? A Comparison of Cases in Patients Less Than 5 Years and 5-18 Years Old, Foodborne Diseases Active Surveillance Network, 1997-2013

Board 165: Giardiasis Outbreaks in the United States, 1971-2011

Board 166: The Seasonality and Climatic Drivers of Cryptosporidiosis

Board 167: Geographical Variation in Listeriosis Incidence, United States, 2001-2012

Board 168: Assessment of Food Safety Regulations for Norovirus Prevention: A State by State Analysis

Board 169: Investigation of Trichinosis Outbreak in Ngao District, Lampang Province, August 2014

Board 170: Pathogen-specific Causes of Diarrhea Among Hospitalized Children in Cairo, Egypt

Board 171: Timeliness and Data Quality of the Web Based Enteric Illness Surveillance (WBEIS) in Bangladesh

Board 172: Foodborne Illness Outbreak at Intermediate School in North West Province, South Africa, October 2014

Board 173: Burden of Diarrheal and Bacterial Foodborne Diseases in Thailand
Withdrawn at Author's Request

Board 174: US Foodborne Outbreaks of Cyclosporiasis During 2000-2014

Board 175: Differences Among Types of Restaurant Settings Associated with Foodborne Disease Outbreaks, 2009-2013
Withdrawn at Author's Request

Board 176: Towards the Development of Potent and Selective Antiviral Therapy for Norovirus-induced Gastroenteritis

Board 177: The Burden and Impact of Acute Gastroenteritis and Foodborne Diseases in the Caribbean

Board 178: Foodborne Diseases in the Caribbean, 2005-2014: Changing Epidemiology and Implications for Prevention and Control

Keynote Session

5:00 PM - 7:30 PM | Centennial Ballroom

Moderator:

Rima Khabbaz
Deputy Director for Infectious Diseases
Director, Office of Infectious Diseases
Centers for Disease Control and Prevention, Atlanta, Georgia

Speakers:

Welcome and Opening Remarks
Rima Khabbaz

Thomas Frieden
Director, Centers for Disease Control and Prevention, and Administrator, Agency for Toxic Substances and Disease Registry, Atlanta, Georgia

The 2014-2015 West Africa Ebola Outbreak
Joanne Liu
International President, Médecins Sans Frontières
Geneva, Switzerland

Inconvenient Truths, Social Networks, and the War Against Antibiotic Resistance
Robert A. Weinstein
Professor of Medicine, Rush University Medical College
Former Chairman, Department of Medicine, Cook County Health and Hospitals System
Chicago, Illinois

The Global Health Security Agenda
Thomas Frieden

Opening Reception

7:30 PM - 9:30 PM | Grand Hall

Tuesday, August 25

Poster Set-up for the Day
7:00 AM – 8:00 AM

All posters presented on Tuesday will be available for viewing in the Grand Hall from 10:10 AM to 6:15 PM. Authors will be present at posters for one hour and fifteen minutes as noted under the Scientific Sessions schedule for the day.

Scientific Sessions

E. Concurrent Plenary Sessions
8:00 AM - 9:00 AM

E1. Reemergence of Vaccine-Preventable Diseases
Centennial Ballroom I

Moderator:
Cynthia Whitney; Centers for Disease Control and Prevention, Atlanta, GA

Speaker:
Reemergence of Vaccine-preventable Diseases
Walter Orenstein; Emory University, Atlanta, GA

E2. Ebola
Centennial Ballroom II

Moderator:
Ermias Belay; Centers for Disease Control and Prevention, Atlanta, GA

Speaker:
The West African Ebola Response: Insights from a CDC Perspective
Inger Damon; Centers for Disease Control and Prevention, Atlanta, GA

E3. Dengue
Centennial Ballroom III

Moderator:
Harold Margolis; Centers for Disease Control and Prevention, San Juan, Puerto Rico

Speaker:
Dengue Update: Advances and Challenges
Kathryn Anderson; University of Minnesota, Minneapolis, MN

E4. Increasing Understanding of the Microbiome
Centennial Ballroom IV

Moderator:
David White; U.S. Food and Drug Administration, White Oak, MD

Speaker:
The Human Microbiome: An Emerging Opportunity for Enteric (and Other) Diseases
Phillip Tarr; Washington University School of Medicine, St. Louis, MO

F. Concurrent Plenary Sessions
9:10 AM - 10:10 AM

F1. Global Trade and Emerging Infectious Diseases
Centennial Ballroom I

Moderator:
Alex Thiermann; World Organisation for Animal Health, Paris, France

Speaker:
Global Trade and Emerging Infectious Diseases: Science-Based Solutions for a Changing World
Brian Evans; World Organisation for Animal Health, Paris, France

F2. Influenza
Centennial Ballroom II

Moderator:
Joseph Bresee; Centers for Disease Control and Prevention, Atlanta, GA

In Flew Enza: Surveillance and Control for an Unpredictable Virus
Nancy Cox; Centers for Disease Control and Prevention, Atlanta, GA

F3. The Global Health Security Agenda
Centennial Ballroom III

Moderator:
Kashef Ijaz; Centers for Disease Control and Prevention, Atlanta, GA

Speakers:
The Global Health Security Agenda and the West Africa Ebola Epidemic
Jordan Tappero; Centers for Disease Control and Prevention, Atlanta, GA

The Global Health Security Agenda Implementation and International Health Regulations Compliance
Petri Ruutu; National Institute for Health and Welfare, Helsinki, Finland

F4. Use of Bioinformatics and Big Data in Public Health
Centennial Ballroom IV

Moderator:
Andrew Pavia; University of Utah, Salt Lake City, UT

Speaker:
Pathogen Genomics at the National Center for Biotechnology Information
David Lipman; National Institutes of Health, Bethesda, MD

Break
10:10 AM – 10:30 AM | Grand Hall

G. Concurrent Panel Sessions
10:30 AM - 12:00 PM

G1. Integrating Public Health and Infectious Disease Clinicians
International Ballroom South

Moderators:
James Hughes; Emory University, Atlanta, GA

Scott Santibanez; Centers for Disease Control and Prevention, Atlanta, GA

Speakers:
The Power of Provider Reporting to Protect the Public's Health
Marci Layton; New York City Department of Health and Mental Hygiene, New York, NY

The Emerging Infections Network: Bridging the Gap between Clinical Medicine and Public Health
Philip Polgreen; University of Iowa, Iowa City, IA

Experience with Ebola, TB, Measles and Other Public Health Issues: Collaboration of Infectious Disease Specialty and Public Health
Thomas File; Summa Health System, Akron, OH

Experience of the IDSA Rapid Communications Network
Marguerite Neill; Brown University, Providence, RI

G2. Emerging Fungal Diseases
International Ballroom North

Moderators:
Tom Chiller; Centers for Disease Control and Prevention, Atlanta, GA

David White; US Food and Drug Administration, White Oak, MD

Speakers:
Biologic Therapy: A Growing Population of Persons Susceptible to Fungal Infections
Kevin Winthrop; Oregon Health and Science University, Portland, OR

Valley Fever, Coming to a State Near You: Expanding Geographic Distribution of Coccidioidomycosis
David Engelthaler; Translational Genomics Research Institute, Flagstaff, AZ

Emerging Azole Resistance in Aspergillus: From Pesticide to Bedside
Paul E. Verweij; Radboud University Nijmegen Medical Center, Nijmegen, Netherlands

G3. Emerging Tick-Borne Diseases
Centennial Ballroom II

Moderators:
Christopher Paddock; Centers for Disease Control and Prevention, Atlanta, GA

Danielle Stanek; National Association of State Public Health Veterinarians, Tallahassee, FL

Speakers:
The Increasing Recognition of Tick-borne Rickettsioses on the African Continent
Phillipe Parola; Aix-Marseille University, Marseille, France

Recognition of Novel *Ehrlichia* and *Borrelia* spp. Infections of Humans in the Upper Midwestern United States
Bobbi Pritt; Mayo Clinic, Rochester, MN

Increasing Awareness of Lyme Carditis as a Cause of Sudden Cardiac Death
Paul Mead; Centers for Disease Control and Prevention, Fort Collins, CO

Clinical and Epidemiological Aspects of Heartland Virus Infection in the United States
Erin Staples; Centers for Disease Control and Prevention, Fort Collins, CO

G4. Culture-Independent Diagnostics and Their Impact on Public Health Functions
Centennial Ballroom III

Moderators:
Jacqueline Lawler; National Association of County and City Health Officials, Newburg, NY

Michael Shaw; Centers for Disease Control and Prevention, Atlanta, GA

Speakers:
Culture-independent Diagnostic Tests: Challenges and Opportunities
John Besser; Centers for Disease Control and Prevention, Atlanta, GA

The Changing Diagnostic Microbiology Landscape
Angela Caliendo; Brown University, Providence, RI

Culture-independent Diagnostic Tests: A Global Public Health Perspective
Martyn Kirk; The Australian National University, Canberra, Australia

Pathogen Characterization in a Post-isolate World
Duncan MacCannell; Centers for Disease Control and Prevention, Atlanta, GA

G5. Global Issues Concerning Vaccine-Preventable Diseases

Centennial Ballroom IV

Moderators:

Bonnie Maldonado; American Academy of Pediatrics, Stanford, California

Cynthia Whitney; Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Future Directions for Global Health Vaccine Discovery
Chris Wilson; Bill & Melinda Gates Foundation, Seattle, WA

Impact and Challenges of New Vaccine Introduction in Developing Settings
Thomas Cherian; World Health Organization, Geneva, Switzerland

Vaccine Hesitancy: An Emerging Obstacle to Global Immunization
Saad Omer; Emory University, Atlanta, GA

G6. Global Water and Sanitation Challenges and Opportunities

Centennial Ballroom I

Moderators:

Michael Beach
Rick Gelting
Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Unknown Knowns: Measuring Sanitation's Health Impacts
Joe Brown; Georgia Institute of Technology, Atlanta, GA

Ebola, Engineering and the Environment: New Approaches to Tackling Emerging Challenges of Disease Transmission
Huw Taylor; University of Brighton, Brighton, United Kingdom

Understanding Pathogen Transport and Contamination via Droplets Using Fluid Dynamics
Lydia Bourouiba; Massachusetts Institute of Technology, Cambridge, MA

Lunch

12:00 PM – 12:30 PM | On your own

Poster Session with Authors – III

12:30 PM - 1:45 PM | Grand Hall

Director's Tour of Posters

Rima Khabbaz
Deputy Director for Infectious Diseases
Director, Office of Infectious Diseases

Effective and Sustainable Surveillance Platforms

Board 179: Tuberculosis Case Finding Using Population Based Disease Surveillance Platforms in Kenya

Board 180: Surveillance for Avian Influenza Viruses in Live Bird Markets, Bangkok, Thailand, 2013

Board 181: Annual Deaths from Selected Waterborne Pathogens in the United States

Board 182: Reassessing the Global Capacity for Timely Detection and Reporting of Emerging Infectious Diseases

Board 183: Validation of an Estimating Procedure as an Alternative Method for Lyme Disease Surveillance

Board 184: Enhanced Surveillance for Novel H7 Avian Influenza Virus Among Poultry in Dhaka City Live Poultry Markets, 2013-14

Board 185: The Influenza Electronic Surveillance System in Kazakhstan

Board 186: Laboratory-based Sentinel Surveillance for Bacterial Etiologies of Acute Infectious Diarrheal Disease in Southern Coastal Region of China, 2007-2013

Board 187: Hospitalization Surveillance for Severe Acute Respiratory Infection in Vietnam, 2011-2013

Board 188: Active Surveillance for Oseltamivir Resistance Among Influenza Viruses, Northern Vietnam, 2009-2013

Board 189: Estimated Numbers of Community Cases of Non-typhoidal *Salmonella* Infections in Guangdong Province, China

Board 190: Timeliness of Oman Communicable Diseases Surveillance System

Board 191: The Potential Impact of Changing Diagnostics on Surveillance for Invasive Bacterial Infections: Emerging Infections Program's Active Bacterial Core Surveillance (2014)

Board 192: The NCBI Pathogen Pipeline: Supporting Surveillance of Bacterial Foodborne Pathogens with a Whole Genome Sequencing Analysis Pipeline to Deliver Real Time Results

Board 193: Hospital-based Severe Acute Respiratory Infection (SARI) Surveillance System in Indonesia, 2013-2014

Board 194: Population-based Rates of Diarrheal Disease Associated with Norovirus, Sapovirus, and Astrovirus in Kenya

Board 195: Coccidioidomycosis: A Possibly Underreported Cause of Death—Arizona, 2008-2013

Board 196: Annual Burden of Acute Infectious Diseases in Ambulatory Care Settings—United States, 2006-2010

Board 197: Global Health Benefits from Investments in Robust Surveillance Systems

Board 198: Ability of the National Influenza Surveillance, Bangladesh (NISB) to Inform Influenza Response in Bangladesh

Board 199: Enhancing Surveillance of Emerging Infectious Diseases Using Mobile Data Collection and Open Data Kit (ODK) Technology: A Cross-sectional Study of Febrile Patients in Kilombero, Tanzania

Board 200: Understanding Lyme Disease Surveillance: Burden, Alternative Approaches, and Degree of Misclassification

Board 201: Flu News Europe—A Joint Collaboration of Influenza Surveillance in the European Region

Board 202: Suite for Automated Global Electronic BioSurveillance (SAGES) Update: Re-engineering Software to Improve Ease of Installation, Use, and Sustainability

Board 203: Multiagency and Multidisciplinary Collaboration for Improved Integrated Real-time Whole Genome Sequence Surveillance of Foodborne Pathogens in the United States

Board 204: Surveillance: Nontuberculous Mycobacteria Isolations from Residents of Three Counties, North Carolina, 2006 - 2010

Board 205: Two Year Findings from an Acute Febrile Illness Enhanced Surveillance Study in Puerto Rico

Board 206: Serological and Vector Surveillance Studies to Reported Rift Valley Fever Free Status in South Korea

Board 207: Evaluation of the National Case-based Measles Surveillance in South Africa, January 2009 to December 2013

Board 208: Estimating the Burden of Foodborne Illness for *Campylobacter*, *Salmonella* and *Vibrio parahaemolyticus* in Japan from Laboratory Confirmed Numbers of Infections and Data from Telephone Surveys

Board 209: Biosurveillance Ecosystem—A Sustainable, User-friendly System That Meets the Needs of Global Biosurveillance Stakeholders, Analysts, and Decision Makers Alike

Board 210: Influenza Sentinel Surveillance in Ukraine and Characteristics of Isolates During the 2014-2015 Season

Board 211: Influenza in District Hospital Patients in Bangladesh: Results from National Influenza Surveillance

Board 212: Development and Piloting of *Enterobiasis vermicularis* Surveillance System in Sri Lanka

Board 213: Surveillance for Severe Disseminated Disease Among Reported Coccidioidomycosis Cases, Arizona, 2009 - 2013

Novel Surveillance Systems

Board 214: Variation by Age Group in Exposures Associated with *Salmonella* Serotype Enteritidis Infection—Foodborne Diseases Active Surveillance Network, United States, 2014

Board 215: Early Indicators of Dengue Based on Date Post Onset of Fever Among Children and Adults in Puerto Rico

Board 216: Enhanced Surveillance for Severe Group A Streptococcal Infections in Three Active Bacterial Core Surveillance Sites, 2010

Board 217: Rabies Response: A Novel Approach to Animal Bite Surveillance in Georgia

Board 218: Medical Examiner Investigated Norovirus Deaths, Minnesota, 2006-2014

Board 219: Linking HIV Diagnostic Testing Algorithm Electronic Laboratory Reports by Local Codes in the New York State Surveillance System

Board 220: Claims Data Evaluation for Lyme Disease Surveillance—Tennessee, 2011-2013

Board 221: Lyme Disease Surveillance Using Sampling Estimation: Evaluation of an Alternative Methodology in New York State

Board 222: Developing a Surveillance Definition for Binational Tuberculosis Cases

Board 223: Epidemiology of Carbapenem-resistant *Acinetobacter baumannii* Identified Through the Emerging Infections Program, 2012-2013

Board 224: Fatal Cases of *Listeria monocytogenes* Infection Among Pregnancies and Children in Phuket, November 2013 *Withdrawn at Author's Request*

Board 225: *Coccidioides immitis*: Developing a One Health Approach for Surveillance of a Newly Emerging Fungal Pathogen in Washington State

Board 226: Optimal Surveillance Network Design: A Value of Information Model

Board 227: Integrating Area Profile and Environmental Surveillance in Monitoring the Risk of Arboviral Disease Transmission in Harris County

Board 228: Enhanced Testing of Norovirus-negative Gastroenteritis Outbreaks

Board 229: Using Multiple Data Sources to Monitor Influenza Epidemics

Board 230: Participatory Surveillance: The Influenza Experience

Board 231: *Coccidioides immitis*: Developing a One Health Approach for Surveillance of a Newly Emerging Fungal Pathogen in Washington State

Board 232: Genetic Heterogeneity of *Listeria monocytogenes* in Northern Italy

Board 233: Real Time Surveillance of Influenza Using Wireless Reporting of RIDT Results

Board 234: Crowdsource Reporting of Infectious Diseases

Early Warning Systems

Board 235: A Girl Infected with *Salmonella* Typhimurium Due to Pet Turtle Contact in Guangdong, China

Board 236: A Review of Dengue Deaths in 2013 in Vientiane Capital and Champasack Province of Lao PDR

Board 237: National Dengue Surveillance in the Lao PDR, 2006-2012: Epidemiological and Laboratory Findings

Board 238: NoroSTAT: Enhanced Norovirus Outbreak Surveillance Network

Board 239: Evaluation of Enhanced Surveillance Strategies for World Pride Celebration in Toronto, Canada

Board 240: Hantavirus Fever Without Pulmonary Syndrome in Panama

Board 241: An Evaluation of the Pacific Outbreak Early Warning Detection System—The Pacific Syndromic Surveillance System

Board 242: Use of Surveillance Data to Estimate Seasonal Influenza Thresholds in Canada

Board 243: Ebola Response in the District of Columbia: Early Warning Surveillance in the United States Capital

Board 244: Sporadic Norovirus Surveillance and Outbreak Trends, Tennessee, 2012-2014

Board 245: Rabies Surveillance Evaluation in an Area Without Human Cases in Brazil

Improving Preparedness for Infectious Disease Emergencies

Board 246: Utility of Established Severe Acute Respiratory Illness Surveillance in the Early Identification of EV-D68 in Minnesota

Board 247: Risk Assessment and Mitigation Strategies Associated with Testing Persons Under Investigation for Ebola Virus Disease

Board 248: Surveillance of ILI/SARI in Republic of Djibouti for Pandemic Influenza Preparedness

Board 249: A North/South Collaboration Between Two National Public Health Institutes: A Model for Global Health Protection

Board 250: Rapidly Detecting and Containing Ebola Virus Disease When Introduced Into a Previously Unaffected Country, 2014

Board 251: Training and Capacity Building Initiatives in Support of the Global Health Security Agenda, 2012-2014

Board 252: Surveillance of Prion Diseases in São Paulo State—A Pioneer Experience in Brazil

Board 253: Association of Public Health Laboratories: Partnering in the 2014 Ebola Outbreak Response

Board 254: Ranking Infectious Disease Risks to Support Public Health Prioritization in the European Union

Board 255: Ebola Virus Disease Outbreak Management System for Case Management, Contact Tracing, and Symptom Monitoring in Tennessee

Board 256: A Multi-site Knowledge, Attitude and Practice Survey of Ebola Virus Disease in Nigeria

Board 257: Public Knowledge, Perception and Source of Information on Ebola Virus Disease—Lagos, Nigeria; September, 2014

Board 258: Chikungunya in Georgia: Preventing Local Transmission Through Rapid Response, 2014

Board 259: Perception, Attitude and Acceptability of Ebola Virus Screening Among Travelers at the Murtala Muhammed International Airport, Lagos, Nigeria

Board 260: Stuck at Home During a Public Health Emergency? There's an App for That!

Board 261: Local Health Department Measles Outbreak Response: Use of the Public Health Incident Command System

Board 262: Evaluating Mass Influenza Vaccination Clinics in Puerto Rico, 2013-2014

Board 263: Building Multi-agency Response Capacity to Emergent or Bioterrorism-related Zoonotic Disease Outbreaks in Georgia

Board 264: Ebola Virus Networks in the News: Transmission Dynamics in the West African Outbreak

Lessons Learned from Recent Flu Preparedness Activities and Flu Season

Board 265: Risk Investigation of Multiple Avian Influenza Viruses Based on Seroprevalence in Occupational Exposure Populations in China

Board 266: Burden of Influenza-associated Deaths in the Americas, 2002-2008

Board 267: Characterizing Influenza Cases in China's First Sentinel Severe Acute Respiratory Infection (SARI) Surveillance System, February 2011 – June 2014

Board 268: Epidemiology of Childhood Influenza Illness in the Post-pandemic Period in Bangladesh: 2010-2014

Board 269: Comparison of the Seasonality of Influenza A and B in Thailand, 2009-2014

Board 270: Lessons Learned During the Influenza Pandemic of 2009-2010 in Kazakhstan

Board 271: Epidemiologic, Virologic and Clinical Characteristics of Adenovirus-associated Respiratory Illness at Five US Military Hospitals, 2009-2014

Board 272: Comparison of the Fall 2013 and Spring 2014 Waves of the Avian Influenza A(H7N9) Outbreak of Human Infections in China

Board 273: Effectiveness of Using Standard Case Definitions for Influenza-like Illness in the Republic of Kazakhstan During the Epidemic Seasons of 2010-2011 and 2012-2013

Board 274: Use of Rapid Influenza Diagnostic Tests: Impact on Treatment and Health Outcomes of Hospitalized Influenza Cases

Board 275: Human Infection with a Novel, Highly Pathogenic Avian Influenza A (H5N6) Virus: Virological, Pathological and Clinical Findings

Board 276: Dynamic Re-assortment of Novel Influenza A (H7N9) with Circulating Influenza Viruses in Guangdong, China, 2013-2014

Board 277: Significance of Phenotypic and Genotypic Characteristics of Influenza Viruses Identified in the Republic of Moldova

Board 278: Application of the World Health Organization (WHO) Case Definition for Suspect Influenza A(H5N1) Case Detection in the Primary Health Setting, Indonesia: Big Effort, Low Yield

Board 279: Establishing the Sentinel Surveillance System for Severe Acute Respiratory Infections in Lebanon, 2014: Better Understanding the Epidemiology of Influenza

Board 280: Has H7N9 Spread Beyond China? An Assessment Based on Lessons Learned from H5N1

Board 281: Severe Acute Respiratory Infections in Border Populations in Southern Arizona, 2010-2014

Board 282: Measured Voluntary Avoidance Behavior During the 2009 A/H1N1 Epidemic

Board 283: Triple Combination Antiviral Drug Therapy Against H3N2 Variant Influenza Virus

Board 284: Influenza Surveillance Networks and Response to Seasonal Influenza in Brazil, 2013

Board 285: Laboratory Control of Influenza in the Republic of Armenia, 2009-2014

Board 286: Flu on Call: Improving Access to Antivirals during a Severe Pandemic

Board 287: Global Mortality Impact of the 1957-1959 Influenza Pandemic

Board 288: Influenza Surveillance Networks and Response to Seasonal Influenza in Brazil, 2013 and 2014, Advances and Challenges

H. Concurrent Panel Sessions

1:45 PM - 3:15 PM

H1. New Challenges in the Prevention of Healthcare-Associated Infections

Centennial Ballroom I

Moderators:

Clifford McDonald; Centers for Disease Control and Prevention, Atlanta, GA

Jacie Volkman; Association for Professionals in Infection Control and Epidemiology, Asheville, NC

Speakers:

Actionable Data for US Hospitals: How Widespread HAI Reporting Empowers Public Health Action at the Hospital Level
Denise Cardo; Centers for Disease Control and Prevention, Atlanta, GA

Reassessing Attributable Mortality with Multidrug-resistant Gram Negatives, MRSA, and *Clostridium difficile* Infection
Richard Nelson; University of Utah School of Medicine, Salt Lake City, UT

Determining Appropriate Use of Chlorhexidine to Reduce Healthcare-associated Infections Across the Healthcare Delivery Spectrum
Thomas Talbot; Vanderbilt University Medical Center, Nashville, TN

H2. Infectious Diseases in Humanitarian (Disaster) Settings

International Ballroom South

Moderators:

Mark Anderson
Clive Brown
Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Vaccination in Crisis: Minimizing the Muddle Through
Rebecca Freeman Grais; MSF Epicentre, Paris, France

Monitoring and Managing Acute Infectious Disease Outbreaks in the World's Largest Refugee Camp: Dadaab, Kenya
Nina Marano; CDC Kenya, Nairobi, Kenya

Things Fall Apart: Managing Endemic Infectious Diseases in the Wake of the Ebola Outbreak in Port Loko District, Sierra Leone
Leo Liu; Lawrence General Hospital, Lawrence, MA

H3. Emerging Mosquito-Borne Diseases

Centennial Ballroom II

Moderators:

Danielle Stanek; National Association of State Public Health Veterinarians, Tallahassee, FL

Mary Wilson; American Society of Tropical Medicine and Hygiene, San Francisco, CA

Speakers:

Chikungunya: Here Today, Where Tomorrow?
Scott Weaver; University of Texas Medical Branch, Galveston, TX

Progress on Vaccine Programs to Prevent Infection with Japanese Encephalitis
Susan Hills; Centers for Disease Control and Prevention, Fort Collins, CO

Changes in Malaria Epidemiology in the Americas and Their Implications for Elimination/Pre-elimination Settings
Reyaud Rahman; Ministry of Public Health Guyana, Georgetown, Guyana

H4. The Ethics of Research During Infectious Disease Epidemics

Centennial Ballroom III

Moderators:

Marta Gwinn
Taraz Samandari
Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Ethical Considerations in the Conduct of Research During Public Health Emergencies
Oliver Morgan; Centers for Disease Control and Prevention, Atlanta, GA

Clinical Trials, Ancillary Care, and Research Ethics
Andrew Vernon; Centers for Disease Control and Prevention, Atlanta, GA

Application of Ethics for Public Health Research
Kata Chillag; Presidential Commission for the Study of Bioethical Issues, Washington, DC

H5. Emerging Issues in Foodborne Diseases

Centennial Ballroom IV

Moderators:

Harry Chen; Vermont Department of Health, Burlington, VT

Robert Tauxe; Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Everything in Sequence: Listeriosis Investigations in the Era of Whole Genome Sequencing
Brendan Jackson; Centers for Disease Control and Prevention, Atlanta, GA

Novel Transmission Dynamics of *Salmonella* and Contamination of Ground Beef
Guy Loneragan; Texas Tech University, Lubbock, TX

Development of a Molecular Surveillance System for Foodborne Diseases in the European Union
Johanna Takkinen; European Centre for Disease Prevention and Control, Stockholm, Sweden

H6. Rabies
International Ballroom North

Moderators:

Jeffrey Bender; Association of American Veterinary Medical Colleges, St. Paul, MN

Christine Hoang; American Veterinary Medical Association, Schaumburg, IL

Speakers:

Global Efforts to Prevent and Eliminate Rabies
Thomas Mueller; Friedrich-Loeffler-Institut, Greifswald-Insel Riems, Germany

Update on Rabies Elimination in the Americas
Marco Vigilato; Pan American Health Organization, Lima, Peru

Advances in Understanding Rabies Pathogenesis and Treatment
Alan Jackson; University of Manitoba, Winnipeg, Canada

Break
3:15 PM – 3:30 PM | Grand Hall

I. Oral Presentations
3:30 PM - 5:00 PM

I1. Vector-Borne Diseases
Centennial Ballroom I

Moderators:

Patrick Kachur
Centers for Disease Control and Prevention, Atlanta, GA

Harold Margolis
Centers for Disease Control and Prevention, San Juan, Puerto Rico

3:30 PM - 3:45 PM

Jamestown Canyon Virus as an Emerging Cause of Human Disease in Minnesota
E. Schiffman; Minnesota Department of Health, St. Paul, MN

3:45 PM - 4:00 PM

Unveiling the Burden of Dengue and Dengue-like Illnesses Through Enhanced Fatal Case Surveillance in Puerto Rico
T. M. Sharp; Centers for Disease Control and Prevention, San Juan, PR

4:00 PM - 4:15 PM

Climate Change and Chikungunya Transmission in Europe: A Preparedness Priority in Europe
J. E. Suk; European Centre for Disease Prevention and Control, Stockholm, Sweden

4:15 PM - 4:30 PM

Clinicopathologic Characteristics and Immunolocalization of Viral Antigens in Chikungunya-associated Fatal Cases—Puerto Rico, 2014
R. S. Levine; Centers for Disease Control and Prevention, Atlanta, GA

4:30 PM - 4:45 PM

Outbreak of Phlebovirus Infection in Lombardia, a Northern Italy Region, in Summer 2013
E. Percivalle; Fondazione IRCCS Policlinico San Matteo, Pavia, Italy

4:45 PM - 5:00 PM

The Factors Contributing to Seven Hundred Percent Increase in Malaria Incidence in Thailand-Lao PDR-Cambodia Border Province, Ubonratchathani Province, Thailand, 2014
A. Sathawornwiwat; Field Epidemiology Training Program, Nonthaburi, Thailand

I2. Vaccine-Preventable Diseases
International Ballroom North

Moderators:

Stephen Hadler
Andrew Kroger
Centers for Disease Control and Prevention, Atlanta, GA

3:30 PM - 3:45 PM

Efficacy of Inactivated Trivalent Influenza Vaccine Among Children in Rural India: A Three-year Randomized Controlled Trial
W. Sullender; University of Colorado Denver, Denver, CO

3:45 PM - 4:00 PM

Reduction in HPV Precursor Incidence in Connecticut Between 2008 and 2013
J. Hadler; Yale School of Public Health, New Haven, CT

4:00 PM - 4:15 PM

Varicella Seroprevalence of Beijing Residents in 2012
L. Suo; Beijing Center for Disease Prevention and Control, Beijing, China

4:15 PM - 4:30 PM

Clinical Characteristics of Vaccinated and Unvaccinated Pertussis Cases—United States, 2010-2012
L. A. McNamara; Centers for Disease Control and Prevention, Atlanta, GA

4:30 PM - 4:45 PM

Epidemiology of Bacterial Meningitis Among Bangladeshi Children <5 Years, 2005-2013
S. Saha; Child Health Research Foundation, Dhaka, Bangladesh

4:45 PM - 5:00 PM

Adult Measles Outbreaks Associated with Endemic H1 and Imported D8 Measles Viruses in Beijing, China
Y. Zhang; National Institute for Viral Disease Control and Prevention, Beijing, China

I3. Surveillance I

International Ballroom South

Moderators:

Fred Angulo
Lori Armstrong
Centers for Disease Control and Prevention, Atlanta, GA

3:30 PM - 3:45 PM

Ebola Knowledge, Attitudes, and Practices Among Community Members in Three Low-incidence Counties: Liberia, September 2014
K. D. Beer; Centers for Disease Control and Prevention, Atlanta, GA

3:45 PM - 4:00 PM

Centralizing and Mapping Surveillance Data During the 2014 West African Ebola Virus Disease Outbreak
E. L. Cohn; Boston Children's Hospital, Boston, MA

4:00 PM - 4:15 PM

The Georgia Ebola Active Monitoring System for Travelers from Ebola-affected Countries—2014-2015
L. Edison; Centers for Disease Control and Prevention, Atlanta, GA

4:15 PM - 4:30 PM

USAID-EPT-PREDICT—A New Approach to Preventing Pandemics and Targeting Control by Detecting Potentially Zoonotic Pathogens Before They Spill over from Wildlife
P. Daszak; EcoHealth Alliance, New York, NY

4:30 PM - 4:45 PM

An Evaluation of Psychological Distress and Social Support of Survivors and Contacts of Ebola Virus Disease Infection and Their Relatives in Lagos, Nigeria—2014
A. Mohammed; Federal Neuro-psychiatric Hospital Kaduna, Kaduna, Nigeria

4:45 PM - 5:00 PM

Seasonal Influenza Forecasting in Military Populations
A. L. Buczak; Johns Hopkins University Applied Physics Laboratory, Laurel, MD

I4. Antimicrobial Resistance

Centennial Ballroom II

Moderators:

Brandi Limbago
J. Todd Weber
Centers for Disease Control and Prevention, Atlanta, GA

3:30 PM - 3:45 PM

The Impact of an Educational Intervention Among Drug Sellers in Pharmacies on Antibiotic Dispensing Practices for Acute Respiratory Illness, a Pilot Study in Dhaka City, Bangladesh
K. Sturm-Ramirez; Centers for Disease Control and Prevention, Atlanta, GA, and International Centre for Diarrhoeal Diseases Research, Bangladesh (ICDDR,B), Dhaka, Bangladesh

3:45 PM - 4:00 PM

Development of an Electronic Bidirectional Public Health Information Exchange to Control Extensively Drug-resistant Organisms (XDROs)
W. E. Trick; Cook County Health and Hospitals System, Chicago, IL

4:00 PM - 4:15 PM

A Summary Index for Antimicrobial Resistance in Food Animals in the Netherlands
M. Bouwknegt; National Institute for Public Health and the Environment, Center for Infectious Disease Control, Bilthoven, Netherlands

4:15 PM - 4:30 PM

Antimicrobial Treatments for *Clostridium difficile* Infection in the Outpatient Setting in Maryland: Implications for Stewardship
R. Perlmutter; Maryland Department of Health and Mental Hygiene, Baltimore, MD

4:30 PM - 4:45 PM

Critical or Fatal Illness Caused by Community-associated *Staphylococcus aureus* (CA-SA) Infection—Minnesota (MN), 2005-2013
A. Beaudoin; University of Minnesota, Minneapolis, MN

4:45 PM - 5:00 PM

Can the Past Inform the Current Response to Cephalosporin-resistant *Neisseria gonorrhoeae*? A Comprehensive Review of Prior Public Health Responses to Gonococcal Antimicrobial Resistance
R. Kirkcaldy; Centers for Disease Control and Prevention, Atlanta, GA

I5. Foodborne Diseases I

Centennial Ballroom III

Moderators:

Thomas Gomez; U.S. Department of Agriculture, Animal and Plant Health Inspection Service, Atlanta, GA

Kristin Holt; U.S. Department of Agriculture, Food Safety and Inspection Service, Atlanta, GA

3:30 PM - 3:45 PM

Quantitative Microbial Risk Assessment of Salmonellosis for Owners of Backyard Poultry Flocks, Seattle, Washington
H. N. Fowler; University of Washington School of Public Health, Seattle, WA

3:45 PM - 4:00 PM

Outbreak of *Salmonella* Newport Infections Linked to Cucumbers—United States, 2014
K. Angelo; Centers for Disease Control and Prevention, Atlanta, GA

4:00 PM - 4:15 PM

Tracing *Brucella suis* Infection in a Human, Oregon, 2013
E. E. Debess; Oregon Department of Human Services, Portland, OR

4:15 PM - 4:30 PM

Climate Change Blunts Progress Reducing Infectious Diseases Attributable to Unsafe Water and Sanitation in China
J. V. Remais; Emory University, Atlanta, GA

4:30 PM - 4:45 PM

Genotypic and Epidemiologic Trends of Norovirus Outbreaks in the United States, 2009-2013
J. Vinje; Centers for Disease Control and Prevention, Atlanta, GA

4:45 PM - 5:00 PM

Astrovirus and Sapovirus in Children Under Five Years of Age with Acute Diarrhea in Guatemala
M. B. Lopez; University del Valle de Guatemala, Guatemala City, Guatemala

I6. Late Breakers I

Centennial Ballroom IV

Moderators:

Marta Gwinn
Allan Pillay
Centers for Disease Control and Prevention, Atlanta, GA

3:30 PM – 3:45 PM

Cross-sectional Study of Influenza Viruses at Swine Slaughterhouses in Vietnam, 2013–2014
L. V. Nguyen; Department of Animal Health of Vietnam, Hanoi, Vietnam

3:45 PM – 4:00 PM

Pregnancy as the Main Driver of Sex Disparities Among Adult Influenza Hospitalizations Across 14 FluSurv-NET Sites, 2010–2012
K. E. Kline; Connecticut Emerging Infections Program and Yale School of Public Health, New Haven, CT

4:00 PM – 4:15 PM

Influenza Outbreak in Hematology/Oncology Unit of Pediatric Hospital in April 2015, Tbilisi, Georgia
O. Tarkhan-Mouravi; National Center for Disease Control and Public Health, Tbilisi, Georgia

4:15 PM – 4:30 PM

"Wash My Hands? Where and with What?!"—Water and Hygiene Conditions in Healthcare Facilities in Honduras, Rwanda, and Ghana
M. N. Gallegos; Emory University, Atlanta, GA

4:30 PM – 4:45 PM

Use of Supervised Machine Learning to Identify Subsets of WgMLST Loci Associated with Human *Listeria monocytogenes* Isolates from Different Food Sources
W. Gu; Centers for Disease Control and Prevention, Atlanta, GA

4:45 PM – 5:00 PM

Lessons Learned from a Time-limited Surveillance Pilot of Enterovirus D68 in Canada
F. Reyes Domingo; Public Health Agency of Canada, Ottawa, Canada

Poster Session with Authors – IV

5:00 PM - 6:15 PM | Grand Hall

Director's Tour of Posters

Tom Kenyon
Director, Center for Global Health

Modeling

Board 289: Modeling Triple-diffusions of Infectious Diseases, Information, and Preventive Behaviors Through a Metropolitan Social Network—An Agent-based Simulation

Board 290: The Economics of Pandemic Prevention: SARS, Ebola and New Strategies to Mitigate Disease Emergence at Source

Board 291: Estimation of MERS-Coronavirus Reproductive Number and Case Fatality Rate for the Spring 2014 Saudi Arabia Outbreak: Insights from Publicly Available Data

Board 292: The Global Distribution and Burden of Melioidosis, an Overlooked Emerging Infectious Disease

Board 293: Estimating Etiology Distributions for Foodborne Disease Outbreaks with Missing Etiologies Using CART Analysis, 1998-2012

Board 294: EPIPOI: A User-friendly Software for Inspecting Seasonality, Burden and Spatial-patterns of Epidemiological Time-series

Board 295: Ebola in West Africa: Impact of Exponential Growth on Case Fatality Estimates
Withdrawn at Author's Request

Board 296: Transmission Dynamics and Control of Ebola Virus Disease Outbreak in Nigeria, July to September 2014

Board 297: Estimating the Effective Reproduction Number, Ebola Virus Disease Epidemic, 2014

Board 298: Impact of Interventions on the Effective Reproductive Number of the 2014 West African Ebola Outbreak

Board 299: A Method for Calculating the Lifetime Risk Reduction of Infection Induced by Newly Implemented Vaccination Program

Board 300: Mortality Patterns of the 1957 Influenza Pandemic in Maricopa County

Geographic Information Systems (GIS)

Board 301: Evaluation of Neighborhood-level Risk Factors on *Campylobacter* Infection Using Geographically Weighted Regression—FoodNet

Board 302: Geographic Expansion of High Lyme Disease Incidence Foci in the United States

Board 303: Mapping Recent Chikungunya Activity in the Americas

Board 304: Spatial and Temporal Analysis of *Campylobacter* spp. and *Salmonella* spp. in England

Board 305: Software to Facilitate Remote Sensing Data Access for Infectious Disease Surveillance and Forecasting

Board 306: Is Listeriosis Really Sporadic in England?

Board 307: Mapping Insecticide Resistance in Malaria Vectors: Latest Updates from IR Mapper®

Strengthening Public Health Systems

Board 308: Advances in Influenza Surveillance in Latin America and the Caribbean, 2010-2014

Board 309: Enhancing Notifiable Disease Surveillance Systems in Middle-income Countries to Improve Detection of Possible Intentional Biological Events

Board 310: United States Centers for Disease Control and Prevention Domestic and International Laboratory Response to Middle East Respiratory Syndrome Coronavirus (MERS-CoV)

Board 311: Knowledge, Attitude, Practices and Training Needs for Food-handlers in Large Canteens in Southern Vietnam, 2012

Board 312: Factors Driving Customers to Seek Health Care in Pharmacies for Acute Respiratory Illness: A Pilot Study in Dhaka City, Bangladesh

Board 313: Implementing Automated Reporting of Outbreak Data to the National Outbreak Reporting System (NORS)

Board 314: A Pilot Program of Joint Veterinary and Human Epidemiology Training in Armenia: A One Health Approach

Board 315: Underreporting of Tick-borne Disease in Residents of a High-incidence County, Minnesota, 2009

Board 316: Competencies for Public Health Laboratories: Strengthening the Workforce to Improve Public Health Practice

Board 317: Poliomyelitis Surveillance System and Environmental Monitoring in São Paulo State, Brazil—Tools to Prevent the Reintroduction of Wild Poliovirus

Board 318: Improving Sample Management to Decrease Contamination Rates in Blood Culture Process During Population Based Surveillance, Egypt, 2010-2014

Board 319: Enhanced Surveillance for Severe Pneumonia, Thailand, 2010-2014

Board 320: Characterizing Investigation Steps and Public Health Responses Taken on Emergency Department Visit and School Absenteeism Syndromic Surveillance Aberrant Events

Board 321: The Impact of Standard Tools on the Investigation of Emergency Department Visit Syndromic Surveillance Aberrant Events in Ontario, Canada

Board 322: Rabies Awareness in a Community of Bangladesh

Board 323: Leveraging Partnerships for Improved National Public Health Institutes

Board 324: Teaching Modern Disease Surveillance and Investigation Skills in Low-income Nations: DTRA Cooperative Biological Engagement Program (CBEP) in Kenya and Uganda

Board 325: Phylogenetic Analysis of Avian Influenza AH5N1 from a Recent Outbreak in Egypt (2014/2015)

Board 326: Adult Immunization Programs and Chronic Disease Partnerships

Board 327: Need for Effective Public Health Strategies: Evidence From Hospital-based Mortality Records in Federal Medical Centre, Owo, Ondo State, Nigeria, 2006-2014

Global Health Initiatives

Board 328: From Idea to Activation: The Vietnam Ministry of Health EOC and the US CDC Global Health Security Agenda

Board 329: Teaching Modern Disease Surveillance and Investigation Skills in Low-income Nations: DTRA Cooperative Biological Engagement Program (CBEP) in Kenya and Uganda
Withdrawn at Author's Request (See Board 324)

Board 330: Global Health Capacity Building Through the Global Health Security Agenda

Immigrant and Refugee Health

Board 331: Tuberculosis and Diabetes Among United States-bound Adult Refugees, 2008-2012

Board 332: Evaluation of Annual Selective Supplementary Immunization Activities Among Pre-school Migrant Children in Beijing, 2006-2013

Social Determinants of Health and Infectious Diseases

Board 333: Profile of Viral Hepatitis in Saudi Arabia

Board 334: Predictors of Condom Use Among Sexually Active Young Women—National HIV Communication Survey, South Africa, 2012

Board 335: Multidrug Resistant Tuberculosis and Treatment in KwaZulu-Natal, South Africa: A Long Distance Relationship

Gender and Infectious Diseases

Board 336: HIV/AIDS and Disclosure to Partners: A Situation Analysis of HIV Positive Women in Oyo State, Nigeria

Vulnerable Populations

Board 337: Neighborhood Poverty and Influenza-related Hospitalizations, FluSurv-NET 2010-2012

Board 338: Epidemiology of Skin and Soft-tissue Infections in US Army Trainees at Fort Benning

Board 339: Infectious Causes of Mortality in an Urban Slum in Nairobi, Kenya, 2009-2013

Board 340: Description of Dengue in Children Aged Less Than 18 Months—Puerto Rico, 1999–2011
Withdrawn at Author's Request

Board 341: Silent Risk of Tick-borne Diseases in Georgia, USA

Board 342: A Mysterious Case of Spontaneous *Streptococcus dysgalactiae* subsp. *equisimilis* (SDSE) Bacteremia and Epidural Abscess: A Case Report

Board 343: Bacterial Etiology of Postpartum Endometritis in Peri-urban Karachi, Pakistan—Data from a Prospective Evaluation Study

Board 344: Influenza-like Illness and Influenza Vaccination During Pregnancy in Quetzaltenango, Guatemala

Board 345: Increase of Invasive *Haemophilus influenzae* Cases and *Haemophilus influenzae* Serotype A Cases in Minnesota, 2005-2014

Board 346: Methicillin Sensitive *Staphylococcus aureus* Bacteremia from Soft Tissue Infection Presenting as Septic Pulmonary Embolism: A Case Report and Review of Literature

Board 347: Intestinal Parasitic Infection and Associated Symptoms Among Children in Tea Plantation Sector, Sri Lanka

Board 348: Incidence of Influenza-associated Respiratory Infection Among Pregnant Women in Bangladesh, 2013-2015

Board 349: Coxsackievirus B3: An Ethiologic Agent of Acute Febrile Illness in Bandung, Indonesia

Board 350: *Salmonella*-related Hospitalizations in Seniors in Canada: Current Status to Inform Potential Future Burden

Board 351: High Prevalence of Intestinal Parasitic Infections Among School-age Children in Thailand: A Comparative Study

Board 352: Exposure to Zoonotic Disease Among Oncology Patients: A Pilot Study in Romania

Poverty and Infectious Diseases

Board 353: Costs of Hospitalization for Respiratory Syncytial Virus Illness Among Children Aged <5 Years and Associated Economic Impact on Households in Bangladesh, 2010

Board 354: Does Socioeconomic Disadvantage Account for Unfavorable Treatment Outcome of Tuberculosis? A Taiwanese Cohort Study

Board 355: *Salmonella* Incidence and Census Tract Poverty Level, California FoodNet, 2008-2013

Board 356: Survey of Rotavirus Infection in Iraqi Pediatric Patients at Three Hospitals

Outbreak Investigation: Lab-Epi Response

Board 357: Investigation of a Group A *Streptococcus* Outbreak in a Long-term Care Facility—Georgia, 2014

Board 358: Linking Listeriosis to Recalled Foods: Use of Whole-genome Sequencing to Enhance Public Health Investigations

Board 359: Increase in *Salmonella* Serotype IIIa 18:z4,z23: Isolated from Retail Meats and Humans—United States, 2003-2012

Board 360: Finding Outbreaks Faster: Measuring the Time to Detection

Board 361: Dengue Virus Infection Among Members of the Uganda People's Defense Force Deployed to Somalia

Board 362: Investigation of an Outbreak of Cholera in Diepsloot, Gauteng Province of South Africa, September 2014

Board 363: Measles Outbreak Investigation in an Urban Slum—Ghazipur Village, Delhi, India

Board 364: An Outbreak of Foodborne Salmonellosis Linked to a Bread Takeaway Shop in Ben Tre City, Vietnam

Board 365: Improving Foodborne Disease Outbreak Response Capacity in State and Local Health Departments Through the Foodborne Diseases Centers for Outbreak Response Enhancement (FoodCORE)

Board 366: Household Cluster Investigations During the Early Stages of the Chikungunya Epidemic in Puerto Rico, 2014

Board 367: Dengue Outbreak in South Texas, 2013

Board 368: Emergence of Rabies Clusters Among Owned Dogs in Thai-Laos Border Area, Wiangkan District, Chiang Rai Province, Thailand, November 2013 - February 2014

Board 369: An Outbreak of Cholera in the Context of Scarce and Intermittent Water Supply in Netrokona Municipality, Bangladesh, 2013

Board 370: Investigation of Diarrhoeal Disease Outbreak in Swaziland in July 2014

Board 371: A Tale of Two Receptions: Two Norovirus Outbreaks at a Banquet Facility—Connecticut, 2013

Board 372: Outbreaks of Listeriosis in England Linked to Crabmeat: A Novel Food Vehicle

Board 373: Acute Gastroenteritis Cases at a Home for Abandoned Children, Johannesburg, South Africa, May 2014 *Withdrawn at Author's Request*

Board 374: Use of an Information Technology Platform to Facilitate Data Sharing in Multistate Enteric Disease Outbreak Investigations

Board 375: Emerging Zika Fever Outbreaks in Thailand, 2012-2013

Board 376: Outbreak of Dengue Fever in Ouagadougou, Burkina Faso, 2013

Board 377: Investigation of a Diarrhea Outbreak in a Public Hospital Refectory in São Paulo City, São Paulo State, June 2014

Board 378: Re-emergence of Urinary Schistosomiasis in Europe? Investigation of a Cluster of *Schistosoma haematobium* Infections Acquired in Southern Corsica

Board 379: Outbreak of *Vibrio parahaemolyticus* Associated with Raw Shellfish, Connecticut, 2013

Board 380: Estimating Remaining Risk for Use in Targeted Follow-up in an Outbreak of Fungal Infections Due to Contaminated Methylprednisolone Injections, Tennessee, 2012

Board 381: Review of Antifungal Treatment Regimens and Clinical Outcomes in an Outbreak of Fungal Infections Due to Contaminated Methylprednisolone Acetate Injections in Tennessee

Board 382: Risk Factors for Fungal Infection Following Injection with Contaminated Methylprednisolone Acetate in Tennessee

Board 383: Investigation of a Cluster of Methicillin-sensitive *Staphylococcus aureus* Infections Among Patients who Received Joint Injections in a Tennessee Outpatient Clinic

Board 384: An Investigation of a Fatal Hand, Foot, and Mouth Disease (HFMD) Prompts Health Alert with a Survey of Knowledge, Attitude, and Practice (KAP) in Prevention and Control in Child Care Centers (CCCs) in Surin Province, Thailand 2014

Board 385: An Outbreak of Ocular Bacterial Conjunctivitis Due to Unencapsulated *Streptococcus pneumoniae*

Board 386: Investigation of an Outbreak of Infections with Rare *Salmonella* Serotypes Linked to Pet Bearded Dragon Lizards, 2012 - 2014

Board 387: Utilization of CDC Serologic Assays to Detect Antibodies to Middle East Respiratory Syndrome Coronavirus (MERS-CoV) in Two US Imported Cases

Board 388: Measles Outbreak in Urban Slums of Lagos State, Southwestern Nigeria, April 2013

Board 389: Hospital-based Quarantine for Ebola Virus Disease Contact Tracing at Fousseyni Daou Hospital—Kayes, Mali, 2014

Board 390: Outbreak of Odyssean Malaria, Gauteng Province, South Africa, January 2015

Board 391: Mobile IT Supporting Contact Tracing in the Ebola Outbreak Surveillance and Outbreak Response Management and Analysis System (SORMAS) to Support the Control of Epidemic-prone Diseases

Board 392: Diarrheal-illness Outbreak in Siyanda District, Northern Cape Province, South Africa, 2013

Board 393: Crimean Congo Hemorrhagic Fever, Sudan, 2013 and 2014

Board 394: Cluster of Ebola Viral Disease Linked to a Single Funeral Event—Sierra Leone, 2014

Board 395: Evaluation of the Timeliness of Enteric Disease Surveillance: Is Achieving the Benchmark Good Enough?

Board 396: Data Management in the West Africa Ebola Outbreak—Lessons Learned from Piloting a New Software Tool

Board 397: Explosive Post-disaster Diarrhea Outbreak in the Solomon Islands, April - June 2014

Wednesday, August 26

Poster Set-up for the Day
7:00 AM – 8:00 AM

All posters presented on Wednesday will be available for viewing in the Grand Hall from 10:10 AM to 1:45 PM. Authors will be present at posters for one hour and fifteen minutes as noted under the Scientific Sessions schedule for the day.

Scientific Sessions

J. Concurrent Plenary Sessions
8:00 AM - 9:00 AM

J1. Comparisons in the Control of HIV and Ebola
Centennial Ballroom I

Moderator:
Kashef Ijaz; Centers for Disease Control and Prevention, Atlanta, GA

Speaker:
Reflections on HIV and Ebola, 2015
Kevin DeCock; Centers for Disease Control and Prevention, Nairobi, Kenya

J2. Infectious Diseases in Popular Culture (Cinema)
Centennial Ballroom II

Moderator:
Marian McDonald; Centers for Disease Control and Prevention, Atlanta, GA

Speaker:
Bad Bugs on the Big Screen: Science Fiction and Fact in Hollywood
W. Ian Lipkin; Columbia University, New York, NY

J3. Global Water and Sanitation
Centennial Ballroom III

Moderator:
Michael Beach; Centers for Disease Control and Prevention, Atlanta, GA

Speaker:
Recent Research on Water Quality and Sanitation in Low Income Settings: What Works, What Doesn't
Thomas Clasen; Emory University, Atlanta, GA

J4. Middle East Respiratory Syndrome (MERS)
Centennial Ballroom IV

Moderator:
Susan Gerber; Centers for Disease Control and Prevention, Atlanta, GA

Speaker:
Epidemiology and Outbreak Investigation of MERS CoV in Saudi Arabia: An Update
Abdullah Assiri; Ministry of Health, Riyadh, Saudi Arabia

K. Concurrent Plenary Sessions
9:10 AM - 10:10 AM

K1. Global Expansion of Chikungunya
Centennial Ballroom I

Moderator:
Christopher Paddock; Centers for Disease Control and Prevention, Atlanta, GA

Speaker:
Chikungunya: Emergence and Spread in the Americas
Sylvain Aldighieri; Pan American Health Organization, Washington, DC

K2. Advanced Molecular Detection
Centennial Ballroom II

Moderator:
Greg Armstrong; Centers for Disease Control and Prevention, Atlanta, GA

Speaker:
Implementing an Integrated Whole Genome Sequencing Solution for Microbial Pathogens: A Challenge for Us All
Derrick Crook; University of Oxford, Oxford, United Kingdom

K3. 20 Years of Accomplishments of the Emerging Infections Program
Centennial Ballroom III

Moderator:
Richard Danila; Council of State and Territorial Epidemiologists, St. Paul, MN

Speakers:
CDC Perspective
Robert Pinner; Centers for Disease Control and Prevention, Atlanta, GA

State Perspective
Ruth Lynfield; Minnesota Department of Health, St. Paul, MN

Academic Perspective
William Schaffner; Vanderbilt University School of Medicine, Nashville, TN

K4. Polio
Centennial Ballroom IV

Moderator:
Allen Craig; Centers for Disease Control and Prevention, Atlanta, GA

Speaker:
Polio Eradication: Completing the Endgame
Hamid S. Jafari; World Health Organization, Geneva, Switzerland

Break
10:10 AM – 10:30 AM | Grand Hall

L. Concurrent Panel Sessions
10:30 AM - 12:00 PM

L1. Emerging Infections in Immunologically Unique Hosts
International Ballroom South

Moderators:
Eleanor Click; Centers for Disease Control and Prevention, Atlanta, GA

Bonnie Maldonado; American Academy of Pediatrics, Stanford, California

Speakers:
Tuberculosis in Peripartum Women and Infants
Amita Gupta; Johns Hopkins University School of Medicine, Baltimore, MD

Emerging Infections in Adult Transplant Patients
Steven Pergam; University of Washington, Seattle, WA

Respiratory Viral Infections in Pediatric Transplant Recipients
Angela Campbell; Centers for Disease Control and Prevention, Atlanta, GA

L2. Public Policy and Infectious Diseases
Centennial Ballroom I

Moderators:
Sharon Ricks; U.S. Department of Health and Human Services, Region IV, Atlanta, GA

Sarah Wiley; Centers for Disease Control and Prevention, Atlanta, GA

Speakers:
Ethics and Ebola: Public Health Planning and Response
Lisa Lee; Presidential Commission for the Study of Bioethical Issues, Washington, DC

The Role of Public Policy in Strengthening America's Ability to Respond to Pathogens of Pandemic Potential
Michael Osterholm; University of Minnesota, Minneapolis, MN

The Roles of Policy in Controlling Vaccine-preventable Disease and Enhancing Immunization
Anne Schuchat; Centers for Disease Control and Prevention, Atlanta, GA

L3. Moving from Early Detection to Prediction of Outbreaks
Centennial Ballroom II

Moderators:
Christine Hoang; American Veterinary Medical Association, Schaumburg, IL

Denise Pettit; Association of Public Health Laboratories, Raleigh, NC

Speakers:
Using One Health Surveillance to Predict and Prevent Pandemics
Jonna A. K. Mazet; University of California, Davis, Davis, CA

Crowdsourcing an End to Pandemics
Mark Smolinski; Skoll Global Threats Fund, San Francisco, CA

Outbreak Detection—How Can We Do Better?
Brian McCloskey; Public Health England, London, United Kingdom

L4. Emerging Respiratory Infections in the Eastern Mediterranean Region
International Ballroom North

Moderators:
Susan Gerber
Centers for Disease Control and Prevention, Atlanta, GA

Wasiq Khan
World Health Organization, Regional Office for the Eastern Mediterranean, Cairo, Egypt

Speakers:
The Epidemiology of MERS-CoV in the United Arab Emirates
Farida Al Hosani; Abu Dhabi Health Authority, Abu Dhabi, United Arab Emirates

Risk factors for MERS CoV Transmission in Household and Healthcare Settings: Experience from Saudi Arabia
Abdullah Assiri; Ministry of Health, Riyadh, Saudi Arabia

Monitoring the Next Pandemic Threat: Updates on the Current Surge of H5N1 Infection and Other New Influenza Viruses in Egypt
Samir Refaey Abu-Zid; Ministry of Health, Egypt, Cairo, Egypt

Emerging Respiratory Infections in the Eastern Mediterranean Region: Current Challenges, Opportunities, and Lessons for Global Health Security
Mamunur Malik; World Health Organization, Regional Office for the Eastern Mediterranean, Cairo, Egypt

L5. One Health
Centennial Ballroom III

Moderators:
Ermias Belay; Centers for Disease Control and Prevention, Atlanta, GA

Elizabeth Hilborn; US Environmental Protection Agency, Research Triangle Park, NC

Speakers:

The One Health Approach is Gaining Momentum Instead of Fading Away: Reviewing a Decade of Tipping Points
Carol Rubin; Atlanta, GA

One Health Training Programs and Funding Opportunities
Gregory Gray; Duke University, Durham, NC

Challenges of Multidisciplinary Research and Developing Partnerships
Cheryl Stroud; One Health Commission, Apex, NC

L6. Challenges in Control of Bloodborne Pathogens
Centennial Ballroom IV

Moderators:

Taraz Samandari
John Ward
Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Hepatitis C Virus Epidemiology in the United States
Scott Holmberg; Centers for Disease Control and Prevention, Atlanta, GA

Outbreak of HIV and Hepatitis C Linked to Injection Drug Use in Rural Indiana
Pamela Pontones; Indiana State Department of Health, Indianapolis, IN

Opportunities for Public Health Control of Hepatitis C Virus Using Directly Acting Antivirals
Mark Hull; University of British Columbia, Vancouver, Canada

Lunch
12:00 PM – 12:30 PM | On your own

Poster Session with Authors – V
12:30 PM - 1:45 PM | Grand Hall

Director's Tour of Posters
Jonathan Mermin
Director, National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention

Infectious Diseases and Policy Implications

Board 398: Effectiveness of the Influenza Vaccine Against Laboratory-confirmed Influenza in Young Children Using a Test-negative Design in Bangkok, Thailand, 2013-2014

Board 399: Anatomy of a Shigellosis Outbreak: Treatment Policies and Implications for Antibiotic Resistance—Central Indiana, 2014

Board 400: Risk Factors for *Vibrio parahaemolyticus* Infection in Southern Coastal Region of China

Board 401: Epidemiological and Etiological Characteristics of Hand, Foot, and Mouth Disease in Henan, China, 2008-2013

Board 402: Lyme Disease Surveillance in New York State: An Assessment of Patient Underreporting

Board 403: Knowledge, Attitude and Practice Related to Malaria Infections Among Liberian Armed Forces at Camp Edward Binyah Kesselly, Liberia

Board 404: Comparative Analysis of Culture-confirmed and Culture-independent Tests for Enteric Infections in Georgia, 2011-2013

Board 405: Evaluation of Control and Prevention Measures for Visceral Leishmaniasis Using Mathematical Model

Role of Health Communication

Board 406: The Impact of a Behavior Change Communication Intervention to Prevent Nipah Virus Transmission in Bangladesh

Board 407: Chinese Social Media Reaction to Information About 42 Notifiable Infectious Diseases

Board 408: Global Handwashing Day 2012: A Qualitative Content Analysis of Chinese Social Media Reaction to a Health Promotion Event

Board 409: Facts and Rumors: Social Media Reaction to Information and Misinformation on Ebola

Travelers' Health

Board 410: Increase in Paratyphoid Fever Cases Among Japanese Travelers Returning from Cambodia in 2013

Vector-Borne Diseases and Climate Change

Board 411: The Dynamics of Vector-host Interaction in Unraveling the Complexity of Eastern Equine Encephalitis as an Emerging Public Health Threat in Northeastern USA

Board 412: Identification of Lyme Borreliosis in a Dog in Thailand

Board 413: Predicting the Spread of Vector-borne Disease: Chikungunya in the Americas

Board 414: Effectiveness of a Single Peridomestic Application of Acaricide to Prevent Lyme and Other Tickborne Diseases

Board 415: Abundance and Infection Rates of *Ixodes scapularis* Nymphs Collected from Residential Properties in Lyme Disease-endemic Areas of Connecticut, Maryland and New York

Board 416: First Detection of *Babesia microti* in *Ixodes scapularis* Ticks, Maryland, USA

Board 417: Dengue Cluster Investigation in Two Districts, Ubon Ratchathani, January-July 2013: Epidemiological Characteristics and Key Vector Containers

Board 418: Human-tick Encounters as a Surrogate Measure for Disease in Tickborne Disease Intervention Studies

Board 419: Meteorological Factors Associated with Hand, Foot and Mouth Disease in a Central Highlands Province, Vietnam: An Ecological Study

Board 420: Spatial Epidemiology of Lyme Disease in an Endemic County

Board 421: Hunter-killed Deer as a Predictor of Notifiable Disease Rates for Lyme Disease and Babesiosis in New Jersey Counties, 1996 to 2013

Board 422: Molecular Identification of the *Anopheles gambiae* Complex (Diptera: Culicidae) from Five Counties in Liberia

Board 423: Risk Assessment for Rickettsial Pathogens in *Dermacentor occidentalis* Ticks from Southern California

Board 424: Characterization of the Bacterial Community of Species and Populations of *Dermacentor* Ticks

Board 425: Analysis of the Metagenome of the Tick Vector *Amblyomma americanum*
Withdrawn at Author's Request

Board 426: Diagnosis of Travel Related and Locally Transmitted Chikungunya Virus in Florida

Board 427: Clinico Epidemiological Profile of Acute Encephalitis Syndrome in West Bengal, India

Board 428: Autochthonous Malaria Case in Johannesburg, Gauteng Province, South Africa, September 2014

Board 429: Molecular Epidemiology and Specific Detection of *Anaplasma* sp. Related to *Anaplasma phagocytophilum* in Sika Deer and Its First Detection in Wild Brown Bears and Rodents in Hokkaido, Japan

Board 430: Interaction Studies of Extrinsic and Intrinsic Dengue Virus Types in Disease Affected Households of Rajasthan, India

Board 431: Characterization of Chikungunya Virus Infections in Children in Managua, Nicaragua

Board 432: Incidence of and Reasons for Hospitalization of Chikungunya Patients—Puerto Rico, 2014

Zoonotic and Animal Diseases

Board 433: Spatial Ecology and Epidemiology of Soilborne Human and Animal Bacterial Pathogens and Their Public Health Significance in Pakistan

Board 434: Lymphocytic Choriomeningitis Virus Outbreak and Risk Assessment—Multiple States, 2012

Board 435: Seroconversion and Risk Factors for Highly Pathogenic Avian Influenza A (H5N1) Virus Infection Among Live Bird Market Workers in Bangladesh During 2009-2010

Board 436: Pet Ownership Increases the Risk of Encountering Ticks in the Household

Board 437: Bat Hunting and Bat-human Interactions in Bangladeshi Villages: Implications for Zoonotic Disease Transmission

Board 438: Point Prevalence Survey for Tickborne Pathogens in Military Working Dogs, Shelter Animals, and Pet Populations in Northern Colombia

Board 439: Long-term Impact of Chikungunya Virus Infection in Florida

Board 440: Seroprevalence of West Nile Virus in Wild Birds in Bangladesh

Board 441: Tickborne Relapsing Fever Outbreak at a High School Football Camp—Arizona, 2014

Board 442: Small Commercial Poultry Farmers' Perception of Avian Influenza and Biosecurity, Bangladesh, 2011-12

Board 443: A Cross-sectional Study to Examine Exposure and Risk Factors for Emerging Infectious Diseases Among Febrile Patients in Kilombero, Tanzania

Board 444: Human Brucellosis and Goat Farms in Ratchaburi, Thailand, 2013

Board 445: Community-based Rotavirus Surveillance Among Pigs and the Children of Pig-raisers in Bangladesh, 2013-2014

Board 446: Human *Salmonella* Serotype Dublin Infections and Antimicrobial Resistance, United States

Board 447: Environmental Contamination with *Salmonella* Species in Homes with Reptile Pets, Minnesota, 2003-2014

Board 448: Chikungunya Virus Infections in Florida, 2014

Board 449: Leptospirosis Surveillance—Using Dogs as Sentinels for Human Infection in New York City, 2006-2014

Board 450: Development and Implementation of One Health Surveillance and Research Activities at the Animal-Human Interface in Vietnam, 2009-2015

Board 451: Early Indicators of Fatal Leptospirosis During an Epidemic in Puerto Rico: A Case-control Study

Board 452: Investigation of Q Fever in Dairy Farms in Mae-On District, Chiang Mai, Thailand

Board 453: Canine and Livestock Husbandry Practices Among Ohio Farmers and Potential for Zoonotic Disease Transmission

Board 454: Changing Trends in Backyard Flocks: Review of Outbreaks of Human Salmonellosis Linked to Contact with Live Poultry—United States, 1990-2013

Board 455: Shiga-toxin Producing *Escherichia coli* O157 Infections in England, 2009-2011: Effects of Climate and Land Use

Board 456: Novel PCR Exclusion Assay to Detect Pathogenic Spotted Fever Group Rickettsia in the Lone Star Tick (*Amblyomma americanum*)

Board 457: The Ecology of Nipah Virus in its Natural Reservoir, *Pteropus giganteus*, in Bangladesh

Board 458: High Resolution Genotyping of *Bacillus anthracis* and Spatio-temporal Patterns of an Anthrax Epizootic in White-tailed Deer, *Odocoileus virginanus*

Board 459: Outbreaks of Cutaneous Anthrax Among Humans in Bangladesh: Understanding the Risk Factors from a Case-control Analysis

Board 460: Use, Characterization, and Potential Zoonotic and Antibiotic Resistant Organisms Among Dogs Using Dog Parks in the Minneapolis/St. Paul Metropolitan Area

Board 461: Self-reported Acute Health Symptoms and Exposure to Companion Animals

Board 462: Molecular Characterization of Zoonotic Poxviruses Circulating in the Amazon Region of Colombia, 2014

Board 463: Spatial-temporal Distribution of Rodent-borne Hantavirus Infection (*Oligoryzomys fulvescens*) in Tonosi—Panama

Board 464: Influenza A Prevalence in Two Swine Populations in Guatemala, 2012

Board 465: The Results of Epizootic Studies on Plague and Tularemia in the Plague Natural Foci of Transcaucasian Plain-foothills

Board 466: Comparison of Highly Pathogenic Avian Influenza A(H5N1) Viruses Isolated From Humans in Vietnam Provides Evidence for Recent Reassortment and Emergence of a Novel Clade 1 Genotype

Board 467: Prevalence of and Risk Factors for Q fever in Dairy Animals and Agricultural Workers in the Central Lowland Regions of Azerbaijan

Board 468: First Incidence of Detection of Infection with a Zoonotic Parapoxvirus in Humans in the Country of Georgia

Board 469: Global Dissemination of *Bartonella* Infections by Invasive *Rattus* Rats

Board 470: Epidemiological Characteristics of Brucellosis on the Territory of Municipality of Veles for the Period Between 1990-2014

Board 471: Active Surveillance for Avian Influenza A/H7N9 Virus in Poultry in the North of Vietnam, 2013 - 2014

Board 472: Rabies Prevalence in Iraq: Diagnostic Efforts of Iraqi Central Veterinary Laboratories

Board 473: Detection and Genetic Analysis of Norovirus from Dogs in South Korea

Board 474: Comparing Seasonality of Bats' Feeding Behavior to Seasonality of Nipah Virus Transmission to Humans in Bangladesh

Board 475: Human Exposures to Ferret-badgers and Gem-faced Civets after Reemergence of Wildlife Rabies—Taiwan, 2014

Board 476: The Human-animal Interface in Peri-urban Slums of Kenya

Tropical Infections and Parasitic Diseases

Board 477: Population-based Surveillance for Bacteremic Melioidosis in Northeast Thailand: An Update on Incidence and Case Fatality Rate, 2006-2013

Board 478: Survival Estimates of *Lutzomyia longipalpis* in an Endemic Area of Visceral Leishmaniasis in São Paulo State, Brazil

Board 479: Prevalence and Factors Associated with Buruli Ulcer in Ayamelum Local Government Area of Anambra State, Nigeria

Board 480: Description of Dengue-related Hospitalization and Disease Severity from an Enhanced Dengue Surveillance System in Puerto Rico

Board 481: Investigation of Visceral Leishmaniasis Caused by *Leishmania martiniquensis* in Non-endemic Area of Thailand

Board 482: Evaluation of a Novel Intervention to Improve the Clinical Management of Patients with Dengue—Puerto Rico, 2012-13
Withdrawn at Author's Request

Board 483: A Helminthiasis Prevalence and Ecological Study in the Aragacotn Region of Armenia, 2013

Board 484: Trends of Visceral Leishmaniasis in Armenia, 1999-2014

H1N1

Board 485: Active Surveillance for Respiratory Pathogens Among DoD Beneficiaries

Board 486: Epidemiology of Fatal Cases Associated with Pandemic Influenza Reported in Yemen

Board 487: Molecular Characterization and Phylogenetic Analysis of Circulating Strains of Influenza A (H1N1) pdm09 and Influenza B from 2013-2014 in Egypt

Board 488: Pandemic Influenza (A/H1N1pdm09) in Older Adults in Kashmir, India: Did the Population Not Get Exposed to Earlier Epidemics?

Board 489: Air and Railway Travels Accelerated Spatial Spread of 2009 Pandemic Influenza A (H1N1) in Mainland, China

Board 490: Circulation Dynamics of Seasonal and Pandemic Influenza Viruses in Nigeria (2009-2013)

Board 491: Not a Total Failure: Influenza Vaccine Associated with a Reduction in Symptom Severity Among Patients with Influenza A/H3N2 Disease

Board 492: Quantifying the Mortality Impact of the 1918-1920 Influenza Pandemic in Arizona
Withdrawn at Author's Request

Board 493: Analyzing the Adverse Side-effects of the Influenza A/H1N1 Vaccine in Health Care Staff in Selected Provinces of Afghanistan

Board 494: Risk Factors for Death from Influenza A(H1N1) pdm09 in Pregnant Women, State of São Paulo, Brazil, 2009

Challenges in Controlling Respiratory Infections in Special Settings

Board 495: Pneumonia Associated with *Chlamydia pneumoniae* Infection at a US Army Training Installation

Board 496: Acute Respiratory Infection Outbreaks in Postpartum Nursing Centers: An Emerging Public Health Threat—Taiwan, 2007-2014

Board 497: Outbreak of 2009 Pandemic Influenza A (H1N1) Caused by Over Crowded Party at a Valve Production Company, Samutprakan Province, Thailand, 2014 *Withdrawn at Author's Request*

Board 498: An Outbreak of Respiratory Syncytial Virus Pneumonia in an Orphanage Home, Thailand, July - August 2014

Board 499: Containing Influenza Outbreaks with Antiviral Use in Jails and Prisons in Taiwan, 2005-2014

Board 500: Detection of Non-influenza Viruses in Acute Respiratory Infections in Children Under the Age of Five in Côte d'Ivoire

Board 501: Possible Evidence of Antibody-dependent Enhancement of Illness During Influenza Pandemic of 1918 in Military Officer Trainees

Board 502: A One Health Approach for Studying Swine Influenza Virus Transmission at Pig Farms, China

Board 503: Characterization of Viral Load and Persistence of Influenza A Virus in Air and on Surfaces of Swine Production Facilities

Board 504: Influenza Surveillance in the Tropics: A United States DoD Perspective

Board 505: Incidence of Influenza and Influenza Re-infection in a Cohort of Nicaraguan Children

Prevention Challenges for Respiratory Diseases in Community and Healthcare Settings

Board 506: Hospitalization for Respiratory Infections, ICU and Mechanical Ventilation in the United States, Using Medical Claims Data

Board 507: Middle East Respiratory Syndrome Coronavirus Infection of New Zealand Rabbits

Board 508: Mathematical Model to Calculate Cost-effectiveness of Vaccination Against Influenza in the Republic of Kazakhstan, 2014

Board 509: Laboratory Monitoring for Influenza Under the Influenza Sentinel Surveillance During the 2013-2014 Epidemic Season in West Kazakhstan Province, Republic of Kazakhstan

Board 510: Influenza Trends in an Urban Area of Indonesia, 2011 - 2014

Board 511: Tailoring the Timing of Influenza Public Health Measures to Local Needs: Experience from East Jakarta District in Indonesia

Board 512: Healthcare Seeking Behavior for Respiratory Illness in a Northern Province of Vietnam

Board 513: Seasonality of Circulating Influenza Types and Subtypes in a Rural Indian Community Under Active Surveillance

Board 514: The Impact of Seasonal Influenza Vaccination Among Persons 60 Years and Older on Rates of Influenza-associated Mortality and Hospitalization from 1994 to 2009 in São Paulo State, Brazil

Board 515: Immunity to Influenza A (H3N2v) Virus in Semirural Communities in Peru

Bacterial/Viral Co-Infections

Board 516: Potential Impact of Co-infections and Co-morbidities Prevalent in Africa on Influenza Severity and Frequency: A Systematic Review

Board 517: Investigation of Other Respiratory Viruses in Influenza Negative Samples in Sentinel Sites, Burkina Faso, 2010-2012

Board 518: Prevalence of Respiratory Viruses Among Hospitalized Children Under 5 Years with Severe Acute Lower Respiratory Infection in Kashmir, North India

Novel Agents of Public Health Importance

Board 519: Salivirus in Children and Its Association with Childhood Acute Gastroenteritis: A Paired Case-control Study

Board 520: Clinical and Pathological Evaluation of a Large Outbreak of *Mycobacterium marinum* Skin Infections Associated with Fish Markets in New York City

Board 521: Chikungunya Surveillance in New York City, 2014

Board 522: Serial RNA Detections of Middle Eastern Respiratory Syndrome Coronavirus (MERS-CoV) Among Laboratory Confirmed Cases—Abu Dhabi, United Arab Emirates, 2013-2014

Board 523: The Epidemiology of Invasive *Haemophilus influenzae* (nontype b) Disease—Ontario, Canada: 2004-2013

Tuberculosis

Board 524: Evaluating Cell-mediated Immune Response and the Role of Transfer Factor in Immunotherapy of Tuberculosis

Board 525: Tuberculosis Contact Investigation at an Island Resort in Michigan, 2014

Infectious Causes of Chronic Diseases

Board 526: Hantavirus Infection in Ho Chi Minh City, Vietnam: A Case Report, 2013

Board 527: Mutational Analysis of Hepatitis E Virus ORF1 "X-Domain" Identifies an Evolutionary Conserved Macrodomain Protein/Appr-1"-pase Active-site, Critical for Virus Replication

Viral Hepatitis

Board 528: Burden and Factors Associated with Sero-positivity to Hepatitis C Virus Among Hospital Attendees in Plateau State, Nigeria

Emerging Aspects of HIV

Board 529: HIV Molecular Epidemiology: How Much Have We Missed?

Board 530: Determinants of Infant-feeding Choices of HIV-positive Women Attending Prevention of Mother-to-child Transmission Clinics in Oyo State, Southwestern Nigeria, 2013

Board 531: Risk Perception for HIV Infection Using Multi-stage Stratified Random Cross-sectional Survey, South Africa, 2012

Sexually Transmitted Diseases

Board 532: Epidemiology of *Chlamydia trachomatis* and *Neisseria gonorrhoeae* in Air Force and Navy Beneficiaries

Board 533: Antimicrobial Susceptibility Pattern and Molecular Characterization of Resistance Genes of *Neisseria gonorrhoeae* Isolates in Bhutan

Board 534: Seroprevalence and Seroincidence of Herpes Simplex Virus (2006-2010) and Vaccine-preventable Human Papilloma Virus Subtypes (2000-2010) Among United States Military Personnel

Board 535: Antibiotic Resistance in *Neisseria gonorrhoeae* Isolates from Five Clinics in Accra and the Western Region of Ghana

Board 536: Occupational Factors and Their Influence on Sexually Transmitted Infections in Active Duty Air Force Members

Late Breakers II

Board LB-11: Chromogenic Clinical Media to Quantify Antimicrobial Resistant Enteric Bacteria in Environmental Samples as an Indicator System for Environmental Surveillance

Board LB-12: Biomarkers on Patient T Cells Diagnose Active Tuberculosis and Monitor Treatment Response

Board LB-13: The Tale of Two Neglected Tropical Infections: Using GIS to Assess the Spatial and Temporal Overlap of Schistosomiasis and Leprosy in a Region of Minas Gerais, Brazil

Board LB-14: Risk Assessment for Local Dengue Virus Transmission During a Binational Dengue Outbreak on the United States–Mexico Border—Yuma County, Arizona, October–December 2014

Board LB-15: Introduction of Mosquito-borne Diseases into Non-endemic Locations: Infected Human Travelers Versus Mosquitoes

Board LB-16: The U.S. Department of Defense Experience with Chikungunya Following Introduction of CHIKV into the Americas, January 2014–February 2015

Board LB-17: MERS-CoV: When Men Kiss Camels—An Anthropological Study About Human-Camel Relationships in Qatar

Board LB-18: An Investigation of a Potential Increase in Pertussis Cases Identified Through Sentinel Surveillance in South Africa, June 2012–December 2014

Board LB-19: Vaccination, Contact Precautions and Antivirals: What Best Controls Influenza Spread in a Hospital?

Board LB-20: Lassa Fever and Contact Tracing in a Large Population

M. Concurrent Panel Sessions

1:45 PM - 3:15 PM

M1. Social Determinants of Emerging Infectious Diseases

International Ballroom South

Moderators:

Sharon Ricks; U.S. Dept. of Health and Human Services, Region IV, Atlanta, GA

Scott Santibanez; Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Use of Area-based Socioeconomic Measures for Analyzing Surveillance Data and Monitoring Trends in Disparities
James Hadler; Yale School of Public Health, New Haven, CT

The Role of Hispanic Origin and Nativity in Hispanic Health
Ken Dominguez; Centers for Disease Control and Prevention, Atlanta, GA

Religion as an Invisible Determinant of Health: Its Role in Shaping Life Conditions Around the World and in Ongoing Epidemics
Ellen Idler; Emory University, Atlanta, GA

M2. Current Issues in Sexually Transmitted Diseases

Centennial Ballroom I

Moderators:

Sarah Kidd; Centers for Disease Control and Prevention, Atlanta, GA

Jacqueline Lawler; National Association of County and City Health Officials, Newburg, NY

Speakers:

The Making of a Superbug: Updates on Antibiotic-resistant Gonorrhea
Robert Kirkcaldy; Centers for Disease Control and Prevention, Atlanta, GA

The Reemergence of Syphilis among Men Who Have Sex with Men
Khalil Ghanem; Johns Hopkins University School of Medicine, Baltimore, MD

Pre-exposure Prophylaxis for HIV Prevention: Bridging the Gaps
Mark Thrun; Gilead Sciences, Denver, CO

M3. Pathogen Discovery and Investigation of New Syndromes

Centennial Ballroom II

Moderators:

Sam Dominguez; Pediatric Infectious Diseases Society, Aurora, CO

Denise Pettit; Association of Public Health Laboratories, Raleigh, NC

Speakers:

Development of a Next Generation Sequence Platform for Clinical Diagnosis and Novel Pathogen Discovery
Charles Chiu; University of California, San Francisco, San Francisco, CA

Pathologic Approach to Investigation of New Syndromes and Pathogen Discovery
Sherif Zaki; Centers for Disease Control and Prevention, Atlanta, GA

Discovering Novel Viral Lineages in Bat Populations: Public Health Implications
Suxiang Tong; Centers for Disease Control and Prevention, Atlanta, GA

M4. New Data Systems/Platforms for Surveillance
Centennial Ballroom III

Moderators:

Paul Freeman; American Public Health Association, Seattle, WA

Robert Pinner; Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

CDC Surveillance Strategy and a Shared Surveillance Data Platform
Brian Lee; Centers for Disease Control and Prevention, Atlanta, GA

Uber Operations
Eduardo Loumiet; Uber Operations, Tallahassee, FL

CalREDIE Surveillance System
James Watt; California Department of Public Health, Richmond, CA

Public Health Surveillance Architecture and the National Healthcare Safety Network
Barry Rhodes; Centers for Disease Control and Prevention, Atlanta, GA

M5. Respiratory Diseases
Centennial Ballroom IV

Moderators:

Stephen Hadler
Cynthia Whitney
Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Tracking Travel-associated Legionnaires' Disease in Europe
Birgitta de Jong; European Centre for Disease Prevention and Control, Stockholm, Sweden,

RSV Maternal Immunization
Flor Munoz-Rivas; Baylor College of Medicine, Houston, Texas

Pneumococcal Conjugate Vaccine Effects on Severe Disease in South Africa—the First 5 Years
Cheryl Cohen; National Institute for Communicable Diseases, Johannesburg, South Africa

M. Oral Presentations
1:45 PM - 3:15 PM

M6. Tropical and Zoonotic Infections
International Ballroom North

Moderators:

Seth Irish
Audrey Lenhart
Centers for Disease Control and Prevention, Atlanta, GA

1:45 PM - 2:00 PM

First Outbreak of Locally Acquired Hepatitis E Virus Infection in Australia
C. Yapa; Health Protection NSW, Sydney, Australia

2:00 PM - 2:15 PM

Epidemiology of Ebola Virus Disease and Impact of Isolation and Treatment in Remote Outbreaks in Liberia
K. A. Lindblade; CDC-Thailand, Bangkok, Thailand, and Centers for Disease Control and Prevention, Atlanta, GA

2:15 PM - 2:30 PM

Ebola Virus Disease Outbreak in Nigeria: Investigation and Epidemiological Profile of Affected Persons, July-September 2014
E. B. Adedire; Nigerian Field Epidemiology and Laboratory Training Program, Abuja, Nigeria

2:30 PM - 2:45 PM

The Epidemiology and Clinical Features of *Balamuthia mandrillaris* Disease in the United States, 1974 - June 2014
J. Gomez; Mississippi State University College of Veterinary Medicine, Starkville, MS

2:45 PM - 3:00 PM

Comparing the Natural History of Human Nipah Infection in Bangladesh by Route of Exposure
H. M. Sazzad; International Centre for Diarrhoeal Diseases Research, Bangladesh (ICDDR,B), Dhaka, Bangladesh

3:00 PM - 3:15 PM

Severe Fever with Thrombocytopenia Syndrome Has Long Been Circulating in South Korea: A 6-year Study
K-H. Kim; Pusan National University School of Medicine, Busan, South Korea

Break
3:15 PM – 3:30 PM | Centennial Foyer

N. Oral Presentations
3:30 PM - 5:00 PM

N1. Healthcare-Associated Infections
Centennial Ballroom I

Moderators:
Brandi Limbago
J. Todd Weber
Centers for Disease Control and Prevention, Atlanta, GA

3:30 PM - 3:45 PM

Treatment and 12-month Outcomes Among Patients with Fungal Meningitis (FM) and Epidural Abscess (EA) Due to Contaminated Epidural Methylprednisolone Acetate (MPA) Injections—United States, 2012-2013
O. McCotter; Centers for Disease Control and Prevention, Atlanta, GA

3:45 PM - 4:00 PM

Geographic Distribution of CRE Cases in Tennessee Informs a Regional Strategy to Strengthen Prevention Practices and Control Measures in Healthcare Facilities
M. A. Kainer; Tennessee Department of Health, Nashville, TN

4:00 PM - 4:15 PM

Shedding of Nipah Virus and Contamination of Hospital Surfaces During an Outbreak in Bangladesh, 2013-2014
M. Z. Hassan; International Centre for Diarrhoeal Diseases Research, Bangladesh (ICDDR,B), Dhaka, Bangladesh

4:15 PM - 4:30 PM

Validation of Risk Score to Identify Future *Clostridium difficile* Infection Following Hospital Discharge in a Cohort of Hospitals Submitting Data to a Hospital Drug Database
J. Baggs; Centers for Disease Control and Prevention, Atlanta, GA

4:30 PM - 4:45 PM

Importance of Adherence to Targeted Screening for *Strongyloides stercoralis* Infection in Solid Organ Transplantation
F. Abanyie; Centers for Disease Control and Prevention, Atlanta, GA

4:45 PM - 5:00 PM

Healthcare-associated Outbreak of Legionnaires' Disease in a Leukemia Unit—Alabama, 2014
L. Francois Watkins; Centers for Disease Control and Prevention, Atlanta, GA

N2. Respiratory Diseases
International Ballroom North

Moderators:
Larry Anderson
Michael Shaw
Centers for Disease Control and Prevention, Atlanta, GA

3:30 PM - 3:45 PM

Direct and Indirect Benefits of Pediatric Influenza Immunization on US Hospitalizations
C. Viboud; National Institutes of Health, Bethesda, MD

3:45 PM - 4:00 PM

Use of Disease Clusters to Estimate Severity of H7N9 Infection in China
M-A. Widdowson; Centers for Disease Control and Prevention, Atlanta, GA

4:00 PM - 4:15 PM

Viral Identification in Children with Previously Undiagnosed Pneumonia
K. Queen; Centers for Disease Control and Prevention, Atlanta, GA

4:15 PM - 4:30 PM

Human Adenovirus Infections Associated with Severe Respiratory Disease, Oregon, 2013-2014
C. Chommanard; Centers for Disease Control and Prevention, Atlanta, GA

4:30 PM - 4:45 PM

Enhanced Transmission of *Streptococcus pneumoniae* Serotype 5 Among Unaccompanied Children with Severe Respiratory Infections
M. Kobayashi; Centers for Disease Control and Prevention, Atlanta, GA, USA

4:45 PM - 5:00 PM

Synthesizing Data and Models for the Spread of MERS-CoV, 2013: Key Role of Index Cases and Hospital Transmission
G. Chowell; Arizona State University, Tempe, AZ

N3. Advances in Microbial Detection and Characterization
Centennial Ballroom II

Moderators:
Duncan MacCannell
Scott Sammons
Centers for Disease Control and Prevention, Atlanta, GA

3:30 PM - 3:45 PM

Quality Laboratory Systems in an Era of Emerging Technologies and Infectious Disease Threats
M. Sullivan; Minnesota Department of Health, St. Paul, MN

3:45 PM - 4:00 PM

Simultaneous Detection and Identification of Thirty-one Enteric Bacteria, Viruses and Parasites Associated with Gastroenteritis Using PCR Assay: Five Real-time Multiplex Reactions and Its Clinical Application
Q. Hu; Shenznen Center for Disease Control and Prevention and Shenzhen University, Shenzhen, China

4:00 PM - 4:15 PM

Next Generation Molecular Epidemiology for Pathogenic Fungal Outbreaks
D. M. Engelthaler; Translational Genomics Research Institute, Flagstaff, AZ

4:15 PM - 4:30 PM

Advanced Molecular Detection of Waterborne and Zoonotic Pathogen *Cryptosporidium*
L. Xiao; Centers for Disease Control and Prevention, Atlanta, GA

4:30 PM - 4:45 PM

Employing Short Read Pneumococcal Whole Genome Sequence Data for Routine Extraction of Invasive Strain Parameters and for Fine Resolution of a Disease Cluster
B. Beall; Centers for Disease Control and Prevention, Atlanta, GA

4:45 PM - 5:00 PM

Rapid Identification of Mycobacteria from Paraffin-embedded Pulmonary and Extrapulmonary Tissue Biopsies of Patients by Multigene Targeted PCR and Sequencing: Implications for Diagnostic Pathology
J. Bhatnagar; Centers for Disease Control and Prevention, Atlanta, GA

N4. Surveillance II

International Ballroom South

Moderators:

Lori Armstrong
Eleanor Click
Centers for Disease Control and Prevention, Atlanta, GA

3:30 PM - 3:45 PM

The EpiCore Project: Improving Non-traditional Outbreak Detection Through Collaboration with Field Epidemiology Training Programs (FETPs)
J. Olsen; The Skoll Global Threats Fund, San Francisco, CA

3:45 PM - 4:00 PM

Identification of Potential Source Cases for Young Children with Tuberculosis Infection—New York City, 2006-2012
J. M. Sanderson; New York City Department of Health and Mental Hygiene, Bureau of Tuberculosis Control, New York, NY, and Centers for Disease Control and Prevention, Atlanta, GA

4:00 PM - 4:15 PM

Analysis of Surveillance Data: Trends of Priority Health Problems in Afghanistan from 2007 to 2012
K. Islam Saeed; Afghan National Public Health Institute, Kabul, Afghanistan

4:15 PM - 4:30 PM

Results from the Centers for Disease Control and Prevention's "Predict the 2013-2014 Influenza Season Challenge," United States
M. Biggerstaff; Centers for Disease Control and Prevention, Atlanta, GA

4:30 PM - 4:45 PM

Integrated Food Safety Centers of Excellence (CoEs): Strengthening State and Local Capacity for Foodborne Illness Surveillance and Outbreak Response
E. Pace; Centers for Disease Control and Prevention, Atlanta, GA

4:45 PM - 5:00 PM

The Global Landscape of Participatory Disease Surveillance
M. S. Smolinski; The Skoll Global Threats Fund, San Francisco, CA

N5. Foodborne Diseases II

Centennial Ballroom III

Moderators:

John Besser
Robert Tauxe
Centers for Disease Control and Prevention, Atlanta, GA

3:30 PM - 3:45 PM

Emergence of *Salmonella* Typhimurium in Australia, 2000-2013
M. Kirk; Australian National Universtiy, Acton, Australia

3:45 PM - 4:00 PM

Traceback and Intensified *Salmonella* Testing Approach—a Regional Investigation of Multidrug Resistant *Salmonella* Heidelberg Illnesses Associated with Consumption of Company A Brand Chicken
A. Douris; US Department of Agriculture, Food Safety and Inspection Service, Athens, GA

4:00 PM - 4:15 PM

Giardiasis and Subsequent Irritable Bowel Syndrome: A Longitudinal Study Using Health Insurance Billing Data
J. H. Nakao; Centers for Disease Control and Prevention, Atlanta, GA

4:15 PM - 4:30 PM

A Multi-district *Streptococcus suis* Outbreak Associated with Undercooked Pork Consumed in Chiang Mai Province, Thailand, During July - August 2013
P. Lekcharoen; Ministry of Public Health, Bangkok, Thailand, and Mahidol University, Nakorn Pathom, Thailand

4:30 PM - 4:45 PM

Knowledge, Attitude and Practices Regarding Brucellosis Infection Among Smallholder Farming and Pastoral Populations in Kenya, 2012
E. Ogola; Kenya Medical Research Institute, Kisumu, Kenya

4:45 PM - 5:00 PM

A National Outbreak of Shiga-toxin producing *E. coli* in England, August to September 2014
L. Byrne; Public Health England, London, United Kingdom

N6. Late Breakers II

Centennial Ballroom IV

Moderators:

Joel Montgomery
Monica Parise
Centers for Disease Control and Prevention, Atlanta, GA

3:30 PM - 3:45 PM

Ebola Virus Disease Outbreak in Lagos State, Nigeria, July–September 2014: An Epidemiological Investigation
F. F. Osundina; Nigeria Field Epidemiology and Laboratory Training Programme (NFELTP), Abuja, Nigeria

3:45 PM - 4:00 PM

Emergence of Serogroup C *Neisseria meningitidis*, Niger—2015
M. Zaneidou; Niger Ministry of Health, Niamey, Niger

4:00 PM - 4:15 PM

Risk Factors Associated with the Fatal Henipah Virus Outbreak Infection in Sultan Kudarat, Mindanao, Philippines, 2014
P. G. Ching; Epidemiology Bureau, Department of Health, Manila, Philippines

4:15 PM - 4:30 PM

Demographic Groups Affected by Increase in Campylobacteriosis, Connecticut 2005–2014
P. J. Clogher; Yale School of Public Health, New Haven, CT

4:30 PM - 4:45 PM

A Collaborative Approach to Reducing the Risk of *Salmonella* Newport Linked to Produce Grown on the Delmarva Peninsula
K. Gensheimer; Food and Drug Administration, College Park, MD

4:45 PM - 5:00 PM

Outbreak Investigation of Primary Amoebic Meningoencephalitis Caused by *Naegleria fowleri*—Karachi, Pakistan, 2012–2014 (with 2015 update)
S. A. Memon; Pakistan Field Epidemiology and Laboratory Training Program, Islamabad, Pakistan

Poster and Oral Presentation Abstracts

Molecular Epidemiology

Monday, August 24, 12:30 PM - 1:45 PM

Grand Hall

Board 1. Surveillance System in Guangdong, China: Serovar Distribution, Antimicrobial Resistance Profiles, and PFGE Typing of *Salmonella enterica* Strains

J. Sun[1], B. Ke[2], D. He[2], X. Deng[2], C. Ke[2]; [1]Guangdong Provincial Inst. of Publ. Hlth., Guangdong Provincial CDC, Guangzhou, China, [2]Guangdong Provincial CDC, Guangzhou, China

Background: *Salmonella enterica* includes the major serovars associated with human salmonellosis. In this study, 1,764 clinical *Salmonella enterica* isolates from diarrhea outpatients were collected from fifteen cities in Guangdong Province, China, between 2007 and 2012. **Methods:** The isolates were characterized by serovar determination, antimicrobial susceptibility tests, and PFGE fingerprint typing. **Results:** The serovar distribution results demonstrated that *Salmonella* Typhimurium (29.65%) and *Salmonella* 4,5,12:i:- (13.83%) are the most common serovars causing infant salmonellosis, whereas *Salmonella* Enteritidis (14.57%) mainly causes human salmonellosis in adults. The serovar shift from *Salmonella* Enteritidis to *Salmonella* Typhimurium occurred in 2008. Antimicrobial susceptibility data showed a high burden of multidrug resistance (MDR) (56.58%), and a 20%-30% increase in the number of isolates resistant to ciprofloxacin (8.05%) and cephalosporins (4.99%) from 2007-2012. Only 9.97% of isolates were fully susceptible to all agents tested. A high burden of MDR was observed in *Salmonella* Typhimurium and *Salmonella* 4,5,12:i:- for all age groups, and a reduced susceptibility to third-generation cephalosporins and quinolones occurred particularly in infants. The dominant PFGE patterns were JPXX01.GD0004, JEGX01.GD0006, JEGX01.GD0007, JNGX01.GD0006, JNGX01.GD0007. ACSSuT was the predominant MDR profile in the *Salmonella* Typhimurium & S. 4,5,12:i:- clonal complexes. The predominant PFGE patterns of the *Salmonella* Typhimurium & S. 4,5,12:i:- clonal complexes and *Salmonella* Stanley were most prevalent in infants. However, no obvious relationship was observed between these PFGE profiles and geographic location. **Conclusions:** These data reveal the serovar distribution of isolates recovered from diarrhea patients, the characteristics of resistant strains and fingerprint typing in Guangdong from 2007 to 2012. These results highlight a serovar shift and a worrying percentage of MDR strains with increasing resistance to quinolones and third-generation cephalosporins. Thus, continued surveillance of *Salmonella* and their MDR profiles using combined molecular tools and efforts to control the rapid increase in antimicrobial resistance among *Salmonella* in Guangdong are needed.

Board 2. The Molecular Epidemiology Characteristics and Genetic Diversity of *Salmonella* Typhimurium in Guangdong, China

D. He, J. Sun, B. KE, Y. Huang, X. Li, Z. Liang, C-W. Ke; Guangdong Provincial CDC, Guangzhou, China

Background: *Salmonella enterica* serovar Typhimurium is the most important serovar associated with human salmonellosis worldwide. Here we aimed to explore the molecular epidemiology and genetic characteristics of this serovar in Guangdong, China. **Methods:** We evaluated the molecular epidemiology and genetic characteristics of 294 endemic *Salmonella* Typhimurium clinical isolates which were collected from 1977 to 2011 in Guangdong, China, and compared them with a global set of isolates of this serovar using epidemiological data and Multilocus Sequence Typing (MLST) analysis. **Principal finding:** The 294 isolates were assigned to 13 sequencing types (STs) by MLST, of which ST34 and ST19 were the most common in Guangdong. All the STs were further assigned to two eBurst Groups, eBG1 and eBG138. The eBG1 was the major group endemic in Guangdong. Nucleotide and amino acid variability were comparable for all seven MLST loci. Tajima's D test suggested positive selection in *hisD* and *thrA* genes ($p<0.01$), but positive selection was rejected for the five other genes ($p>0.05$). In addition, The Tajima's D test within each eBG using the global set of isolates showed positive selection in eBG1 and eBG138 ($p<0.05$), but was rejected in eBG243 ($p>0.05$). We also analyzed the phylogenetic structure of *Salmonella* Typhimurium from worldwide sources and found that certain STs are geographically restricted. ACSSuT was the predominant multidrug resistance pattern for this serovar. The resistant profiles ACSSuTTmNaG, ACSSuTTmNa and ACSuTTmNaG seem to be specific for ST34, and ASSuTNa for ST19. **Conclusion:** Here we presented a genotypic characterization of *Salmonella* Typhimurium isolates using MLST, and found two major STs are endemic in Guangdong. Our analyses indicate that genetic selection may have shaped the *Salmonella* Typhimurium populations. However, further evaluation with additional isolates from various sources will be essential to reveal the scope of the epidemiological characteristics of *Salmonella* Typhimurium in Guangdong, China.

Board 3. Examination of PulseNet Data to Assess the Utility of Pulsed-field Gel Electrophoresis (PFGE) for *Campylobacter* Outbreak Investigations

L. A. Joseph, S. G. Stroika, M. C. Judd, C. Fitzgerald, K. B. Hise, M. M. Freeman; CDC, Atlanta, GA, USA

Background: *Campylobacter* species are a leading cause of bacterial diarrheal illness in the United States. In 2004, the Centers for Disease Control and Prevention (CDC) established the PulseNet *Campylobacter* National database. We evaluated these data to determine whether PFGE is beneficial during *Campylobacter* outbreak investigations. **Methods:** PFGE patterns were generated using the PulseNet *Campylobacter* protocol by public health laboratories and the CDC PFGE Reference Laboratory. *Sma*I (primary enzyme) and/or *Kpn*I (secondary enzyme) PFGE patterns were uploaded to the database, analyzed using BioNumerics, and named in accordance with PulseNet pattern naming guidelines. **Results:** Between January 2004 and January 2015, 17,292 isolates (73% clinical) were uploaded to the database. The top 10 *Sma*I patterns (out of 3,243 unique patterns) were associated with 269 unique *Kpn*I patterns. Of the 85 campylobacteriosis clusters identified in the database, 28 (33%) had corresponding epidemiological information and were examined in this study. *Sma*I and *Kpn*I patterns were available for 518 of the 565 (92%) isolates in the 28 selected clusters; however, only 6,057of the 17,292 (35%) total isolates uploaded to the database had been tested by both enzymes. A single *Sma*I/*Kpn*I pattern combination was observed in 14 (50%) clusters; multiple *Sma*I and/or *Kpn*I patterns were observed in the remaining 14 (50%) clusters. The seven most common *Sma*I/*Kpn*I pattern combinations in the database contributed to 10 (36%) of the selected clusters suggesting

that there is not much diversity among strains implicated in these clusters/outbreaks. **Conclusions:** PFGE is informative for *Campylobacter* outbreak investigations. Because *Kpn*I often differentiates isolates with an indistinguishable *Sma*I pattern, it is essential to use both enzymes when analyzing suspected outbreak-associated isolates. It is also important to always interpret PFGE data in the context of epidemiological data, especially when potential outbreaks include multiple *Sma*I and/or *Kpn*I patterns. Currently, we are determining how whole genome sequence data will improve on the ability of PFGE to discriminate among putative outbreak-associated *Campylobacter* isolates.

Board 4. Distribution of Hepatitis C Virus Genotypes in the United Arab Emirates

H. Alnuaimi, B. Hamarsheh, W. Tariq; Tawam Hosp., Al Ain, United Arab Emirates

Objective: To determine the distribution of HCV genotypes among the patients attending Tawam hospital in Al-Ain, UAE. **Methods:** This was a descriptive study using laboratory results from January 2013 to June 2014 in molecular lab at Tawam hospital. The study was designed to include patient's demographics, and nationality. The patients with positive screening test for HCV antibodies referred from the other clinics and peripheral health centers were included in the study. The blood sample was collected and the confirmation of HCV was done by Western blot. The confirmed cases were subjected for HCV RNA levels and subsequently for HCV genotyping and sub-typing. **Results:** A total of 161 patients (36 UAE nationals and 125 expatriates). Among the UAE nationals, 50% had genotype 1, 5.56% had 3, 30.56% had 4 and only 2.78% patients had genotype 2. On the other hand 85.84% Egyptians had genotype 4 and 75% Pakistanis had genotype 3. **Conclusion:** In this study high prevalence of genotype 1 followed by 4 and 3 was seen in UAE nationals which is in contrast to the earlier reports of genotypes 4 being most common in Middle East countries. Among expatriates, genotype 4 was common in Egyptians and 3 in Pakistanis.

Board 5. Multi-locus VNTR-based Diversity of Emerging Monophasic Variant of Serovar Typhimurium for French Outbreak Investigation

A. Brisabois, B. Glasset, S. Granier, R. Lailler, S. Cadel-Six; ANSES, Maisons-Alfort, France

Background: The genus *Salmonella* is one of the most prevalent pathogens involved in foodborne infections worldwide. As monitoring data point out, monophasic variant of serovar Typhimurium (1,4,[5],12:i:-) has been emerging strongly in human, food, and animal sectors for several years. The aim of this study was to evaluate the performance of the Multi-Locus VNTR Analysis (MLVA) for studying genomic diversity of these emerging monophasic variants strains, and the ability for foodborne outbreak investigations. **Methods**: A collection of 210 selected monophasic isolates recovered from various animal and food sources from the *Salmonella* network during two French outbreak periods in 2011 was investigated. Monophasic variant isolates were identified with conventional slide agglutination and confirmed with the EFSA-based PCR protocol targeting presence of *fljB* gene and intergenic region *fliA-fliB*. Then, Multi-Locus VNTR analysis (MLVA) was carried out on the set of strains as well the gold standard reference typing method (PFGE). All molecular typing data were analyzed using the BioNumerics software and standard minimum spanning trees were generated using single and double locus variance priority rules. **Results:** Thirty-nine MLVA profiles resulting from the combination of five VNTR loci were obtained out of which 6 major profiles represented 65% of the studied strains. Among the six main MLVA profiles, two of them were mainly identified in clinical human strains during the two outbreak periods. The first one epidemic MLVA profile was highly identified in dairy products in agreement with a food alert of contaminated milk occurred in a French region. The second one epidemic profile was attributed to pork products as 84% isolates from pork source harbored this profile. Finally, MLVA showed a high capacity for strain discrimination with a Simpson's diversity index of 0.96. Moreover, the most frequently encountered PFGE profile of monophasic variant was split in 17 different MLVA profiles. **Conclusion**: This study underlines the high genetic diversity of the monophasic variant of Typhimurium among animal and food sources and highlights MLVA as a powerful suitable method for epidemic clone identification and outbreak investigation in complement to epidemiological data with a high benefit for public health.

Board 6. Interspecies Transfer of Plasmids Harboring Resistance Genes in a Patient with *Klebsiella pneumoniae* Carbapenemase (KPC)-producing Carbapenem-resistant Enterobacteriaceae (CRE)

K. Shaw[1], T. Johnson[2], M. Hargreaves[1,3], P. Vagnone[1], J. Harper[1], R. Lynfield[1]; [1]Minnesota Dept. of Hlth., St. Paul, MN, USA, [2]Univ. of Minnesota, St. Paul, MN, USA, [3]CDC/APHL Emerging Infectious Diseases Res. Fellowship, St. Paul, MN, USA

Background: Carbapenemase-producing (CP) CRE are an emerging threat. CP-CRE are highly resistant and can spread rapidly in healthcare facilities through clonal dissemination or plasmid transfer of resistance genes. We describe epidemiologic characteristics of a patient harboring 2 species of KPC-producing CRE and genetic characterization of isolates collected. **Methods:** From March-May 2012, we received 10 CRE reports (3 *Enterobacter cloacae* [2 sputum, 1 blood]; 7 *Escherichia coli* [4 sputum, 3 urine]) on a 53 year-old male through routine CRE surveillance; 9 isolates (2 *E. cloacae*, 7 *E. coli*) underwent molecular testing for carbapenemases. Whole genome sequencing (WGS), plasmid profiling and resistance gene typing were also performed on isolates. Medical records were reviewed. **Results:** The patient had a complex medical history including cancer of lung and brain, multiple indwelling devices, and a history of exposure to multiple healthcare settings. He had pneumonia, bloodstream infection and possible urinary tract infection (UTI) with CRE during the 3 months preceding his death. Of 9 isolates tested, 7 were KPC positive by PCR (2 *E. cloacae,* 5 *E. coli*); these were isolated during different time periods. One KPC-positive *E. coli* isolate belonged to the *H*30-R subtype of sequence type 131 (ST131), a predominant extraintestinal strain. Plasmid profiles revealed 2 plasmids (pIncX-SHV; pNJST258N2-like plasmid encoding bla_{KPC}) with multiple resistance genes which were identical in KPC-positive *E. cloacae* and *E. coli* isolates. **Conclusions:** We identified a patient with 2 species of Enterobacteriaceae that produced KPC. Subsequent WGS and plasmid analysis provided evidence of horizontal plasmid transfer of *Klebsiella*-derived plasmids encoding multiple resistance genes between *E. cloacae* and *E. coli*. Identification of *E. coli H*30-R ST131 harboring KPC is particularly concerning because *E. coli* ST131 has recently emerged as the dominant cause of healthcare-associated UTIs, and are commonly resistant to fluoroquinolones and third-generation cephalosporins. The dissemination of such highly resistant pathogens in healthcare settings poses a substantial threat. Surveillance for these organisms is important to determine prevalence and evaluate impact of prevention measures.

Board 7. Optical Mapping and Genome Sequences of Isolates of *Bartonella bacilliformis*

V. N. Loparev, G. A. Dasch, K. M. Knipe, L. A. Rowe, S. L. Lydy; CDC, Atlanta, GA, USA

Background: Pulsed field gel electrophoresis (PFGE), multilocus sequence typing (MLST), amplified-fragment length polymorphism analysis, and intergenic region sequence typing (IGR) are all effective methods for detecting genetic diversity among species and isolates of *Bartonella. B. bacilliformis* (Bb), the etiologic agent of acute Oroya fever and chronic verruga peruana in humans, is sand fly transmitted, and exhibits substantial diversity by MLST and IGR typing. **Methods:** Optical maps of chromosomal DNAs of 36 isolates of Bb were obtained and compared with complete Illumina and Pacific Biosciences genomic sequences of representative MLST/IGR types. **Results:** NcoI was employed for all Bb isolates while BamHI was also excellent. The optical map for reference strain KC583 was nearly identical to that predicted from the complete genome sequences of KC583. Optical mapping clades agreed with MLST/IGR types but detected more genetic variation. Inversions and translocations were identified in some types relative to KC583. The optical maps of Bb were markedly different from those predicted from the complete genome sequences of other species of *Bartonella*. **Conclusions:** Optical mapping of Bb isolates was much simpler, higher resolution, and more rapid than PFGE, MLST, and IGR typing but largely confirmed the previous groupings of Bb isolates obtained by MLST and IGR typing. The outlier MLST/IGR/OpGen type (isolates Vega, Ver097, Peru53, Ramirez) may be a new species. It is intermediate between the newly named *B. ancashi* and the other MLST/IGR groups of Bb from Peru. These isolates all cause similar clinical manifestations but may be transmitted by different vector species.

Board 8. Detection of Human Bocavirus Types 1 and 3 in Egyptian Children with Acute Gastroenteritis

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Background: Human bocavirus (HBoV) is associated with respiratory and enteric infections. The genome has two major ORFs encoding nonstructural proteins (NS1, NP1) and a third ORF that encodes two structural capsid proteins (VP1 and VP2). Based on sequences of these regions, there are four HBoVs species, HBoV1, HBoV2, HBoV3 and HBoV4. All these are detected in diarrheal specimens, stressing gastrointestinal tropism. We studied the prevalence of HBoV in a cohort of symptomatic children seeking medical care at Abu Homos Hospital in the Nile Delta of Egypt during 2006-2007. **Methods:** Stool samples from 364 patients < 5 years of age were screened for HBoV. Genomic DNA was extracted using QIagen DNA mini kit, and NS1 gene was amplified by PCR. Partial genome sequences of NS1 positive cases were obtained using BigDye® Terminator v3.1 Cycle Sequencing Kit and verified against GeneBank databases. Other enteric viruses were detected by RT-PCR. **Results:** Among 364 diarrheal stool samples, 35 (9.6%) were positive for HBOV. Rotavirus was detected in 79 samples (21.7%), norovirus in 39 samples (10.7%), astrovirus in 21 samples (5.8%), and adenovirus in seven samples (2.0%). None of the HBoV-positive patients reported concomitant respiratory symptoms, but showed fever (5.7%), vomiting (94.3%), and bloody diarrhea (8.6%), with 22.9% hospitalized. HBoV1 was predominant (n=30, 86%), with high sequence homology to Brazilian and Chinese strains. The rest of the strains were HBoV3 (n=5, 14%), displayed nucleotide diversity from those reported globally. Co-infection with other enteric viruses was found in 37% of HBoV-positive samples. Rotavirus cases belonged mainly to genotype G2P4, while astrovirus included the novel MLB1 and VA2, with type I being most prevalent. Genotype GII norovirus was the only genotype identified, while adenovirus types 40/41, 1, 2, and 5 characterized the positive cases. **Conclusions:** This is the first report of the detection and genetic characterization of HBoV in Northern Africa. Interestingly, Bocavirus was the sole diarrheagenic agent in 63% of gastroenteritis cases. Understanding of the genetic diversity of enteric viral families will assist in future studies of pathogenicity and distribution of these etiologic agents as well as guide health care officials in presentation of disease and carer of patients.

Board 9. Emergence of Norovirus GI.3 Outbreaks in the United States, 2013-2014

L. Barclay, M. E. Wikswo, N. Gregoricus, A. J. Hall, J. Vinje; CDC, Atlanta, GA, USA

Background: Norovirus is the leading cause of epidemic and sporadic gastroenteritis in the United States. Although the majority of outbreaks are caused by GII.4 viruses, several other genotypes co-circulate at lower levels throughout the year. During the 2013-2014 seasonal year (September-August), we observed an increase in the number of GI.3 outbreaks reported to CaliciNet compared to previous years. To further investigate this emergence, we compared epidemiological characteristics of GI.3 and non-GI.3 outbreaks. **Methods:** Genotype data from norovirus outbreaks were extracted from CaliciNet and matching outbreaks were supplemented with epidemiologic data from the National Outbreak Reporting System (NORS). Stool specimens from 60 GI.3 outbreaks from 2013-2014 were further characterized by sequencing of the P2 region of the genome and compared with GI.3 sequences from 2009-2013 outbreaks. **Results:** From September 2009-August 2013, 4007 norovirus outbreaks were reported to CaliciNet, of which the proportion of GI.3 outbreaks ranged from 1.5% - 3.9% per year (109 GI.3 outbreaks in total). During the 2013-2014 seasonal year, the number of GI.3 outbreaks increased to 175 (16.8%) out of 1041 norovirus outbreaks. Most of these outbreaks occurred in long-term care facilities (61%), restaurants (10%), and schools (10%). Person-to-person contact (66%) was the most common transmission route, followed by foodborne (15%); transmission route was not reported for 19% of the outbreaks. The 866 non-GI.3 outbreaks in 2013-2014 also occurred primarily in long-term care facilities (66%), restaurants (11%), and schools (4.5%) and were spread mostly by person-to-person contact (54%) and foodborne transmission (13%). GI.3 and non-GI.3 outbreaks peaked in January 2014, with non-GI.3 outbreaks yielding a second peak in March 2014. With a few exceptions, GI.3 viruses prior to 2013 were genetically similar to viruses after 2013. **Conclusions:** We report the emergence of GI.3 noroviruses during the summer of 2013, which continued to increase and cause outbreaks over the following winter season. No distinct difference in setting or transmission route between GI.3 and non-GI.3 outbreaks was observed. In October 2014, GI.3 is the second most commonly reported genotype after GII.4 in US norovirus outbreaks.

Board 10. Molecular Epidemiology of Human Adenoviruses in South West India

C. Akhil, S. R. Aswathy, D. Santhosha, N. Sudheesh, J. Anup, G. Arunkumar; Manipal Ctr. for Virus Res., Manipal Univ., Manipal, Udupi, India

Background: Human adenoviruses (HAdVs) usually cause mild, self-limiting infection but can become severe and fatal in immunocompromised

patients. As of today, 68 types of human adenoviruses (HAdV) have been described and the clinical manifestations and severity of infection widely vary depending on the serotype of the virus and the host species. Serotypes 1, 2, 3, 5, 6 and 7 are mainly associated with respiratory tract infections, while types 40 and 41 are diarrheagenic viruses. There is barely any data available from India on the epidemiology of HAdVs. Here we describe the molecular epidemiology of HAdVs circulating in the South-western India. **Materials and Methods:** Respiratory specimens from Influenza virus negative Influenza like illness (ILI) cases during April 2011 to March 2013 were screened for HAdV by real-time PCR. The HAdV-positive cases were subjected for serotyping. The hyper variable region of HAdV hexon gene was amplified using PCR and the amplicons were sequenced using Sangers sequencing. The sequences were aligned by ClustalW; phylogenetic analysis and neighbor joining tree constructed using the software Mega 5.2 to delineate the serotype. **Results:** A total of 391 ILI cases tested, 43 (11%) were positive for HAdVs. Of these 30 samples were subjected for serotyping. However, only 23 could be typed. The commonest serotypes were HAdV- 3 (9/23) and HAdV- 2 (7/23). The other serotypes were HAdV-7 (3/23), HAdV-1 (2/23), HAdV-8 (1/23) and HAdV- 40 (1/23). The most frequent clinical manifestation was respiratory illness and the associated serotypes were HAdV-3, HAdV-2 and HAdV-7. Conjunctivitis cases were caused by HAdV-3, HAdV-7 and HAdV-8. There were four cases of encephalitis which was associated with HAdV-1, HAdV-2 and HAdV-3. While HAdV-1, 2, 3 and 40 were found in children below 5 years of age, HAdV-7 and 8 were detected from adults. Phylogenetic analysis revealed HAdV-1, 2, 7 and 8 exhibit varying degree of divergence from the reference strains. **Conclusion:** This study documents the circulating HAdV strains and their clinical manifestations as well as epidemiology in South-west India. To the best of our knowledge, this is the first report on molecular epidemiology of HAdVs from India. However, a community based study is required to obtain generalizable data on the prevalent HAdV serotypes circulating in India.

Board 11. Molecular Genetic Monitoring in Influenza Sentinel Surveillance Among Patients with Influenza-like Illnesses (ILI) and Severe Acute Respiratory Infections (SARI) in the Republic of Kazakhstan

A. B. Abeyev; Ctr. of Sanitary-Epidemiological Expertise, Astana, Kazakhstan

Introduction: Molecular Genetic Monitoring will enable systematic surveillance of influenza virus population allowing to determine its genetic composition, difference from the vaccine strains, as well as resistance to available antivirals. **Materials and Methods:** We studied 19 influenza isolates from nasal swabs of ILI/SARI patients in 2013/2014 and 2014/2015 epidemic seasons. Nucleotide sequences of influenza virus genes were PCR amplified using the WHO-recommended primers and chemicals produced by Applied Biosystems. GISAID reference sequences of influenza viruses were used for tests. **Results:** The study performed hemagglutinin and neuraminidase phylogenetic tests in 12 A (H3N2) influenza strains - 8 from 2013/14 epidemic season and 4 from 2014/2015. The four strains of A (H3N2) from 2013/14 season matched the A/Norway/3314/2013 strain and belonged to 3C.3 genetic group, and one strain from the 2014/2015 season matched A/Florida/29/2014 and belonged to 3C.2 group. Furthermore, we found that three A(H3N2) strains from 2014/2015 season and four strains from 2013/14 season matched A/Kazakhstan/3319/2013 and A/Korea/3786/2014 strains by hemagglutinin gene, and belonged to genetic groups 3C.3 and 3C.2 by neuraminidase gene. The M2 gene amino acid sequence test revealed that 9 strains of influenza virus A (H3N2) were featured with S31N mutation which determined resistance of the virus to adamantanes. The HA gene amino acid sequence test revealed that 2 A (H3N2) strains from 2014/2015 season had the most expressed A154S mutation responsible for virulence of the virus. The NA gene amino acid sequence test showed that 4 A (H3N2) strains from 2013/14 season had significant Y155F and D251V mutations associated with resistance to antiviral drugs. The neuraminidase phylogenetic analysis helped identify that all seven strains of A (H1N1)pdm09 isolated in the 2013/2014 season belonged to 6B genetic group and did not have H275Y substitution in the neuraminidase gene, which is responsible for resistance to oseltamivir. **Conclusions:** Molecular genetic typing established that 7 influenza strains isolated in the 2013/2014 epidemiological season are identified as A (H1N1) pdm09, 8 strains from 2013/14 and 4 strains from 2014/2015 epidemic season are identified as A (H3N2). The nine strains of A (H3N2) influenza virus had S31N mutation responsible for viral resistance to adamantanes.

Board 12. Identification of a *Janibacter* Species from a Patient with Endocarditis Based on Ultra-deep Sequencing of Bacterial Genomes

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Background: The genus *Janibacter* is composed of nine different species, most of which are found in the environment. Only six cases of human infection have been reported in association with organisms from this genus: *J. melonis* (1), *J. terrae* (4), and an undescribed *Janibacter* sp. We report the isolation and identification of *Janibacter hoylei* from a human case of infective endocarditis. The microorganisms were isolated from cardiac tissue taken from a 60-year-old female from a village near the town of Kareli, in the country of Georgia. **Methods:** The case was diagnosed as endocarditis with several underlying conditions - fever, weakness, and headache. The patient underwent heart valve replacement. Culturing was performed on the cardiac tissue, from which two morphologically distinct colonies were observed. **Results:** Two isolates were obtained after sub-culturing. DNA from both isolates was sent to CDC-Fort Collins for characterization. Both isolates were identified as *J. hoylei* based on amplification and sequencing of the 16S rRNA gene. Independent genomic characterization was performed at the University of Texas Medical Branch (Galveston, USA) using a whole genome sequencing approach. Sequencing of each sample resulted in 2 and 6 million sequencing reads that were 50 nucleotides long, these were trimmed during analysis for quality reasons to 32 base long non-overlapping subsequences. Expositive searches for all resulting reads against a collection of 13,774 complete bacterial, viral, and fungal genomes (every microbial reference genome available at GenBank by fall 2014) has determined that both strains obtained from the endocarditis case are closely related to *J. hoylei* PVAS-1 with small mismatches between the cultures. **Conclusions:** Members of the genus *Janibacter* have not often been isolated from human clinical infections. In collaboration with CDC-Fort Collins, we report the genomic characterization of two isolates closely related to *J. hoylei* from a Georgian endocarditis patient. Previous to this work, *Janibacter hoylei* has yet to be identified in a clinical human infection. Key words: *Janibacter*, genome, next generation sequencing, infective endocarditis.

Board 13. Molecular Epidemiology of Pathogenic and Non-pathogenic Hantaviruses in Slovenia

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Background: Slovenia lies at a junction of the Alps, the Mediterranean, the Pannonian basin, and the Dinaric Mountains. The resulting high biotic and landscape diversity form the foundation for great variability of zoonotic pathogens. Thirty-one species of small mammals can be found in Slovenia and several of them harbor hantaviruses. At least two viruses cause the disease in humans with a significant differences in the severity of HFRS. Nowadays the incidence of PUUV infection is a three-fold higher compared to DOBV and it is still increasing. Increasing amplitude and magnitude of HFRS outbreaks and availability of diverse animal collection has enabled us to perform a detailed study on the phylogenetic diversity and molecular epidemiology of pathogenic and non-pathogenic hantaviruses. **Methods:** A total of 2393 animals of several species and 506 HFRS patients have been included in the study. For screening for pathogenic hantaviruses specifically designed multiplex real-time RT-PCR assay was used. For non-pathogenic hantavirus a broad spectrum nested RT-PCR with degenerated primers was used. For all positive samples partial S, M, and L segment were obtained. Bayesian phylogenetic analysis was performed with three independent MCMC runs of four chains each consisting of 10,000,000 generations. **Results:** We have confirmed presence of 3 pathogenic: DOBV, DOBV-Kurkino and PUUV and 2 non-pathogenic: TULV and SWSV. The diversity within different hantavirus species ranges from 1.3% up to 14.1%. Higher nucleotide diversity was observed in non-pathogenic hantaviruses, whereby DOBV and PUUV seem to be more conserved, and with stronger geographical clustering. It is evident that the distribution of the virus is mainly influenced by the presence of the host species, but the geographic characteristics, like rivers, impact and limit the formation of HFRS endemic areas. **Conclusions:** The study presents one of the largest collections of hantavirus L, M, and S sequences obtained from hosts and patients within a single country. Several genetic lineages were determined for each hantavirus species, with higher diversity among non-pathogenic compared to pathogenic viruses. For pathogenic hantaviruses, a significant geographic clustering of human- and rodent-derived sequences was confirmed. Several geographic and ecological factors were recognized as influencing and limiting the formation of endemic areas.

Board 14. A Simple Genotyping Method for Differentiation of *Blastocystis* Subtypes and Genetic Variation of *Blastocystis* sp. in Thailand

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Background: *Blastocystis* sp. is one of the most common intestinal protozoa of human and animals worldwide. The infections can cause various gastrointestinal symptoms. The genetic diversity of the protozoa has led the suggestion that the subtypes might be associated to the wide range of clinical symptoms. Molecular techniques have revealed extensive genetic diversity of this protozoan. More than 14 subtypes have been reported. Subtype 1-9 has been reported in humans. However, the prevalence of each subtype is different in each country. Until now, there is no standard genotyping method for *Blastocystis* sp. In this study, we developed a simple genotyping method to identify subtypes of *Blastocystis* sp. in human. We also studied the subtype distribution of *Blastocystis* sp. in Thailand. **Methods:** Fecal samples were collected from 1,025 students in 4 regions of Thailand. *Blastocystis* infections were identified by simple smear, formalin ethyl-acetate concentration, Boeck and Drbohlav's Locke-Egg-Serum (LES) medium culture, and polymerase chain reaction (PCR) of small-subunit ribosomal DNA (SSU rDNA). The subtypes of *Blastocystis* sp. were determined by restriction fragment length polymorphism (RFLP). **Results:** Out of 1,025 students, 415 (40.48%) were positive for *Blastocystis* sp. However, PCR method could identify only 109 infected individuals (26.27%). Based on all available published nucleotide SSU rDNA sequences of *Blastocystis* subtypes from GenBank, we developed PCR-RFLP analysis with *Mfe*I, *Ase*I, *BsrG*I, *BspH*I, and *Dra*I for rapid differentiation of human *Blastocystis* (subtype 1-9). Using 2 steps of RFLP reactions, we could determine subtype 1-3 among these students. Subtype 3 was the most prevalent (58.72%), followed by subtype 1 (31.19%) and subtype 2 (10.09%). **Conclusions:** *Blastocystis* sp. was the most common intestinal parasites in Thai students. *Blastocystis* subtype 3 was the most prevalent in students in all regions in Thailand. Subtype distribution of *Blastocystis* in Thailand was different from other countries. Therefore, clinical significance of *Blastocystis* in Thai patients as well as study of immunological aspects should be further investigated for a better understanding of the *Blastocystis* sp. pathogenicity in humans.

Advanced Molecular Detection (AMD)

Monday, August 24, 12:30 PM - 1:45 PM

Grand Hall

Board 15. Detection of Single and Mixed Subtype Influenza Viruses with Next-Generation Sequencing Platform

Z. Xiaohui, L. Yue, Z. Wenfei; Chinese Natl. Influenza Ctr., China CDC, Beijing, China

Background: Influenza virus is consistently threatening public health worldwide. Several influenza A viruses have caused human pandemic in the last centenary, making rapid detection of this pathogen critical for disease control and targeted therapy. The recently developed next generation sequencing (NGS) technology, with high sequencing throughput and requiring little priori knowledge of samples, have greatly improved the sensitivity to identify and subtype influenza virus. **Methods:** In this study, we assessed one of the NGS bench sequencer, the Ion torrent PGM, on its analytical sensitivity or detection limit to influenza virus at moderate amount of reads. Virus genome was quantified by real-time PCR and serially diluted to different titers, followed by amplification with influenza A virus common primer and then subjected to PGM sequencing. Furthermore, there were challenges to subtype low-titer (LT) influenza virus which mixed with high-titer (HT) ones because of exponential amplification in the library construction. The copy-number rate of two mixed virus which could both be subtyped was determined using manual combination of two known influenza viruses followed amplification and deep sequencing. **Results:** Our data showed the PGM can detect influenza virus at titers as low as 5 copy/reaction and subtype a single virus at concentration of 625 copy/reaction. Using 625 copy/reaction as LT virus baseline, only the HT virus could be subtyped when these two viral copies differed more than 100 folds. **Conclusions:** NGS platform can detect influenza virus at high sensitivity, especially for subtyping co-existed influenza virus. Our data set a reference limit to identify and subtype influenza virus with NGS platform at similar output reads.

Board 16. Development of a Flexible, Rapid, High-capacity Sequencing Method for MERS-CoV

C. R. Paden, Y. Tao, A. Tamin, K. J. Queen, Y. Li, S. Tong; CDC, Atlanta, GA, USA

Background: In 2012, Middle Eastern Respiratory Syndrome Coronavirus (MERS-CoV) was identified from patients suffering from a severe respiratory syndrome. The virus was sequenced and confirmed as a distinct human beta-coronavirus. While MERS is associated with a relatively high mortality rate (42.6%), the number of confirmed cases (759) and person-to-person transmissions appear to be limited. However key mutations in MERS-CoV genome may cause enhanced transmission or alter tropism. Therefore, the ability to rapidly identify mutations which are significant and/or describe chains of transmission is of great value to pathogenicity studies, molecular epidemiology and public health. **Methods:** We developed a set of primers to generate nested, tiling amplicons across the 30kb MERS-CoV genome in order to amplify viral genomes for Sanger sequencing from what are typically low copy-number samples. We packaged these primers and reagents into a kit for a quick turnaround time. In order to rapidly sequence many MERS-CoV genomes we adapted this protocol to run on a commercially-available microfluidic PCR system. Amplicons from dozens of samples are generated and sequenced all at once by high-throughput sequencing. **Results:** Using tissue culture-derived MERS-CoV as a proof-of-concept, we are able to obtain >1000-fold coverage from a starting titer of approximately 1000 copies. With this data, we are able to conduct variant analyses of minor virus populations and have observed individual SNPs emerge over several passages in tissue culture, including one in S gene that repeatedly dominates. Further, we have used these methods in responding to MERS-CoV cases in the USA and from Middle Eastern countries. **Conclusions:** Combining the microfluidic PCR platform and high-throughput sequencing allows for efficient use of clinical samples while providing for as many as 48 full genomes in three days. Further, amplification of the viral sequence allows for more efficient use of sequencing flow cells, decreasing the cost of abundant sequencing data. This type of rapid, sensitive, high-capacity amplification and sequencing strategy will be valuable especially when the number of cases is high and there is a need for fast turnaround time.

Board 17. Transforming Public Health Microbiology in the United States with Whole Genome Sequencing (WGS) - PulseNet and Beyond

P. Gerner-Smidt, Enteric Diseases Laboratory Branch, CDC, Atlanta, GA, USA

Background: A number of different methods and technologies are used in public health laboratories to characterize foodborne bacterial pathogens ranging from phenotypic tests e.g., growth characteristics, serotyping and antimicrobial susceptibility testing, to PCR and other molecular methods for detection of e.g., virulence genes, and for subtyping in outbreak investigations e.g., PFGE. This traditional strain characterization is labor and resource intensive and has a turnaround-time of up to several months. Most of this information may be extracted from the genome sequence of any organism. With the introduction of next generation sequencing technologies and advances in bioinformatics it is now possible to characterize foodborne pathogens in a single workflow with a TAT of ≤4 working days in a cost-efficient manner. **Methods:** The Enteric Diseases Laboratory Branch at CDC is working with partners in federal agencies, public health laboratories in the states and internationally to build applications to extract information about genus, species, lineage, serotype, pathotype, virulence profile and antimicrobial resistance markers, and subtyping using gene by gene approaches from the genome sequences. The PulseNet infrastructure and analytical platform and database will be used because of its versatility and because the public health laboratories have worked with it for >15 years. The method will also be validated and replace CLIA related activities in the branch and public health laboratories. **Results:** WGS has successfully been tested for national surveillance of listeriosis since September 2013 and is now being implemented in the daily routine. The technology has proven its power supplementing traditional methods in outbreak investigations by adding phylogenetic relevance and increased resolution compared with current methods thereby enhancing case definitions and source tracking. The method is currently being piloted for surveillance of *Campylobacteraceae*, Shiga toxin-producing *E. coli,* and *Salmonella* with the remainder of foodborne bacteria to be added over the next five years. **Conclusion:** WGS will revolutionize the surveillance of both sporadic and outbreak related foodborne infections by replacing and enhancing current laboratory methods.

Board 18. Transforming Public Health Microbiology for *Campylobacteraceae* with Whole Genome Sequencing

P. S. Kwan[1], D. Wagner[1], H. Carleton[1], J. Pruckler[1], G. Williams[1], C. Bennett[1], L. Joseph[1], E. Trees[1], E. M. Ribot[1], M. C. Maiden[2], W. G. Miller[3], Y. Chen[4], S. Zhao[4], P. McDermott[4], H. Pouseele[5], P. Gerner-Smidt[1], C. Fitzgerald[1]; [1]Enteric Diseases Laboratory Branch, CDC, Atlanta, GA, USA, [2]Dept. of Zoology, Univ. of Oxford, Oxford, United Kingdom, [3]Agricultural Res. Service, USDA, Albany, CA, USA, [4]Ctr. for Vet. Med., U.S. FDA, Laurel, MD, USA, [5]Applied Maths NV, Keistraat 120, Belgium

Background: Conventional phenotypic and genotypic methods employed for the identification and subtyping of *Campylobacteraceae* are labor-intensive, expensive, and imprecise. As part of the Advanced Molecular Detection (AMD) initiative "Transforming public health microbiology with whole genome sequencing - PulseNet and beyond," we have begun developing a *Campylobacteraceae* whole genome sequence (WGS) database. The PulseNet infrastructure (BioNumerics database) will be used in conjunction with the existing BIGSdb platform to build the database, with the goal of characterizing *Campylobacteraceae* in a single workflow using WGS. **Methods:** Reference genomes were provided by FDA and USDA and an additional 100 strains were sequenced at CDC using the Illumina HiSeq (2x100bp). Assemblies and annotations were performed using the Computational Genomics Pipeline (CG-Pipeline) v0.4. These genomes cover the known genus/species of *Campylobacteraceae* and the genetic diversity within *C. jejuni* and will be used to expand on and set criteria for the current PubMLST.org/campylobacter locus definitions. Multiple subschema are being set up within the database to perform identification and scalable, hierarchical subtyping that will include seven locus MLST, ribosomal MLST, core genome MLST, and whole genome MLST. For initial testing of the database, an additional 600 strains will be sequenced, including isolates submitted to CDC for reference identification, as well as a random subset of sporadic NARMS and PulseNet strains to capture outbreak diversity within *C. jejuni*. **Results**: To date all potential reference genomes have been sequenced and annotated and are being chosen for inclusion in the BioNumerics database development. WGS data have been generated for 96/600 isolates that will used to test the prototype isolate database. **Conclusions:** The *Campylobacteraceae* WGS BioNumerics database will provide a single, unified, cost-effective approach for accurate species identification and subtyping to aid the surveillance of both sporadic and outbreak related *Campylobacter* infections. Through continued collaboration with domestic and international partners, we will work to

test and refine the nomenclature and isolate databases and plan to CLIA validate the reference identification subschema within the next year.

Board 19. Metagenomic Pathogen Detection and Gut Microbiome Response to Foodborne Illness

M. R. Weigand[1], A. Huang[2], A. V. Pena-Gonzalez[1], K. T. Konstantinidis[1], C. L. Tarr[2]; [1]Georgia Inst. of Technology, Atlanta, GA, USA, [2]CDC, Atlanta, GA, USA

Background: Current diagnostic testing for foodborne pathogens relies on culture-based techniques even though many microorganisms, including known pathogens, resist cultivation under laboratory conditions, which often precludes identification of a specific causative agent. Powerful sequence-based approaches such as metagenomics hold the potential to derive epidemiological data directly from complex samples, without isolating or culturing individual organisms. However, such methods have seen little application to foodborne pathogen detection because standardized bioinformatics techniques for analysis have not been established. **Methods:** We have applied shotgun metagenomics to stool samples collected from two localized foodborne outbreaks attributed to *Salmonella* to evaluate metagenomics as a diagnostic and disease surveillance tool, as well as gain insight into the gut microbial community responses to foodborne bacterial infection. These outbreaks were geographically isolated (Alabama and Colorado) and the etiologic agents were identified by culture-dependent methods as distinct strains of *Salmonella enterica* subsp. *enterica*, serovar Heidelberg. **Results:** Sample consistency and human sequence contamination varied, often reducing the sequencing depth of the targeted microbial communities, yet referenced-based detection of *Salmonella* Heidelberg was possible by metagenomic read recruitment, even in samples with high contamination. Taxonomic profiling revealed similar microbial communities within localized outbreaks, such that samples from different outbreaks clustered separately and were distinct from a subset of 'healthy' references selected from the Human Microbiome Project. Additionally, coverage estimates of the sequenced microbial communities suggested reduced diversity associated with foodborne illness compared to 'healthy' references. **Conclusions:** These results highlight the potential utility of metagenomic-based diagnostic tools for foodborne pathogen identification and epidemiologically relevant clustering, even in samples heavily contaminated with human host DNA. Furthermore, such shotgun metagenomic approaches offer additional insight into gut microbial community responses to foodborne illness that may hold clues to pathogen ecology.

Board 20. A Bioinformatic Pipeline to Genotype and Compare Hundreds of *Bacillus anthracis* Genomes

L. M. Rodriguez-R[1], M. R. Weigand[1], C. K. Marston[2], C. A. Beesley[2], M. E. Bell[2], M. Frace[2], S. Sammons[2], A. R. Hoffmaster[2], K. T. Konstantinidis[1]; [1]Georgia Inst. of Technology, Atlanta, GA, USA,[2]CDC, Atlanta, GA, USA

Background: Currently, several schemes for genotyping *Bacillus anthracis* are in use, primarily based on Multiple Loci VNTR (Variable Number of Tandem Repeats) Analysis (MLVA) and Single-Nucleotide Polymorphisms (SNPs). However, current schemes lack standardization, and achieving high resolution is particularly challenging due to the low genetic diversity of the group. **Methods:** Here, we present a genome-wide analysis of over 200 genomes of *B. anthracis* isolated from human, animal, and environmental samples recovered from around the world since the 1930s, with special focus on North American isolates. We have applied genome-wide metrics to the comparison of whole genomes such as the Average Nucleotide Identity (ANI) to reconstruct high-resolution clades, and compared genome-based clustering with MLVA. **Results:** We developed a genome-based framework for high resolution genotyping of *B. anthracis*. Using this framework, we have identified geographically restricted clusters, some of which could not be differentiated with previous schemes such as MLVA. In addition, we present a general implementation of the genomic methods, extensible to other bacterial groups. **Conclusions:** In the current work, we used *B. anthracis* to showcase the utility of high-throughput genomic analyses for high-resolution genotyping and its application to molecular epidemiology. This general pipeline can also be adapted for the analysis of other bacterial species. In addition, we examined the geographic distribution of *B. anthracis* in light of genome-based clustering.

Board 21. Implementation of Whole Genome Sequencing (WGS) for Surveillance of Shiga Toxin-producing *Escherichia coli* (STEC) in the United States

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Background: Shiga toxin-producing *Escherichia coli* (STEC) are important foodborne pathogens causing diarrhea, hemorrhagic colitis, and hemolytic uremic syndrome, a life-threatening condition. Current methods for the characterization of STEC are cumbersome and expensive. We therefore began work to replace traditional methods with those using whole genome sequence (WGS) data by developing an allele database of individual *Escherichia* genes in BioNumerics. The database, which will include genes obtained from databases developed by Danish scientists, from genomes sequenced at CDC and from genomes available publically, will allow characterization of *Escherichia* in a single workflow using a multi-locus sequence typing (MLST) approach. **Methods:** High quality annotated reference genomes representing 20 STEC serotypes were sequenced at the CDC or obtained from NCBI. Multiple subschema are being built within the database to perform identification, characterization and scalable, hierarchical subtyping that will include classical, extended, core and whole genome MLST. To test the epidemiologic clustering ability of the subtyping algorithms and increase the allelic diversity of the database, an additional 500 strains from outbreaks and sporadic infections were sequenced and analyzed. **Results:** Sixty reference genomes from CDC and NCBI were included in the BioNumerics allele database to represent genes encoding known virulence factors and O and H antigens. Genomic sequences generated for 500 strains were analyzed using the prototype allele database. **Conclusions:** The *Escherichia* WGS BioNumerics database provides a single, unified cost effective approach for accurate species identification, serotyping, virulence characterization and subtyping for the surveillance of both sporadic and outbreak related *E. coli* infections. The end-users in the public health labs will be able to analyze their own data with little training, making the system equally efficient for local and central investigations. The system will be refined through continued collaboration with domestic and international partners.

Board 22. Rapid Molecular Detection and Characterization of *Legionella* for Outbreak Response

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Background: The incidence of Legionnaires' disease (LD), a severe pneumonia caused by inhalation of *Legionella* bacteria in aerosolized water, has increased 217% in the last decade. To determine the source of an LD outbreak, it is currently necessary to compare both clinical and environmental isolates using one of several potential typing methods. However, *Legionella* culture is difficult, costly, and time consuming. Further, current methods often do not provide enough discriminatory power to be conclusive. We propose using next generation sequencing technology to develop a typing system based on whole genome sequences, and ultimately use a metagenomic approach to investigate outbreaks. This will greatly decrease the time from outbreak recognition to identification of the source and allow comprehensive characterization of the outbreak-associated strains. **Methods:** We have created a prototypical whole genomic pipeline (WGP) to annotate and compare *Legionella* sequence data. The WGP is being beta tested, retrospectively, with data obtained from 3 outbreaks for which conventional typing methods were unable to provide sufficient resolution. **Results:** We have created a Base WGP infrastructure that consists of: 1) A customized and locally operated MySQL database and OrthoMCL program; 2) Bioinformatics programs and scripts for data mining, data parsing, and file manipulation that are housed on the Aspen cluster managed by the Scientific Computing Support Group; and 3) A GUI to be designed for user connectivity. To date, we have constructed and implemented the comparative genomics and phylogenetic analysis modules for the pipeline. We have optimized analytic workflows that allow us to process on average 34,000 genes in a few hours. Further, use of this Base WGP for an outbreak investigation was able to characterize a 30-year-old historic isolate as having an extremely close phylogenetic relationship to the recent outbreak-related strains from the same location, demonstrating a high likelihood of persistence of this single strain for over 3 decades in a building water system. **Conclusions:** This WGP and overall approach has the potential to rapidly identify and characterize legionellae from environmental source(s) and quickly provide genetic matches to *Legionella* sequences obtained directly from clinical specimens.

Board 23. The Application of Whole Genome Multi-locus Sequence Typing to Characterize *Listeria monocytogenes*

H. A. Carleton[1], L. S. Katz[1], S. Stroika[1], A. Sabol[1], K. Roache[1], Z. Kucerova[1], E. M. Ribot[1], P. Evans[2], K. Holt[3], K. Kubota[4], H. Pouseele[5], J. Besser[1], C. Tarr[1], E. Trees[1], P. Gerner-Smidt[1]; [1]CDC, Atlanta, GA, USA, [2]Ctr. for Food Safety and Applied Nutrition, U.S. FDA, College Park, MD, USA, [3]Food Safety and Inspection Service, USDA, Atlanta, GA, USA, [4]APHL, Washington, DC, USA, [5]Applied Maths, Sint-Martens-Latem, Belgium

Background: The introduction of low cost rapid next generation sequencers (NGS) is revolutionizing public health microbiology because traditional phenotypic and genotypic characterization methods now can be replaced by whole genome sequencing (WGS). As part of the Advanced Molecular Detection (AMD) initiative we focused on *Listeria monocytogenes* surveillance and transformation of PulseNet's current pulsed-field gel electrophoresis (PFGE) -based surveillance into a WGS -based infrastructure for public health laboratories. As part of these projects we developed a *L. monocytogenes* whole genome multi-locus sequence typing database (wgMLST) in BioNumerics 7.5 and tested the utility of this approach in surveillance. **Methods:** Since September 2013, WGS has been performed on over 1500 clinical, food and environmental *L. monocytogenes* isolates. Nextera XT DNA libraries were sequenced on the Illumina MiSeq platform. After raw read quality control, sequences with >20x coverage were uploaded in real-time to the Sequence Read Archive at NCBI and further analyzed using wgMLST. A subset of the isolates was also characterized using high quality single nucleotide polymorphisms (hqSNP) (LYVE-SET: github.com/lskatz/lyve-SET) to compare the performance of the two methods. **Results:** The wgMLST database was built using 200 well characterized annotated reference genomes, from which over 5800 unique loci were identified. On average, 3063 loci (range 2223-3526) were identified per genome, and the number of alleles per locus ranged from 1 to 307. For each new genome analyzed an average of 80 new alleles were identified. For isolates identified as part of a cluster/outbreak, there was high correlation in the clustering of isolates by wgMLST and hqSNP analysis for epidemiologically confirmed outbreaks. **Conclusion:** This preliminary analysis suggests that the current *Listeria* wgMLST database adequately captures the diversity of *Listeria* that is characterized as part of real-time surveillance. Additionally wgMLST can be used to identify clusters of epidemiologically related isolates and closely matches results of hqSNP analyses. In addition to the wgMLST scheme, we will include as subset analyses the classical 7 gene MLST and a core MLST recently developed by Pasteur Institute that includes approximately 1,745 genes.

Board 24. Rapid Identification of *Burkholderia pseudomallei* by Using a Pyrosequencing Based Algorithm

A. MacMillan[1,2], S. DasGupta[1], H. Shah[1], O. Shone[1], D. Galkowski[1,3], N. Delgado[1]; [1]New Jersey Dept. of Hlth., Ewing, NJ, USA, [2]APHL/CDC EID Res. Fellow, Ewing, NJ, USA, [3]Rutgers Univ., New Brunswick, NJ, USA

Background: *Burkholderia pseudomallei* is a Tier-1 Select Agent, and the organism responsible for melioidosis in humans and animals. Identification of *B. pseudomallei* can be difficult due to similarity to other related species. Classical microbiology identification techniques require BSL-3 containment practices. Pyrosequencing can be utilized for identification, with increased specificity compared to DNA amplification assays. A pyrosequencing assay was developed to specifically target *B. pseudomallei*. **Methods:** *B. pseudomallei*-specific PCR and sequencing primers were developed to target 3 genes, *orf2*, *orf11* (both members of a *B. pseudomallei* type III secretion system gene cluster) and BPSL3108, a gene with unknown function. Tested organisms include 8 *B. pseudomallei* strains and 11 related *Burkholderia* species. DNA from control organisms was either isolated from culture or obtained commercially (BEI Resources). Different methods of DNA isolation and amplification were utilized to test assay robustness. Pyrosequencing of 40-45 bp of *B. pseudomallei*-specific DNA at each gene was achieved using the QIAGEN PyroMark Q96 ID system. **Results:** PCR resulted in *B. pseudomallei*-specific amplicons of expected size for both *orf2* and *orf11* regions, while amplification of BPSL3108 did produce amplicons with other *Burkholderia* species. However, a third specific primer is utilized in the pyrosequencing reaction, which prevents sequencing of any non-specific amplification. Non-*B. pseudomallei* organisms provided no sequence signal of *orf2* or *orf11*, and produced BPSL3108 sequences with no significant homology compared to *B. pseudomallei*

strains. **Conclusions:** This assay describes the first specific pyrosequencing method for *Burkholderia pseudomallei* identification. Used in conjunction with Real-time PCR-based assays, pyrosequencing can increase specificity and confidence level of *Burkholderia pseudomallei* identification. This technology can overcome some limitations of conventional assays caused by genomic variability (i.e. single nucleotide polymorphisms or genetic engineering). In addition, the assay provides significant savings and reduced processing time, including less complex bioinformatics, in comparison to other next-gen sequencing platforms.

Board 25. Describing Meaningful Starting and Ending Points for a Dynamic Change Process: Advanced Molecular Detection in Public Health

A. E. Montesanti, R. Huggins, D. MacCannell, A. Guinn, C. Prue; CDC, Atlanta, GA, USA

Background: In 2014, the Centers for Disease Control and Prevention (CDC) launched the Advanced Molecular Detection (AMD) initiative to introduce cutting-edge laboratory and bioinformatics approaches to enable faster and more effective infectious disease prevention and control. Efforts focus on: 1) applying AMD technologies in programs; 2) increasing workforce capacity; and 3) developing laboratory and information technology (IT) infrastructure and processes. Evaluation is critical to track AMD adoption and integration. **Methods:** Many measures have been developed to track AMD progress. To measure current and planned use of AMD technologies, the Office of AMD conducted a survey with 44 CDC infectious disease programs. To measure publicly available AMD outputs, a detailed search query on CDC authors who submitted genetic sequences to the National Center for Biotechnology Information (NCBI) was conducted. To measure IT infrastructure to support bioinformatics, the amount of operating time of high performance computers was calculated. To measure AMD impact on public health programs, such as speed of pathogen or cluster detection, stories of applying AMD approaches in on-going outbreaks are shared on CDC's website. **Results:** In 2014, two out of 44 infectious disease programs stated using AMD technology as part of routine work at CDC and/or are piloting in states; 20 have stated they are in the evaluation/validation phase of using AMD technology; and 21 are identifying new AMD applications. One is not currently using AMD methods. From 2013 to 2014, there has been a four-fold increase in the number of genetic sequences in NCBI from known CDC authors and a five-fold increase in the total number of computing hours on high performance computers. **Conclusions:** Tracking adoption and integration of AMD technologies in public health, at CDC and in states, is vital in ensuring investments enable faster and more effective infectious disease prevention and control.

Board 26. Targeted Re-sequencing and Metagenomics Analysis to Identify and Characterize Pathogens in Respiratory Specimens from Unexplained Respiratory Disease Outbreak (URDO) Responses

J. L. Waller; CDC, Atlanta, GA, USA

Background: Rapid identification of causative agents during a respiratory disease outbreak is paramount. Many viruses and bacteria initially present with similar clinical features. Currently, CDC's URDO multipathogen panel relies upon simultaneous detection(s) using real-time PCR technology to identify ~20 common causes of respiratory disease. While useful and rapid, this panel allows only a basic level of information for a select group of pathogens. By transforming this approach to a sequenced-based method, we anticipate a more rapid and complete dataset for all targeted agents that may be present in clinical specimens and also allow for detection of novel or rare pathogens. These sequencing strategies will enable detection of a wide variety of respiratory pathogens as well as characterize clinically-relevant traits such as strain typing and antimicrobial resistance determination in a single sequencing run. **Methods:** A custom primer panel was developed to amplify target regions for specific pathogen detection and characterization of relevant features. The SmartChip TE system (WaferGen Biosystems) was used to generate specific "seq-ready" libraries. Following this amplification step, all products will be pooled and sequenced on the MiSeq, with subsequent sequence data to be analyzed using custom-generated genetic databases. **Results:** We have designed a custom panel for 54 targets for 12 specimens in 8 replicates for a variety of agents. We have assessed oligos, amplicons, and enzyme formulations to strategically align the procedure for consistent performance. We have successfully generated "seq-ready" amplicons from both DNA and RNA targets in wet chemistry format, including: the detection of *M. pneumoniae*, Flu A, & RSV; strain typing of *L. pneumophila* & *S. pneumoniae* 19A; oseltamivir resistance of H3N2. **Conclusions:** Our initial results show promise for this method being expanded to cover the entire respiratory target panel. Development and implementation of this approach in URDO investigations would reduce time to results and provide a more comprehensive picture of the outbreak. This would lead to faster outbreak response(s) and informed public health intervention strategies, likely resulting in improved outcomes. This strategy represents a powerful advance in current capabilities to support local, state and global health security efforts.

Board 27. Point-of-care Multiplex Detection and Differentiation of Chikungunya and Dengue Viruses in Whole Blood

N. Venkateswaran, T. Fecteau, P. Valencia, W. M. Nelson; Tetracore, Inc., Rockville, MD

Background: Dengue (DENV) and Chikungunya (CHIKV) viral infections are emerging and re-emerging with an expanded geographical distribution due to urbanization, increased human travel, and climate changes. These two infections also show a substantial overlap in clinical presentation and are co-prevalent in many countries. A recent infection can only be confirmed by detection of the virus in whole blood because positive results in serological assays may indicate prior infection. As antibodies develop in response to the infection, the viral load in the blood decreases. Thus to meet the need for sensitive detection and accurate differentiation of CHIKV and DENV in whole blood we designed a multiplex real time reverse transcription polymerase chain reaction assay for portable thermocycler T-COR 8™. The objective of the study was to develop an assay that may be used in both point-of-care (POC) and laboratory settings. **Methods:** For optimization of this assay we spiked cell culture derived viruses purchased from ZeptoMetrix Corporation in normal human blood samples. This multiplex assay included reagents to amplify DENV, CHIKV, and an internal control (IC) to monitor the reaction inhibition. DENV assay was designed as PAN assay that can detect all four serotypes of DENV. Conditions to dry down the multiplex assay were optimized to make the assay amenable for use in low resource settings. A simple sample collection device and a cartridge with dried down reagents were also developed for field use. **Results:** Dried down DENV assay was previously found to be 98.77% sensitive and 100 % specific on Cepheid SmartCycler using set of 81 confirmed positive and 25 negative samples. SF9, L929, Hela, SL29, Vero 76, c6/36 and BHK-2 cell line DNA extracts were not cross reactive. Individual DENV and CHIKV assays showed a wide dynamic range with 4 logs of linearity using spiked samples. Comparison of individual with multiplex assay showed similar sensitivity. Multiplex format is being further optimized and validated

for portable T-COR 8 system. Detailed results from this study will be described in this presentation. **Conclusions:** The data from this study shows that presence of DENV and CHIKV can be detected in blood samples effectively in centralized labs, on nursing cart or at the patient bed side using our novel multiplex assay and POC platform T-COR 8.

Laboratory Support for Strengthening Infectious Disease Surveillance and Monitoring Infections

Monday, August 24, 12:30 PM - 1:45 PM
Grand Hall

Board 28. Little Effect of Varying Specimen Storage Temperature on Influenza PCR Results

A. Hawksworth, M. Balansay, S. Vo, J. Radin, C. Myers, G. Brice; Naval Hlth. Res. Ctr., San Diego, CA, USA

Background: The perceived need to maintain cold or frozen temperatures of specimens collected for virologic testing presents a major obstacle to performing surveillance in many regions and populations. Few studies have examined the effect of long-term storage temperature on polymerase chain reaction (PCR) results. **Methods:** Grown influenza A/H1N1(09) and human cells were spiked into universal transport medium and divided into 52 identical aliquots. Thirteen aliquots were stored at each of 4 different temperatures (-70°C, -20°C, 4°C, and ambient temperature). Specimens were tested for influenza A, the H1(09) subtype, and RNAse P in triplicate by real-time PCR using FDA-approved tests at specified intervals from 1 to 168 days. Mean crossing threshold (Ct) was calculated for each time point and storage temperature and compared using general linear models. **Results:** All specimens at all storage temperatures were PCR positive for influenza A through the 168 day period. Although there was a trend toward increasing Ct over time and at ambient storage temperature, all specimens remained strongly positive for influenza A and the H1 subtype, with mean Ct below 29 at every time point. RNAse P Ct values were higher from the outset, but showed the same trends and also remained positive through day 168. **Conclusions:** These data suggest that, at least for influenza surveillance, maintaining the cold chain is not necessary. This could remove a prohibitive cost and logistical barrier, allowing surveillance in regions and populations (e.g., developing countries and transient military populations) that had previously been considered impractical. Further investigation of other pathogens and more extreme environmental conditions is warranted.

Board 29. PulseNet Promotes Global Health Security and Enhances Disease Surveillance in Mexico Through Laboratory Training

M. M. Freeman, G. Gonzalez-Aviles, J. Concepcion-Acevedo, E. M. Ribot, P. Gerner-Smidt; CDC, Atlanta, GA, USA

Background: International travel and food trade impact our everyday lives; unfortunately foodborne infections are not prevented by borders. PulseNet USA and PulseNet International play important roles in detecting and investigating international outbreaks of foodborne bacteria by sharing data and by providing effective means of communication across PulseNet networks. A main objective of the PulseNet networks is to ensure accurate comparison of data across laboratories worldwide. **Methods:** PulseNet ensures that data is comparable by conducting hands-on laboratory trainings using standardized protocols. We also play a major role in technology transfer in the international arena through trainings. An important tool is frequent communication with our partners through the PulseNet International web forum hosted by Public Health Agency of Canada and periodic teleconferences, especially during possible outbreaks. **Results:** Collaborations and laboratory trainings between PulseNet USA, COFEPRIS (Mexican FDA counterpart) and InDRE (the national public health laboratory in Mexico) have increased lab capacity, and strengthened cross-border, inter-agency relationships, as evidenced by the quick and effective joint-response to a cholera outbreak in September of 2013 by COFEPRIS and InDRE. **Conclusions:** As whole genome sequencing (WGS) is incorporated into public health laboratories, cooperation and communication between the U.S. and Mexico are keys to ensuring data comparability, safety of imported food and continued outbreak detection. SENASICA, (Mexican USDA counterpart), recently consulted PulseNet USA regarding a preliminary WGS implementation plan. The proper contacts have been established so we can work together preventing, detecting and responding to foodborne disease to achieve our ultimate goal of food safety.

Board 30. Molecular Epidemiological Characterization of *Brucella canis* from Humans in Zhejiang, China

H. Jiang[1], H. Wang[2], J. Luo[3]; [1]Natl. Inst. for Communicable Disease Control and Prevention, China CDC, Beijing, China, [2]Hangzhou CDC, Hangzhou, China, [3]Jiaxing CDC, Jiaxing, China

Background: Brucellosis is a neglected disease and yet is the most common zoonotic disease worldwide. In China, brucellosis is an endemic disease typically caused by *Brucella melitensis* infection (biovars 1 and 3). Although, *Brucella canis* infection has not been the major cause of brucellosis in China, recent outbreaks in Beijing and other provinces suggest that this infection may be on the rise. On November 10, 2011, a 45-year-old woman was diagnosed as *Brucella canis* infection. The blood culture was identified as *Brucella canis* by phenotypic and genotypic methods. To compare the molecular epidemiological relationship between strains of *Brucella canis* isolated from the patient and the dog strains isolated from Hangzhou and from other Chinese regions, MLVA-16 was performed. In order to detect genetic mutations which could ultimately be correlated with the different LPS genetic loci between human and animal *B. canis* strains, twenty-one genes, involved in the lipopolyscaccharide-synthesis, were sequenced and compared with the *Brucella canis* RM6/66 strain. **Methods:** To compare the molecular epidemiological relationship between *B. canis* strains isolated from China, MLVA-16 was performed. A total of 21 genes involved in LPS synthesis were also analyzed. **Results:** The 2011 human *B. canis* strain was compared with three *B. canis* strains isolated in 1986 from dogs born and raised in the same geographical area, Hangzhou city. All four isolates were indistinguishable using panel1 (genotype 3: 2-3-9-11-3-1-5-2) and panel 2A (genotype 28: 6-20-9) markers. The three dog MLVA genotypes were very similar, harboring only one single-locus variant or double-locus variants in bruce07 and bruce21, respectively. However, the human isolate shared only one marker (bruce30), but differed at the other panel 2B markers from the dog isolates. Differences were observed among all *B. canis* China isolates using MLVA-16 dedongram. 21 genes involved in LPS synthesis were amplified and sequenced. No mutations were detected among these strains, demonstrating the presence of the same LPS genetic loci responsible for the rough morphology. **Conclusions:** The occurrence of a *B. canis* human infection was confined to a community-acquired sporadic case, which might raise new awareness and interest for such infection in humans.

Board 31. Improving Laboratory Quality Management Systems in Selected Public Health Laboratories in Egypt

M. E. Morales-Betoulle[1,2], A. Safwat[3], N. Hanna[3], A. Naguib[3], S. Andrews[4], X. Liu[4], C. Sanders[4,5], H. Mansour[5], N. Fathy[3]; [1]The QED group LLC contractor, Washington, DC, [2]CDC- Global Disease Detection Program-Contractor, Cairo, Egypt, [3]Central Publ. Hlth. Lab., Ministry of Hlth. and Population, Cairo, Egypt, [4]CDC, Atlanta, GA, USA, [5]U.S. Naval Med. Res. Unit No. 3, Cairo, Egypt

Background: Responding to the International Health Regulations (IHR) requirements, the Egyptian Central Public Health Laboratory (CPHL) monitors and improves quality management systems in public health laboratories across the country. To support this mission, CDC Global Disease Detection Program (GDD) has initiated a collaborative project with CPHL to improve and standardize laboratory quality management in central and regional laboratories. **Methods:** A Laboratory Quality Management System (LQMS) improvement program by phases was designed to include: 1) Laboratory Assessments using standardized WHO Lab Assessment Tool (LAT Annex 2, 2012) and gap analysis. 2) Workforce Development by Training of Trainers (TOT) and a cascade of trainings on LQMS and 3) Follow-up visits to monitor and evaluate QMS implementation of gaps identified during initial assessments, following WHO stepwise implementation plan. Laboratories assessed were in Cairo and four other governorates in Upper Egypt and Central Nile Delta regions. **Results:** From February 2013 to July 2014, sixteen laboratories were assessed using the LAT standardized checklist containing eleven QMS indicators. Average scores ranged from 64-89% for six central level laboratories located in Cairo, three intermediate laboratories in Cairo and Giza scored 55-71%; intermediate and peripheral laboratories had average scores varying from 34-80% in Upper Egypt (N=5) and of 42%, 57% in Central Nile Delta Region (N=2). The major gaps identified across all laboratories referred to documents and records, sample and biorisk management. During this period, eight CPHL scientists received the TOT and became qualified trainers on LQMS, providing training to >40 laboratorians from different governorates. Initial results from monitoring and evaluation showed progress on first phase of stepwise implementation with constitution of quality teams, infrastructure improvements and enhancement of document management. **Conclusions:** Our results using LAT assessments provide baseline data on LQMS for public health laboratories in Egypt. This is an important step to effectively measure the success of laboratory quality improvement programs integrated in the national strategic plan for public health laboratories in order to meet IHR requirements.

Board 32. Overview of FilmArray™ Respiratory Panel Results from the Department of Defense Global Laboratory-based Influenza Surveillance Program

J. Thervil[1,2], S. Zorich[2], R. Yohannes[2]; [1]Oak Ridge Inst. for Sci. and Ed., Oak Ridge, TN, [2]United States Air Force Sch. of Aerospace Med., Wright-Patterson AFB, OH

Background: The Department of Defense (DoD) Global Laboratory-Based Influenza Surveillance Program is a sentinel-based program with over 90 DoD sites worldwide that submit respiratory specimens to USAFSAM for diagnostic purposes and surveillance tracking. **Methods:** For the 2013-2014 and 2014-2015 influenza seasons, the FilmArray™ Respiratory Panel (BioFire Diagnostics, Salt Lake City, UT) was utilized to identify twenty common respiratory pathogens among submitted specimens. Specimens meeting an influenza-like illness case definition underwent viral culture and real-time reverse transcriptase-polymerase chain reaction (rRT-PCR) tests. Specimens testing negative for influenza by rRT-PCR underwent further testing by FilmArray™ with prioritization for specimens from a site with an ongoing outbreak. This prioritization was utilized for a pneumonia outbreak at the United States Air Force Academy (USAFA) in Colorado. **Results:** For the 2013-2014 influenza season, 2,678 specimens were tested via FilmArray™. Among these specimens, 1,489 (56%) tested positive for a respiratory pathogen: 83 adenovirus (5%), 232 coronavirus (15%), 143 human metapneumovirus (10%), 470 human rhinovirus/enterovirus (31%), 35 influenza (2%), 84 parainfluenza (6%), 189 respiratory syncytial virus (13%), 32 *Chlamydophila pneumoniae* (2%), 50 *Mycoplasma pneumoniae* (3%), and 171 co-infections (11%). For the 2014-2015 influenza season so far, 1,191 specimens have been tested with 599 (50%) positive for a respiratory pathogen: 31 adenovirus (5%), 1 *Chlamydophila pneumoniae* (0.2%), 55 coronavirus (9%), 20 human metapneumovirus (3%), 177 human rhinovirus/enterovirus (29%), 25 influenza (4%), 29 *Mycoplasma pneumoniae* (5%), 68 parainfluenza (11%), 113 respiratory syncytial virus (19%), and 80 co-infections (13%). Twenty-seven of the 32 specimens testing positive for *C. pneumoniae* originated from USAFA. **Conclusions:** The FilmArray™ platform enabled the DoD Influenza Surveillance Program to identify numerous pathogens that would have otherwise gone undetected. Laboratory testing of USAFA's pneumonia outbreak specimens by FilmArray™ provided the diagnosis of *C. pneumoniae*. Use of this platform for surveillance of respiratory pathogens has proven beneficial for the DoD population.

Board 33. Assessment of Public Health Laboratory System in Cambodia

S. Sokunna, Alex Coastaal, Toni Whistler; Ministry of Hlth., Phnom Penh, Cambodia

Background: Laboratory services are fundamental parts of all health systems and purpose is to improve health by providing evidence base for detection, management and prevention of diseases. A national policy and national strategy for medical laboratory were signed in 2009 and 2010. The paper focuses on assessment of public health laboratories in Cambodia, particularly communication of public health laboratory system. **Methods:** This paper is part of assessment of national laboratory system in 2013-2014. We conducted in-dept interview with key informant. Twenty two laboratories were assessed by using WHO tool adapted by IQLS system. **Results:** In assessment of the national laboratory system, public health functions received the lowest average score (30%) among 22 lab. Most laboratories are focused on diagnosis to support patient treatment and do not actively participate in public health activities including surveillance, notification and reporting of events of public health importance, and outbreak response. There is lack of knowledge of public health laboratory functions and IHR framework amongst laboratory staff, particularly within Department of Hospital Services, where laboratory is perceived as solely diagnostic service delivery unit for patient care. Laboratory staff is seldom involved in information sharing, strategic decision making and planning for improvement of surveillance programs. **Conclusions:** Public health laboratory functions need to be understood well with implemented, management and policy levels to improve public health laboratories.

Board 34. Severe Acute Respiratory Infection (SARI) and Pandemic Influenza Preparedness Central Public Health Laboratories, Egypt (2007-2014)

A. M. Hasanin, Sr., A. E. Sheta, A. Safwat, N. Fathy, E. Abass, M. Fahim, S. El-Refaey, A. Kandeel; Central Publ. Hlth. Lab., Cairo, Egypt

Background: The national strategy of influenza surveillance in Egypt includes different types of surveillance, sentinel sites for (SARI & ILI),

mission-wide surveillance for influenza including avian & MERS-CoV in 450 hospitals. Also, there is a survey during Hajj season since 2011. Our objective is to detect the predominant virus circulating during influenza season and study the pattern of virus, and any viral mutation that may occur. SARI was implemented on November 2007, and ILI in 2004 under WHO umbrella Sampling, storage and transportation was one of the challenges during our lab work. **Methods:** Samples collected according to SARI and ILI case definition. 2 swabs, oropharyngeal (O.P), and nasopharyngeal (N.P) swabs are taken & both of them put in the same (VTM) viral transport media, then divided into 2 parts, one examined by MOH & the other sent to NAMRU-3 as a quality control. Total nucleic acid (TNA) was extracted, all samples was tested using Real Time PCR for (RNP, serve as internal positive control and against a panel of respiratory pathogen using CDC primers & probes following CDC protocol. Testing for MERS-CoV by RT PCR for all suspected cases as a part of surveillance. Identification and isolation of influenza virus subtypes on virus isolation unit. **Results:** The total SARI samples examined from November 2007 until August 2014 is 16872 samples,119 samples FluA/H1(1%), 676samples FluA/H3(4%), 1199 samples PndH1N1(7%),15 samples H5N1(0.1%), 905 samples FluB(5.4%). The total ILI samples examined from February 2010 until September 2014 is about 9000 samples. The total number of samples examined in CPHL for influenza as our routine work from different governorate on 2014 was 6447 samples. The total number of MERS-COV examined in CPHL was about 2700 samples; only one positive case was detected in Egypt until now. **Conclusions:** The Laboratory And Epidemiology are responsible for implementation of surveillance program, process analysis & report the data, integrating lab results, train staff in the sentinel sites, on sample management, data collection, transportation, preservation. Follow up & regular training of personal decrease the gaps & improve the quality of samples which impacted on the quality of samples arrived to CPHL.

Board 35. The Public Health Laboratory System Database: Developing a National Public Health Laboratory Test Directory

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Background: Detection and control of outbreaks and emerging infectious diseases requires ready access to information on public health testing capacity. The Public Health Laboratory System Database (PHLSD) was developed to improve management of public health laboratory (PHL) data and information and enable creation of a national PHL test directory. The national directory will make detailed test capability information available to PHLs for use in emergency situations or for potential sharing of test services. The PHLSD will also allow each PHL to manage and update data regarding the laboratory's infrastructure, regulatory compliance, and equipment. **Methods:** CDC's Infectious Diseases laboratories' Microsoft Access database was customized for PHL use and includes environmental and other unique PHL testing services and methods, multiple regulatory requirements (e.g., CLIA, FDA, EPA), and a general framework for personnel and equipment inventories. A standardized list of over 2,000 tests and methods was developed and embedded into the database, which has report generation and data export functions. **Results:** The PHLSD is being implemented as a pilot at PHLs; comprehensive test lists are being submitted and shared with neighboring states for emergency preparedness. Full national implementation will involve a Sharepoint webform version of the PHLSD to allow for frequent updates, faster data aggregation, and addition of new variables for emerging diseases and regulatory purposes (e.g., laboratory developed tests). Test service information will be aggregated by APHL to compile a searchable national PHL test directory. **Conclusions:** The PHLSD provides a strategic approach for organizing, sharing, and reporting information, as well as increasing the efficiency of PHL information management. A comprehensive PHL test directory will allow for greater transparency, enhance opportunities for collaboration, and be a resource in times of emergency or surge. The ability to easily modify the database will allow capture of evolving data needs as PHLs fulfill their roles in public health surveillance, outbreak investigations, and emergency preparedness and response that includes rapidly changing technologies and emerging infectious diseases such as MERS-CoV, chikungunya, and Ebola.

Board 36. Disparate Detection Outcomes for Anti-HCV IgG and HCV RNA in Dried Blood Spots

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Background: Dried blood spots (DBS) expedite the collection, storage and shipping of blood samples, thereby facilitating large-scale serologic studies. The sensitivity of anti-HCV IgG testing and HCV-RNA quantitation was evaluated using freshly prepared and stored DBS derived from HCV-infected patients. **Methods:** Protocols for elution were optimized using DBS prepared from plasma of 52 HCV-infected persons and 51 uninfected persons (control DBS), then applied to DBS from 33 chronic hepatitis C patients that had been stored at -20°C for 5 years (stored DBS). Control and stored DBS, and their corresponding plasma, were processed for anti-HCV IgG testing using the VITROS chemiluminescence assay (CIA) and the HCV 3.0 enzyme immunoassay (EIA) (Ortho-Clinical Diagnostics), and for HCV RNA quantitation by quantitative (q) RT-PCR. HCV genotyping was conducted by nucleotide sequencing. **Results:** The sensitivity of CIA and EIA in control DBS was 92% and 90% respectively, compared to 100% and 97%, respectively, in stored DBS. The sensitivity of HCV RNA detection was 88% in control DBS, compared to 36% in stored DBS. Specificity was 100% for all the assays in both control and stored DBS. Genotypes 1, 2 and 3 were detected in 10 (71%), 2 (14.3%), and 2 (14.3%) samples, respectively. Sequences generated from DBS and their corresponding plasma samples were identical. **Summary:** Whereas the sensitivity of anti-HCV IgG detection in stored DBS was equivalent to that in recently prepared DBS, the sensitivity of HCV RNA detection was markedly lower in stored DBS compared to recently prepared DBS. Stored DBS may be reliably used for anti-HCV detection but for HCV-RNA-based testing freshly prepared DBS is preferable to stored DBS.

Board 37. Cluster of False-positive Influenza Rapid Antigen Tests, Denver, Colorado, 2013-14: Impact on Clinical Management and Public Health Surveillance

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Background: Reverse transcription polymerase chain reaction (RT-PCR) testing for influenza at the state public health laboratory of admitted patients in the Denver area revealed a higher-than-expected false positive rate among hospitals using a specific rapid influenza diagnostic test (RIDT) during the height of the 2013-14 season. We examined how these cases may have burdened the healthcare system and the implications for including these cases in public health surveillance systems. **Methods:** Colorado conducts enhanced population-based surveillance for

laboratory confirmed (by any test) influenza hospitalizations (cases) in the 5-county Denver area. Medical charts were reviewed to collect clinical and epidemiologic information, including reason for admission and antiviral treatment. **Results:** The mean false positive rate among cases reported from the subset of surveillance hospitals using a specific RIDT ranged was 40% (range: 19% to 72%); the mean false positive rate among all surveillance hospitals was 21%. Among the false positive cases, 97/185 (52%) were admitted for an acute respiratory illness; 48% were admitted for another reason. Of those admitted for another reason, 73/88 (83%) received antiviral treatment. Although all age groups were affected, including these false positive cases into surveillance had the largest impact on the incidence rates among cases 50-64 and 65+ years of age, increasing the rate by 17% and 33%, respectively. **Conclusions:** This study revealed a high rate of antiviral use in a population of patients not admitted for an acute respiratory illness, possibly due to incorrect results of an RIDT. This finding is concerning, as it unnecessarily contributed to the cost of hospitalization. In addition to poor sensitivity, RIDTs can lead to unwarranted antiviral treatment, and can overestimate the true burden of influenza hospitalizations among certain groups. More sensitive tests such as RT-PCR or culture should be encouraged, particularly among hospitalized patients for whom confirmatory testing may result in a change in clinical management.

Board 38. Evaluation of the Microscopic Observation Drug Susceptibility (MODS) Assay for Direct Detection of MDR-TB and XDR-TB

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Background: The emergence of multidrug-resistant tuberculosis (MDR-TB) and extensively drug-resistant TB (XDR-TB) is widely considered a serious threat to global TB control. Our objectives was to evaluate the MODS assay for direct detection and drug susceptibility testing of TB directly from sputum specimens at the Abbasia Chest Hospital (ACH) and Central Public Health Laboratories (CPHL), Cairo, Egypt, and assess the performance of the MGIT 960 and MODS in second-line TB drug testing. **Methods:** A total of 1,327 sputum specimens were collected from TB suspected cases at ACH and CPHL between June 2010 to May 2012. Samples were tested directly by AFB smear microscopy. Positive and negative AFB smear samples were tested against the MODS assay and the MGIT 960 system to evaluate the diagnostic accuracy of MODS in the detection of TB and the drug susceptibility to isoniazid (INH) and rifampicin (RIF). MDR-TB isolates were tested against second-line TB drugs that included amikacin (1.0 µg /ml), ofloxacin (2.0 µg /ml), levofloxacin (2.0 µg /ml), kanamycin (4.0 µg /ml) using both MODS and MGIT. **Results:** Smear microscopy detected 869 (65.5%) positive AFB specimens of these, MGIT detected a slightly higher number of positive TB cultures: 857 (98.6%) versus the MODS assay which determined 842 (96.7%). Testing the AFB smear negative specimens by using the MGIT yielded a higher percentage of TB positive results: 85 (18.5%) versus 50 (10.9%) detected by the MODS assay. For detection of resistance to INH and RIF, the MODS assay was 88.6% sensitive and 96.6% specific, and 93.2% sensitive and 98.4% specific, respectively. The median time for culture turnaround was shorter for MODS (11 days; IQR 7-15 days) than in MGIT (12 days; IQR 7-17 days). The cost per test for MODS was only $1.16 vs. $58 for MGIT. Second line TB drugs showed a high agreement between MODS and MGIT, reaching 91% for amikacin and kanamycin and 82% for levofloxacin and ofloxacin, respectively (mean = 86.5 %). **Conclusion:** To augment TB detection and drug susceptibility testing in developing countries, MODS was found to offer a simple, rapid and economical assay, not only for delineating MDR strains, but also for testing second-line drugs. It demonstrates comparable sensitivities and specificities to MGIT, but MODS = 2.2% of MGIT cost.

Board 39. A TaqMan Array Card (TAC) for Detection of Pathogens Causing Acute Febrile Illness in East Africa

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Background: Acute febrile illness (AFI) is associated with significant morbidity and mortality worldwide yet an etiologic agent is seldom identified. We developed a TaqMan Array Card (TAC) which enables simultaneous detection of 25 AFI associated organisms, including Chikungunya, Crimean-Congo hemorrhagic fever virus, Dengue, Ebola virus, Bundibugyo virus, Sudan virus, Hantavirus, Hepatitis E, Marburg, Nipah virus, O'nyong-nyong virus, Rift Valley fever virus, West Nile virus, Yellow fever virus, Bartonella spp., Brucella spp., Coxiella burnetii, Leptospira spp., Rickettsia spp., Salmonella spp. and Salmonella Typhi, Yersinia pestis, Leishmania spp., Plasmodium spp., Trypanosoma brucei. **Methods:** The card was validated based upon analytical and clinical performance. Extrinsic controls (PhHV and MS2) were included to monitor the inhibition and assure the validity of testing results. Nucleic acid was extracted and assayed on TAC with a ViiA 7 Real time system. The analytical performance was validated for linearity, repeatability, reproducibility, and matrix inhibition. The clinical performance of the card was measured using 704 blood or serum specimens from outbreak and surveillance investigation from 4 regions of Tanzania from 2012 to 2014. **Results:** On analytical specimens PCR efficiencies of the assays ranged from 85 to 98%. All assays showed good linearity (R2 = 0.992 - 1). The Ct values of had within-run variance from 0.6% to 2.4% (repeatability, n = 8) and between-run variance from 1.0% to 10% (reproducibility, n = 10). Matrix inhibition was rare with only 3.3% of 704 reactions exhibiting inhibition of extrinsic control amplification. On the 704 clinical specimens we obtained 235 positive results (Ct < 45) which were then compared with wet assays and sequencing as the gold-standard. We derived Ct cutoffs such as 34.2 for Dengue, 34.9 for Brucella, 35.7 for Rickettsia, 35.6 for S. Typhi, and 32.8 for Plasmodium which led to an overall 79.4% sensitivity and 99.6% specificity, 91.4% positive predictive value and 99.0% negative predictive value. **Conclusions:** This TAC can be used as a rapid screen for organisms associated with AFI in surveillance and/or clinical care settings. Detection of targets at lower Cts is confirmable by sequencing. Further validation on other pathogens is ongoing.

Board 40. Passive Hepatitis Delta Surveillance in the United States: 2012-2014

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Background: Hepatitis D virus (HDV), also called hepatitis delta virus, is a small circular negative single-stranded RNA virus of approximately 1,700 nucleotides. HDV is considered a defective virus because it requires the hepatitis B surface antigen (HBsAg) to assemble. Like many

RNA viruses, HDV exhibits a high level of genetic diversity. Eight genotypes of HDV have been reported, with genotype 1 being prevalent world-wide, and other genotypes being endemic to different parts of the world. Co-infection or superinfection with HDV can cause more severe hepatitis than HBV infection alone, including more rapid progression to liver disease and higher mortality rates. Currently assays for the detection of HDV RNA are not commercially available. **Methods:** A one-step TaqMan quantitative reverse transcription-polymerase chain reaction (qRT-PCR) assay was developed in-house using primers designed downstream of the HDV antigen gene for the detection of HDV RNA from all eight HDV genotypes. Between 2012 and 2014, 36 clinical samples collected from hepatitis B infected individuals, referred to our laboratory from various parts of the country, were tested for HDV RNA by this newly developed method. **Results:** HDV RNA was detected in 17 (47.2%) of the samples. Of these 17 HDV RNA positive samples, 16 (94.1%) were also HBsAg and anti-HDV positive, while 1 was HBsAg positive, but anti-HDV negative. Of the remaining 19 HDV RNA negative samples, 16 had sufficient volume to test for HBsAg and anti-HDV, of these 10 (71.4%) were HBsAg positive/anti-HDV positive, 4 (25%) were HBsAg positive/anti-HDV negative, 1 (6.3%) was HBsAg negative/anti-HDV positive, and 1 (6.3%) was HBsAg negative/anti-HDV negative. Five individuals were noted to have chronic HBV/HDV infection. Follow up samples were available for four of the samples following anti-viral therapy, three of which had viral loads suppressed by one to five logs. HDV genotype 1 was the only genotype detected among these patients. **Conclusions:** Clinicians should consider HDV infection among HBV-infected individuals in the United States.

Board 41. Performance of a Hepatitis C Virus Core Antigen Assay for Identifying Persons in the United States with Current Hepatitis C Virus Infection

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Background: Hepatitis C Virus (HCV) core antigen is a serological marker other than HCV RNA that is indicative of current HCV infection. The aim of this study was to evaluate the performance characteristics of the Abbott HCV core antigen (cAg) assay applied to blood specimens of HCV-infected persons in the United States. **Methods:** HCV RNA and HCV cAg levels were measured from 551 samples using, respectively, the COBAS Ampliprep/COBAS Taqman HCV v2.0 and the Abbott ARCHITECT HCV Ag test. **Results:** Sensitivity of the HCV cAg assay was >94% in anti-HCV-positive/HCVRNA-positive samples, and 100% in anti-HCV-negative/HCVRNA- positive samples. **Conclusions:** Correlation between HCVcAg and HCV RNA levels was 0.959. HCV cAg testing may be reliably used to identify current HCV infection.

Board 42. Combined Anti-hepatitis E Virus IgG Serotesting for Resolving Hepatitis E Virus Epidemiology in the United States

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Background: One puzzle of the epidemiology of Hepatitis E Virus (HEV) infection in the United States emanated from the report of Kuniholm *et al.* (*J Infect Dis* 2009: 200:48) which showed an unexpectedly high anti-HEV-IgG detection rate of 21% (confidence interval: 19%-22.9%) obtained after testing 18,695 participants of the NHANES III (conducted between 1994 and 1998). Whether that estimate could be due to the performance characteristics of the in-house immunoassay used by Kuniholm *et al.* was examined in the current study, which involved testing with 3 other assays: 2 commercially available anti-HEV IgG assays (DSI and Wantai) and an in-house western blot (WB) assay. **Methods:** Serial dilutions of the WHO reference HEV standard showed that the limit of detection was 1000 mIU/mL for the DSI assay, 100 mIU/mL for the Wantai assay and 200 mIU/mL for the WB assay. These were higher than the detection limit of 40 mIU/ml reported for the assay used by Kuniholm *et al.* A total of 1804 NHANES III sera previously tested by Kuniholm *et al.* and weighted to over-represent reactive samples were then selected and tested by the DSI, Wantai, and WB assays. **Results:** Of that total, 727 (41%) and 202 (11%) were reactive and non-reactive, respectively, in all 4 assays. Of the remaining 875 specimens, 456 (25% of total) were reactive in 3 assays, 203 (11% of total) in 2 assays, and 216 (12% of total) in 1 assay. Overall, the Wantai assay generated 1354 (75%) reactivities, of which 1159 (86%) were concordantly reactive by WB. Using reactivities in both Wantai and WB assays as referent, sera that were tested in the assay of Kuniholm *et al.* were 98% concordantly reactive. However, 39% of sera that were reactive in the assay of Kuniholm *et al.* were unreactive in both the Wantai and WB assays. **Conclusions:** Such discordance that could have been contributed by the higher sensitivity and the lower specificity of the assay of Kuniholm *et al.* compared to the other assays. Further resolution of the extent of HEV transmission in the United States would require judicious application of anti-HEV assays, severally and in combination, and formulation of anti-HEV testing algorithms.

Board 43. Investigation of Acute Neurological Disease Using a Simple Differential Diagnostic Tool for 29 Etiological Agents of Febrile Disease in South Africa

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Background: Acute febrile disease often remains undiagnosed in Africa because of a lack of capacity to test for a wide range of pathogens. We recently described a simple macroarray-chip of high specificity and sensitivity that can detect 29 etiologies of febrile disease, hemorrhagic fever, and meningo-encephalitis in low resource settings. Here we applied itthe chip for differential diagnosis of acute febrile and neurological disease in South Africa. **Methods:** >1800 CSF samples from hospitalized patients with acute neurological disease were collected over 2 years (2012-2014) from microbiology and virology departments, National Health Laboratory Services, Tshwane serving 3 hospitals in Pretoria, South Africa. Clinical data was collected from diagnostic records and entered into a database. 27 known positive cases including rabies, Crimean-Congo hemorrhagic fever (CCHF), Rift Valley fever (RVF), West Nile virus (WNV), chikungunya, and dengue, and 50 meningoencephalitis CSF specimens from other parts of Africa were used for proof of principle. The chip was applied to screen total nucleic acids of both blinded positives and specimens from patients with unsolved neurological or fever signs. All positives results were confirmed by single PCR and sequencing. **Results:** All 29 positive controls and 27 known positive febrile, neurological and hemorrhagic fever cases were correctly identified. Screening of 181 randomly selected CSF specimens from unsolved acute neurological cases from South Africa identified two enterovirus, 3 Epstein-Barr, one hepatitis B, one rabies virus and three *Neisseria meningitides* positives, while 8 *Plasmodium falciparum* positives were identified from the rest of Africa. All cases were confirmed by PCR and sequencing. **Conclusion:** Screening of 181 unsolved neurological cases in hospitalized patients

identified several common viral and bacterial pathogens as well as rabies in patients with neurological disease in hospitals in South Africa. Screening of neurological cases continues to describe the cause of neurological disease in this setting. Implementation of the chip as differential diagnostic tool in low resource settings may help to solve febrile, neurological or hemorrhagic fever outbreaks in Africa.

Board 44. The Detection of Anti-dengue Virus IgM in Urine as a Putative Marker for Severe Disease

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Background: Dengue is globally the most important arbovirus disease with an estimated 300 million dengue virus (DENV) infections however, only 100 million dengue cases are reported per year. It is estimated that 5-10% of cases result in severe dengue, which may include glomerular changes associated with renal dysfunction. We looked for the presence of anti-DENV IgM antibodies in urine as an indicator for severe dengue among patients identified with acute febrile illness in our Sentinel Enhanced Dengue Surveillance System (SEDDS) site in Ponce, Puerto Rico. **Methods:** Between May 2012-March 2013, 1560 patients with fever or history of fever for ≤7 days were enrolled, a past medical history of chronic illnesses was obtained, and they were followed through their febrile illness. Serum and urine specimens were collected during the acute (days post onset of fever (dpo)=0-5) and convalescent phase (dpo=6-14) of their illness. Acute sera were tested for DENV RNA by RT-PCR. All urine specimens were tested for anti-DENV IgM. The results from the urine anti-DENV IgM were compared to serum to determine sensitivity and specificity. To determine if IgM in urine might be an indicator of disease severity, we compared this result to the WHO 2009 classification of severe dengue, dengue with warning signs and dengue without warning signs. **Results:** The sensitivity of urine anti-IgM was 37% and specificity was 98% compared to serum. When compared to serum RT-PCR results, the sensitivity of IgM in urine was 24% and the specificity was 93%. Patients classified with severe dengue were more likely to test positive for IgM in the urine after dpo≥6 compared to dpo=0-5 (p=.001) and those classified as dengue with warning signs were more likely to test positive for IgM in the urine after dpo≥6 compared to dpo=0-5 (p<0.01). There was no significant difference in IgM in urine between dpo=0-5 and dpo≥6 for patients classified with dengue without warning signs. There was no correlation between the presence of IgM in urine with sex, age or pre-existing chronic diseases such as diabetes, high blood pressure, or anemia. **Conclusion:** While detection of anti-DENV IgM in urine lacked adequate diagnostic sensitivity when compared to serum, its presence may be a marker for hospitalization or disease severity.

Board 45. Differences in Viral Antigens Distribution Between Wild Type and Vaccine-associated Viscerotropic Yellow Fever Fatal Cases

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Background: Yellow fever (YF) virus is endemic in tropical regions of South America and Africa. Vaccine is indicated for patients for travel to these areas. Although considered a safe vaccine, reports published since 2001 indicate that vaccine can cause a severe, often fatal, multisystemic illness named vaccine-associated viscerotropic disease (YEL-AVD). From 2008 to 2009, two outbreaks of YF occurred in Brazil in previously unvaccinated populations. Over 5.5 million doses of 17DD yellow fever vaccine were administered. Vaccine-associated adverse events were associated with YEL-AVD and resulted in fatal cases. **Methods:** From 2008 to 2009, 22 yellow fever cases were submitted to the Adolfo Lutz Institute in Brazil for pathologic evaluation. Immunohistochemistry (IHC) and reverse transcription polymerase chain reaction (RT-PCR) in paraffin-embedded tissues confirmed the diagnoses in 19 cases. History of vaccination and other epidemiologic data were collected from all patients. This study was designed to compare histopathologic features and IHC localization and distribution of viral antigens in wild type (WT) and YEL-AVD, and was done by two pathologists in a blinded fashion. **Results:** Out of 22 cases, 7 cases of YEL-AVD and 7 cases of WT were identified, and 5 could not be differentiated by using PCR. Histopathology in both groups was similar. IHC staining was seen in hepatocytes and Kupffer cells in WT; while in YEL-AVD staining was observed in hepatocytes, Kupffer cells and mesenchymal cells. Extrahepatic immunostaining was observed in mesenchymal cell in different organs. **Conclusions:** Mesenchymal cell immunostaining is pathognomonic for YEL-AVD. The difference in viral antigen distribution can be used to distinguish the YF fatal cases and is most likely associated with different viral and host factors. Further studies are needed to better understand the pathogenesis of YEAL-ADV.

Board 46. Reference Laboratory of Malaria as an Element of Vigilance in Armenia

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Background: The concept of vigilance for malaria was first introduced in the Global Malaria Eradication Program. A critical component of vigilance is a reference laboratory. **Methods:** The Parasitological Laboratory of the National Center for Disease Control and Prevention in Armenia was established as the national reference laboratory for malaria. The laboratory conducts laboratory confirmation of all suspected malaria blood films following primary diagnosis by clinical laboratories. The diagnosis is confirmed microscopically with thick and thin blood smears stained with Giemsa stain. The laboratory also conducts monthly quality assurance monitoring by randomly testing 10% of all negative slides from the marz-level (district-level) clinical laboratories. **Results:** The establishment of a reference laboratory for malaria has resulted in prompt and accurate parasitological diagnosis of malaria. The laboratory is also the national center for epidemiological monitoring of malaria and is the main authority of expertise. The laboratory carries out educational campaigns and trainings; conducts research on diagnostics and relevant aspects of diagnosis and prevention; collects and analyzes all records of malaria; and maintains a national database on malaria cases. This improved laboratory surveillance contributed to the elimination of the disease. In 2011, Armenia was declared malaria-free. **Conclusion:** The establishment of a malaria reference laboratory has strengthened the quality of malaria diagnosis in the country, and has contributed to Armenia's malaria-free status.

Board 47. Laboratory Diagnostics of Equine Influenza

M. Peknyi[1], S. Nychyk[1], V. Synycyn[1], M. Sytiuk[1], R. Kapraliuk[1], V. Evtushenko[1], N. Hudz[1], S. Doleckiy[2]; [1]Inst. of Vet. Med. of the NAAS, Kyiv, Ukraine, [2]Natl. Academy of Agrarian Sci. of Ukraine, Kyiv, Ukraine

Background: There were registered cases of equine influenza in Ukraine in 2002, 2004, and 2010, and still there is a threat of new outbreaks. Today the majority of farms have blanket vaccination against equine influenza, so in many cases laboratory tests should be used to check the effectiveness of vaccination by determining the titer of antiviral antibodies in the blood serum of horses. That is why the aim of the work was to develop native

tests for serological diagnosis of equine influenza for HI and ELISA. **Methods:** Equine influenza virus strains A(Equine)2(Miami)63(H3N8) and A(Equine)1(Cambridge)63(H7N7), positive reference serum against the strains, set of antigens and sera for diagnosis of equine influenza produced by Kursk biofactory, serum of vaccinated horses were used in this work. Sera were divided into aliquots and investigated simultaneously in test systems of our production based on hemagglutination-inhibition test (HI), ELISA and Kursk biofactory test-kit for HI test. In the research we used sera samples which were previously determined to be positive to compare antibody titers in various reactions. **Results:** A simultaneous study of 60 sera samples using our test system in HI test there were registered 40 positive samples, using Kursk biofactory test-kit in HI test - 41 positive samples, using our test system in ELISA - 43 positive samples. Antibody titers in HI test coincided in 70% with the difference up to 1 log2, all sera antibody titers were higher on 2-3 log2 in ELISA. **Conclusions:** The difference in antibody titers between HI test and ELISA could be due to the fact that HI test detects only hemagglutinins while ELISA different antibodies. Based on the results we believe that developed test systems sensitivity and specificity are equal to foreign analogues and can be widely used in practice of veterinary medicine laboratories.

Board 48. Genetic Diversity of *Mycobacterium tuberculosis* and Mutation Profiles in Drug Resistance Associated Genes in Bagamoyo District, Tanzania

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Background: Tuberculosis (TB) remains one of the most infectious diseases and a major public health problem globally. The emergence and spread of TB drug resistance aggravates the burden of this disease to the community. In many resource-limited countries, there is no regular TB drug resistance surveillance and treatment is initiated without drug sensitivity testing. Hence, TB drug resistance in these countries remains largely unknown. Moreover, the prevalence of resistance-associated mutations may vary by geographic area, as do the distribution of *M. tuberculosis* strains. This calls for concrete efforts to stop development and spread of TB resistance in the community. **Method:** Overall, a total of 114 *M. tuberculosis* isolates from TB patients residing in Bagamoyo district in Tanzania were analyzed for genetic diversity, and assessed for drug resistance mutations in nine genes (*KatG, inhA, ahpC-OxyR*, *rpoB*, *pncA*, *embB*, *rrs*, *rpsl*, and *gyrA*) associated with TB drug resistance by employing a rapid and high-throughput Sequenom's massARRAY system. **Results:** We defined 14 *M. tuberculosis* haplotypes and 4 SNP clusters. Predominant haplotypes were BAG8 (36%), BAG14 (24%), and BAG6 (18%). On the other hand, we observed only 5% (3/61) of isolates with *katG*315 SeràThr mutation which is commonly associated with isoniazid resistance. No any other drug resistance associated mutations were detected. We also observed high prevalence of non-synonymous mutations at *embB*1054, SeràPro (14%), *katG*463, ArgàLeu (34%) and *gyrA*384, AlaàVal (21%). **Conclusions:** For the first time, our study demonstrated the genetic diversity of *M. tuberculosis* and presents haplotypes that may be valuable for molecular surveillance of TB transmission in the study area. Furthermore, our study confirmed low-grade TB drug resistance in the Bagamoyo district in Tanzania. We recommend for rational TB treatment to prevent the emergence and spread of resistant strains, and a countrywide study to assess importance of the defined haplotypes in TB epidemiological studies in Tanzania.

Board 49. Detection of *Bacillus anthracis* and Determining the Presence of Plasmid rX01 and rX02 in PCR

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Background: The complexity of the genetic identification of *Bacillus anthracis* caused significant homology genomes of representatives of *Bacillus cereus* and the presence of 4 different plasmid composition variations in anthrax strains. Therefore, research focusing on the identification of virulence-associated markers that discriminate between virulent and avirulent isolates was performed. The study focused on the selection of effective combinations of oligonucleotide primers to identify the major virulence factors of anthrax plasmids pXO1 and pXO2. **Methods:** We used *B. anthracis* (Tsenkovsky-2, UA-07, K79Z, 55, 34F2, CB-072), *B. cereus* 2527, *Bacillus subtilis* 7241, and *Bacillus anthracoides* 1312 strains. These microorganisms are most commonly isolated in Ukraine. *B. anthracis* strains are used for vaccine production in Ukraine. Only Tsenkovsky-2 strain of B. anthracis was pXO1+/pXO2+, other strains were pXO1-/pX02+. The *B. anthracis* strains were tested isolated to determine the virulence on animal model (guinea pigs). The oligonucleotide primers for plasmids pXO1 (pA gene) and pXO2 (capsule gene) were used in PCR tests. Chromosomal DNA isolations and routine DNA techniques were performed by Sambrook et al. (1989). As the positive and negative controls it was used ones from commercial test kit "SibDif", Amplisence, Russia. **Results:** It was designed the primers to detect and identify pXO1 and pXO2 plasmids in multiplex PCR. Experimentally confirmed the ability to detect DNA fragments of plasmids (pA gene of protective antigen) and capsule gene in multiplex PCR. It was found that strain Tsenkovsky-2 revealed the presence of both plasmids. Only this strain has capsule, it confirmed the specificity of the test. All other tested strains were identified as pXO1-/pXO2+. These assay validated by comparing results of in vitro/in vivo testing and PCR. **Conclusions:** Designed primer set for detection and differentiation of capsular and acapsular strains of *B. anthracis* with detection of pXO1 and pXO2 plasmids. It was analyzed the diversity of pXO1 and pXO2 plasmids among *B. anthracis* museum and vaccine strains from our collection. The assay may be an important diagnostic tool to detect virulent strains. It can help to improve control *B.anthracis* infection in Ukraine.

New or Rapid Diagnostics

Monday, August 24, 12:30 PM - 1:45 PM

Grand Hall

Board 50. Performance of Quidel Sofia Rapid Diagnostic Influenza Test, 2012-2014

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Background: Since 2004, the Naval Health Research Center (NHRC) has collaborated with the US Centers for Disease Control and Prevention's Border Infectious Disease Surveillance program and state and local health officials, to conduct influenza-like illness (ILI) surveillance in the US-Mexico border region. Results from this program are used to evaluate rapid influenza diagnostic tests (RIDT). Participating California clinics tested each ILI patient with a commercial RIDT. **Methods:** NHRC provided 3 of 4 clinics with the Quidel Sofia - Fluorescent Immunoassay Analyzer (San Diego, CA) to replace the Quidel QuickVue RIDT (clinics A, B, and C). One clinic (D) continued to use the Quidel QuickVue test. In 2013-2014, all 4 clinics used the Sofia RIDT. All persons of any age meeting the case definition (temperature ≥100°F, and sore throat or cough) were enrolled and sampled. Two nasal swabs were collected: one for the RIDT, the other tested by reverse transcription polymerase chain reaction (RT-PCR). RIDT results were compared with RT-PCR results to determine sensitivity and specificity for each RIDT. **Results:** In 2012-2013, clinics A, B, and C tested 372 ILI patients; clinic D tested 102 ILI patients. Overall sensitivity and specificity of the Quidel Sofia were 83% and 81%, and 59.0% and 100% for the Quidel QuickVue. Influenza A sensitivity and specificity were: Quidel Sofia, 82% and 98%; Quidel QuickVue, 57% and 100%. Influenza B sensitivity and specificity were: Quidel Sofia, 84% and 83%; Quidel QuickVue, 62% and 100%. In 2013-2014, the Quidel Sofia was used to test 499 ILI patients at 4 clinics. Overall sensitivity and specificity were 62% and 92%. Influenza A sensitivity and specificity were 70% and 97%. Influenza B sensitivity and specificity were 53% and 95%. **Conclusions:** *I*n 2012-2013, the Quidel Sofia had higher sensitivity than the Quidel QuickVue test when compared to RT-PCR for all influenza viruses, influenza A, and influenza B. Quidel Sofia had a decreased specificity for all influenza viruses and influenza B. False-positive influenza B results, which were observed with the Quidel Sofia, resulted in decreased specificity. In 2013-2014, Quidel Sofia results were very similar to what we have observed for the Quidel QuickVue in the same population over the last 7 influenza seasons_poor sensitivity and very good specificity.

Board 51. Establishment of a National Influenza Centre (NIC) in a Post Conflict and Resource Limited Country (Afghanistan): Progress and Challenges

G. E. Sharifi, Sr.; Central Publ. Hlth. Lab., Kabul, Afghanistan

Background: Afghanistan's National Influenza Centre was established at the Central Public Health Laboratory (CPHL) as (BSL-II) in March 2007. The centre was created in response to the need for local monitoring of influenza cases in the wake of avian influenza outbreaks across south-east Asia. The NIC receives human samples from hospitals or communities where Influenza-like-illness (ILI) has been detected, through the DEWS system. **Methods:** Initial infrastructure was put in place for a three-suite PCR lab and viral culture room by the US Naval Medical Research Unit No. 3 (NAMRU-3). The suite is currently located in the CPHL virology department and in at the Afghan National Army Hospital Lab (ANA) which provides technical assistance to the MoPH projects and to the Afghan National Army clients. Laboratory technicians have been trained by NAMRU-3 and others to perform selection of influenza PCR assays (a NAMRU-3 assay for A-H3, A-H5, the CDC swine flu assay) and viral culture. Thus far, the facility has successfully partaken in two WHO-EQA Program assessments, with the result that the centre received WHO accreditation in January 2009. Furthermore, the CPHL receives quality control (QC) tests on regular basis and has achieved full score in EQA program 2012 for the detection of influenza virus A by PCR. **Results:** From June 2007 to Dec 2011, over 9,000 respiratory samples were collected by the Disease Early Warning System (DEWS) from different provinces across the country. Of these, 4,163 samples were screened by rapid test (Respi-Strip) for influenza types A and B. The results for rapid test positive samples were confirmed and further sub-typed by real-time reverse transcriptase PCR (CDC swine flu assay). Non-H1N1 Influenza A (not otherwise sub-typed) was identified in 4.6% (82/1778) of PCR-tested samples, while novel variant H1N1 was detected in 15% (266/1778). The highest test positivity rates for seasonal influenza and novel variant H1N1 were observed in Kabul (17%), Herat (10%) and Bamyan (10%) provinces. It was also observed that the month of October of each year has the highest test positivity rate (26%) followed by November (18%) and December (9.5%). Furthermore, the CPHL has received 1380 samples in year 2012 and out of this 202 samples processed with 1% positivity rate and rest 1178 samples are pending for reagents/kits.

Board 52. Evaluation of the Performance of Rapid Diagnostic Tests for Rotavirus and Cholera in Dadaab Refugee Camp and the Kenya/Somali Border

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Background: Refugee camps located in remote areas often have diarrhea outbreaks caused by cholera or rotavirus. Rapid diagnostic tests (RDTs) are feasible alternatives for determining cholera and rotavirus outbreaks in refugee camps with inadequate laboratory capacity. We field tested rotavirus and cholera RDTs in Dadaab Refugee Camp and communities on the Kenya/Somali border. **Methods:** May - December 2014 (mostly dry season), we prospectively enrolled suspected rotavirus (hospitalized child <5 years with acute diarrhea) and cholera (person ≥2 years with acute diarrhea) cases. Acute diarrhea was defined as ≥3 episodes of loose stool in 24 hours for less than 7 days. Trained surveillance clerks tested stool from suspected rotavirus and cholera cases using Immuno*Card* STAT!® Rotavirus (ICS-RV) and Crystal VC® RDTs, respectively, per manufacturers' instructions. We compared the RDTs with the gold standard of culture for *Vibrio cholerae* and an immunoassay for rotavirus (Premier™ Rotaclone® Enzyme Immunoassay). Additionally, we evaluated user acceptability of both RDTs by administering a standardized questionnaire. **Results:** We enrolled 213 suspected rotavirus and 183 suspected cholera cases. The median age of suspected rotavirus cases was 10 (range 1-48) months, and 58.2% were male. The median age of suspected cholera cases was 3.5 (range 2-92) years, and 49.7% were male. The sensitivity, specificity and positive & negative predictive values (PVs) of ICS-RV as compared with the immunoassay were 83.1% (95% CI: 72.3-91.0%), 99.3% (95% CI: 96.1-100%), 98.3% (95% CI 91.1-100%) and 92.1% (95% CI 86.6-95.9%), respectively. The specificity and positive & negative PVs of Crystal VC when compared to culture were 95.6% (95% CI: 91.6-98.1%), 0% (95% CI: 0-36.9%), and 100.0%

(95% CI: 97.9-100%), respectively. There was no culture-confirmed cholera hence the sensitivity of Crystal VC was not applicable. Users found both RDTs easy to use. **Conclusions:** ICS-RV can be useful to determine rotavirus outbreaks since it had high sensitivity, specificity and PVs in field conditions. Crystal VC was evaluated when there was no cholera, hence its performance cannot be assessed. Further evaluation is planned when the rainy season begins. Both RDTs required little technical expertise.

Board 53. Assessment of Arbor Vita A/H7N9 Rapid Subtyping Test

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Background: The Directorate of Operational Infectious Diseases at the Naval Health Research Center (NHRC) has been tasked with evaluating new technologies for pandemic preparedness including furthering the development of point-of-care diagnostics for avian influenza strains. The US Department of Defense is interested in having a rapid diagnostic capable of identifying the dangerous H7N9 virus strain to help protect military populations stationed in Southeast Asia. NHRC has partnered with Arbor Vita Corporation (AVC) in support of achieving FDA approval for the A/H7N9 Influenza Rapid Subtyping Test capable of detecting H7N9. Arbor Vita's assay technology specifically detects the influenza A/H7N9 virus and is based on detection of the influenza virus nonstructural protein 1 (NS1). **Methods:** A prototype of the AVC A/H7N9 Influenza Rapid Subtyping Test was developed by testing the selected monoclonal antibodies (mAb) specific to influenza A/H7N9. The test specificity for influenza A/H7N9 was determined by comparing mAb affinity for A/H7N9 NS1 protein to NS1 proteins based on sequences from the following influenza strains: seasonal A/H1N1, 1918 pandemic A/H1N1, 2009 pandemic A/H1N1, seasonal A/H3N2, and human A/H5N1. The A/H7N9 Flu Test prototype was also tested on influenza viral culture by the Naval Research Laboratory, NHRC, and University of Hong Kong to demonstrate a successful working prototype. **Results:** Proof of concept of the device and development of a working prototype have been completed. Cross reactivity of the A/H7N9 Influenza Rapid Subtyping Test was evaluated at Arbor Vita Corporation, NHRC, Naval Research Laboratory, and Hong Kong University. The strains were tested using viral cultures or recombinant proteins. The A/H7N9 test detects human A/H7N9 and does not detect seasonal influenza A or pandemic H1N1. The pandemic flu A test detects all influenza A strains evaluated. The US Food and Drug Administration (FDA) issued an Emergency Use Authorization for this device on April 25, 2014. **Conclusion:** NHRC will continue to collaborate with AVC to reach the goal of achieving FDA approval for the device, including performing analytical performance studies and being a key performer in the clinical trial.

Board 54. Immunodiagnostic Development for Lyme Disease Targeting *Borrelia burgdorferi* HtrA Protease

X. Tang[1], T. Russell[2], R. L. Pitts[1], J. Lee[1], B. J. Johnson[2], J. M. Goldstein[1]; [1]CDC, Atlanta, GA, USA, [2]CDC, Fort Collins, CO, USA

Background: The bacterium *Borrelia burgdorferi* is the etiological agent of Lyme disease and is transmitted to humans through the bite of infected blacklegged ticks (Ixodes ricinus complex). BbHtrA is a member of the highly conserved HtrA family of chaperone proteases believed to act as virulence factors. Potential BbHtrA contributions to virulence include the recently described degradation of numerous extracellular matrix proteins and the induction of inflammatory signals. **Methods:** In our study, the wild type BbHtrA gene and the enzymatically-inactive point mutant S226A were cloned and expressed in *E. coli*. Soluble protein was extracted and purified by His-tag with extensive washing to remove the bacterial endotoxin followed by positive identification by Mass Spectrometry. To characterize the oligomeric state of purified protein, we employed size exclusion chromatography. To facilitate the investigation of BbHtrA as a suitable biomarker for active disease, S226A was used to immunize mice for the development of mAbs for the clinical detection of BbHtrA. **Results:** 1. Wild type BbHtrA was found to hydrolyze substrates and maintain serine protease activity while S226A remained inactive. In addition to predicted self-cleavage, BbHtrA could degrade casein and native decorin. 2. In the absence of any substrate, both BbHtrA and S226A formed trimers. However, in the presence of the substrate casein, S226A formed hexamer while BbHtrA remained as trimer. 3. Stable hybridoma cell lines were derived that produced high affinity monoclonal antibodies reactive to both forms of BbHtrA. **Conclusions:** The purified IgGs are highly specific and show promise for the development of immunodiagnostics for rapid detection of *B. burgdorferi* infection.

Board 55. Application of Genotypic Characterization for the Direct Detection of Drug Resistant Genes in *Mycobacterium tuberculosis* in Clinical Samples from Children

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Background: With the introduction of multidrug therapy, new forms of drug resistance have emerged. In this study, nine genome regions associated with drug resistance (DR) in *Mycobacterium tuberculosis* were amplified, including *rpoB* for rifampin (RIF), *katG*, *inhA* and *mabA* for isoniazid (INH), *embB* for ethambutol (EMB), *pncA* for pyrazinamide (PZA), *rpsL* and *rrs* for streptomycin (STR) and *gyrA* for levofloxacin. In this study, two clinical samples from children were applied for detection of drug resistance (DR) genes in *Mycobacterium tuberculosis*. **Methods:** A combination of genotypic characterization consisted of multiplex polymerase chain reaction (PCR), high resolution melting (HRM) and sequencing analyses of targeted regions in *rpsL* and *rrs* were conducted. Few steps including the extraction of DNA from clinical samples and quantitation PCR (qPCR) were initially performed for detection of *M. tuberculosis* DNA. Then, the DNA samples were examined with multiplex PCR that consisted of nine genome regions associated with DR genes in two sets of PCR reactions. The analysis was followed with the HRM and sequencing analyses of *rpsL* and *rrs* for STR. **Results:** Using the multiplex PCR, we were able to amplify genotypes that were resistant to at least one drug. Nevertheless, using HRM analysis, the DNA templates from children clinical samples produced a unique and different cluster pattern as compared with the reference strains. As for the sequencing analyses, a guide tree showed branching of the clinical samples and the references strains. **Conclusion:** This genotypic characterization is useful for the detection of DR genes in *M. tuberculosis* from DNA directly extracted from children clinical samples. Thus reducing the time needed to diagnose TB with an enhancement for the detection of DR strains. **Keywords:** Children TB; clinical samples; drug resistant (DR); *M. tuberculosis*

Board 56. Comparison of a Multipathogen Detection Platform to Singleplex qPCR Assays for Detection of Respiratory Infections Among Persons at Nine International Sites

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Background: The Taqman® Array Card (TAC) uses real-time reverse transcriptase polymerase chain reaction (rRT-PCR) to rapidly and simultaneously detect multiple pathogens. We evaluated this platform in ten international sites using previously tested respiratory clinical specimens. The objectives were to evaluate the capacity and performance of TAC using archived specimens containing known pathogens previously identified by molecular methods. **Methods:** Each site identified 60-120 nasopharyngeal and/or oropharyngeal specimens previously tested with singleplex rtPCR assays. Total nucleic acid (TNA) was re-extracted utilizing methods available to each lab and tested for the presence of 30 viral and bacterial pathogens using the TAC platform. Discordant results were retested using the appropriate singleplex assay. To estimate sensitivity of TAC, we used the newly acquired singleplex results as the gold standard where available; otherwise, we used the historic molecular results as the gold standard. Calculations of sensitivity were limited to targets which had ≥5 positive singleplex assay results. **Results:** A total of 875 specimens were tested at ten international sites utilizing six different extraction platforms. Fourteen of thirty total targets had ≥5 positive singleplex results. Sensitivity data for these 14 assays ranged between 72% (Parainfluenza virus 1) and 100% (*Staphylococcus aureus* and Coronavirus HKU1). Eight targets had sensitivity >90% and 5 targets had a sensitivity of 81-90%. Sensitivities of influenza A, respiratory syncytial virus, and *Streptococcus pneumoniae* were 98%, 95%, and 83%, respectively. In 81% of specimens, more than one target was detected on TAC. **Conclusions:** The overall concordance of data between the assessed singleplex assays versus those on TAC suggests that this multipathogen detection platform provides a valuable tool for simultaneously and rapidly detecting respiratory agents. The compared sensitivity data also suggest that extraction methodologies for TNA play a minimal role in detection performance. The high proportion of specimens with multiple detections highlights the potential role of co-infections leading to respiratory disease as well as the need to distinguish carriage from causality.

Board 57. A Loop-mediated Isothermal Amplification Method for Rapid Detection of *Salmonella enterica* Serovar Typhi Infection

M. Yan, F. Fan, P. Du, B. Kan; Natl. Inst. for Communicable Disease Control and Prevention, Chinese Ctr. for Disease Control and Prevention, Beijing, China

Background: Typhoid fever caused by *Salmonella enterica* serovar Typhi remains a public health concern. Patient with typhoid fever presents similar symptoms with other febrile illnesses, making the etiological diagnosis of the disease very important. Blood culture is commonly used but is time-consuming, and antibody detection lacks specificity and sensitivity. The rapid, simple and inexpensive technique for specific diagnosis of *S.* Typhi infection is still needed especially in the regions with high incidence of typhoid. **Methods:** A Loop-Mediated Isothermal Amplification (LAMP) method to detect *S.* Typhi DNA was developed. To obtain the specific genes of *S.* Typhi, two screening rounds were performed. Firstly, the genes shared by two *S.* Typhi strains, CT18 and Ty2, were identified and searched to the genome sequences of other *Salmonella* serotypes on GenBank, and then compared with the human genome. The alignments less than 50% of the gene size were ignored. A total of 125 genes were obtained. In the second round, 22 *S.* Typhi strains and 75 non-typhoidal strains covering 34 *Salmonella* serotypes were used to examine the specificity of these 125 genes by PCR. The resulting specific genes were used as the targets to develop the LAMP assay. The specificity and detection limit of the LAMP reaction was evaluated and compared with the corresponding real time PCR (RT-PCR) using *S.* Typhi simulated stool and blood specimens. **Results:** *S.* Typhi gene STY2879 was selected as the target gene for setting up LAMP detection using Loopamp® DNA amplification reagent. STY2879 can be amplified in all the *S.* Typhi strains isolated in different years and regions, whereas no amplification was observed in non-typhoidal strains. For the sensitivity of STY2879-LAMP assay, 15 copies/reaction of the reference plasmid carrying STY2879 gene can be detected, and 2×10^2 CFU/g in the simulated stool samples, 20 CFU/mL in the simulated blood can be reached, which are 10-100 fold higher than RT-PCR. In addition, the positive reporting time of the LAMP was 3-5 hours earlier than RT-PCR. **Conclusions:** The LAMP assay of *S.* Typhi infection basing on STY2879 gene has higher sensitivity, specificity and short reporting time when compared to RT-PCR and culture methods, combined with its simple performance, indicating a good potential use in the diagnosis of *S.* Typhi infection.

Board 58. Development and Characterization of Mouse Monoclonal Antibodies Against Monomeric Dengue Virus Non-structural Glycoprotein 1 (NS1)

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Background: Dengue virus (DENV) nonstructural-1(NS1) glycoprotein is used for diagnosis of DENV infections in the first 8 days of illness with any of the four serotypes (DENV-1-4). Commercial NS1 tests have been developed but have limited sensitivity in secondary DENV infections since most patients presenting with dengue in endemic countries are predominantly secondary infections. This decrease in sensitivity is the interference of immune complex formation between NS1 antigen and reactive anti-DENV NS1 antibodies from a previous DENV infections. In order to improve the sensitivity of the NS1 test, we propose the incorporation of a heat-mediated immune-complex dissociation (ICD) step prior to testing serum samples which requires monoclonal antibodies (MAbs) reactive to heat-denatured NS1. **Methods:** In order to incorporate a simple heat-mediated ICD step, we developed new MAbs with high affinity and specificity to heat-denatured DENV NS1 protein. In the present study, six new MAbs were isolated from BALB/c mice immunized with recombinant monomeric NS1 of DENV-1 or DENV-2 and characterized by three different immunoassays: indirect enzyme linked immunosorbent assay (ELISA), fixed cell ELISA and western blot. **Results:** Characterization with these three different methods revealed that all six MAbs were serotype-reactive and capable of recognizing NS1 in dimeric and hexameric isoforms as well as heat-denatured NS1 from all four DENV serotypes. No cross-reactivity to NS1 of West Nile virus and Yellow fever virus was observed in the western blot and indirect ELISA. Five of the six MAbs mapped to the DENV NS1 region of 105-119 amino acids. The remaining MAb mapped to DENV NS1 region of 25-39 amino acids. These two NS1 regions were found to be highly conserved among all four DENV serotypes by sequences analysis and database comparison. **Conclusion:** Taken together, our results suggest the use of these newly developed MAbs for the development of immunodiagnostic assays that capture and detect heat denatured NS1 from all four DENV serotypes as a method to improve NS1 ELISA sensitivity in secondary DENV infections.

Board 59. The Utility of a Rapid Dengue Diagnostic Test to Detect Outbreaks in Places Lacking Established Diagnostic Testing — Angola, Republic of the Marshall Islands, Federated States of Micronesia, and Fiji

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Background: Dengue is global public health problem which lacks effective prevention methods (e.g., vaccines, vector control). Dengue presents as an acute febrile illness (AFI) that is not readily differentiated from malaria, leptospirosis, influenza and chikungunya in tropical areas except through laboratory testing. However, many areas where dengue occurs do not have laboratory capacity to conduct dengue diagnostic testing. Rapid diagnostic tests (RDTs) are available for detection of IgM antibody to dengue virus (anti-DENV IgM) and DENV non-structural 1 (NS1) antigen; testing for both increases the accuracy of dengue diagnosis. Based on a recent analytic evaluation of dengue RDTs, we selected one to use in several areas experiencing suspected dengue outbreaks that did not have conventional laboratory testing for dengue. **Methods:** The Standard Diagnostics BIOLINE Duo RDT, which detects both anti-DENV IgM and DENV NS1 antigen, was used during suspected dengue outbreaks in Angola, Federated States of Micronesia, Republic of the Marshall Islands and Fiji to identify dengue cases. In total, 1678 specimens from suspected dengue cases tested with the RDT were sent to CDC Dengue Branch for confirmatory testing by the CDC DENV 1-4 Real Time RT-PCR and InBios anti-DENV IgM ELISA to determine the RDT sensitivity and specificity. **Results:** During all four outbreaks, RDT sensitivity for anti-DENV IgM ranged from 55-91.7% and the specificity from 93.1-98%. For NS1, the test sensitivity ranged from 49.7-92.9% and specificity from 22-89%. Sensitivities varied by days post onset of illness (DPO) for each analyte (NS1 and IgM) and infecting DENV serotypes. The most robust sensitivity for NS1 was observed on DPO=3 (71.4%), and the lowest sensitivity was observed on DPO=5 (50%). The sensitivity of the anti-DENV IgM was best on DPO=5 (83%) and lowest on the day of illness onset (0%). The combined RDT results of NS1 and IgM improved the sensitivity ranged from 2-6.7% of detecting a dengue case during each outbreak. **Conclusions:** This is the first study to evaluate the performance of a dengue RDT during outbreaks caused by each of the four DENV serotypes. RDTs provided accurate diagnostic information in-country to better guide the public health response that would have otherwise not been available in these resource limited settings.

Board 60. Biophysical Characterization of the *Plasmodium falciparum* Biomarker HRP2 Toward High-sensitivity Lateral Flow Immunoassay Infection Detection Tests for Malaria Elimination Campaigns

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Background: Currently available *Plasmodium falciparum* (*Pf*) lateral flow immunoassay rapid diagnostic tests (RDTs) lack the sensitivity required to target the subclinical transmission reservoir. *Pf* infection detection tests (IDTs) with a significantly improved limit of detection would enable more effective malaria elimination interventions while retaining the critical advantages of low cost, ease of use, and rural deployment. Histidine-rich protein 2 (HRP2) is a high-priority target analyte for identifying individuals at risk of *Pf* transmission. However, the highly polymorphic nature of HRP2 makes optimization and standardization of RDTs challenging. Our aim is to facilitate the development of improved malaria HRP2 IDTs through improved understanding of HRP2 structure-function relationships and their impact on epitope-antibody interactions. **Methods:** We have assessed the biophysical characteristics of native and recombinant HRP2 proteins and investigated interactions with a variety of capture and detection immunoreagents in whole blood, plasma, and buffer. Quantitative amino acid analysis, circular dichroism, quantitative enzyme-linked immunoassay, and biolayer interferometery were all utilized to better determine key characteristics for HRP2 antigen diagnostic standards as well as optimal capture/detect immunoreagent pairs. **Results:** From our studies, protein quantitation using the NanoOrange reagent method best approximates HRP2 concentration determination due to low HRP2 sequence complexity and a preponderance of histidine residues. Furthermore, recombinant HRP2 protein that includes an expression/purification tag decreases immunoassay sensitivity. **Conclusions:** Difficulties in HRP2 protein quantitation and variations in epitope sequence, frequency, and arrangement may alter RDT/IDT performance. Ongoing experiments are required to investigate the impact of sequence variations on immunoreagent binding and overall performance of highly sensitive malaria IDTs under development. Well defined HRP2 standards, reference methods, and new HRP2 immunoreagents are needed to enable the most effective use of diagnostics for malaria elimination.

Laboratory Proficiency Testing/Quality Assurance

Monday, August 24, 12:30 PM - 1:45 PM
Grand Hall

Board 61. Clinical Evaluation and Validation of Laboratory Methods for the Diagnosis of *Bordetella pertussis* Infection: Culture, Polymerase Chain Reaction (PCR), and Anti-pertussis Toxin IgG Serology (IgG-PT)

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Background: The appropriate use of clinically accurate diagnostic tests is essential for the detection of pertussis, a poorly controlled vaccine-preventable disease. The purpose of this study was to estimate the sensitivity and specificity of different diagnostic criteria including culture, polymerase chain reaction (PCR), serology, and the use of a clinical case definition. An additional objective was to describe the optimal timing of specimen collection for the various tests. **Methods:** Clinical specimens were collected from patients with cough illness between 2007 and 2011 during routine physician visits for cough illness and CDC-initiated outbreak investigations at seven locations across the US. A nasopharyngeal and blood specimen was collected from each patient during the enrollment visit. Patients who had been coughing for ≤ 2 weeks were asked to return in 2-4 weeks for collection of a second, convalescent blood specimen. Culture was performed at a local or state

health department or hospital laboratory and the CDC laboratory. PCR and serology were performed at CDC. Sensitivity and specificity of each diagnostic test was estimated using three methods_pertussis culture as the "gold standard," composite reference standard analysis (CRS), and latent class analysis (LCA). The effect of timing of specimen collection on diagnostic testing accuracy was also assessed. **Results:** Overall, 868 patients were enrolled and 14% were pertussis positive by at least 1 diagnostic test; 71% of these were positive by convalescent serology. Culture and PCR were most sensitive when performed during the first 2 weeks of cough, while serology was optimally sensitive after the second week of cough. In a sample of 545 participants with non-missing data on all 4 diagnostic criteria, PCR was the most sensitive (92%) and specific (99%) test when culture was considered the gold standard. However, sensitivity estimates for convalescent serology and the clinical case definition were increased through the use of CRS and LCA methods. **Conclusions:** Timing of specimen collection in relation to onset of illness should be considered when ordering diagnostic tests for pertussis. Consideration should be given to including serology as a confirmatory test in the Council of State and Territorial Epidemiologists (CSTE) case definition for pertussis.

Board 62. The Investigation of Infectious Disease Laboratory Management of a Less-developed Province in China

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Background: Uneven economic and social development among different provinces in China has had an adverse affect on overall laboratory quality and safety management, revealing an overall widening gap between the Chinese national public health labs and their leading international counterparts.Site visits were conducted in pilot areas to provide a more clear understanding of current status and needs with respect to laboratory management. **Methods:** An economically developing province was evaluated. Public health and clinical laboratories in the provincial capital, two other cities and four counties were selected. In total, 14 study units were investigated, including 7 CDCs and 7 hospitals. The WHO laboratory assessment tool (LAT) for quality and biosafety management in the infectious disease laboratories was translated, adapted to the China environment and implemented during the investigation. Data was collected and analyzed using the WHO LAT to evaluate the system. **Results:** The results indicated that an overall average laboratory management score was 74%. Within this score, laboratories performed better with respect to categories involving equipment however the public health services of the laboratory lagged behind. Laboratories possess the equipment necessary to meet the basic requirements, but collected data is not been shared in a timely manner between clinical and public health laboratories at any tier of the system. Based on the service level of laboratory (provincial, district, city), average scores for city laboratories were highest, followed by the provincial and county laboratories. The average score of hospital laboratories and public health system laboratory were the same. **Conclusions:** The WHO LAT was used to objectively assess the current situation of laboratory management. Several issues were identified by using the LAT, the next phase of the project is to address specific issues raised to improve laboratory quality. Based on the results, we can draw the conclusion that along with the increase in investment in infectious disease laboratory, the equipment, reagent and staff are meet essential quality needs. The investigation also revealed areas of inadequacy. Further cooperation and information exchange between hospital and CDC laboratory systems is required to make the laboratory management system fully functional.

Board 63. Quality of HIV Testing in Zambia (2009-2012): The Impact of National Quality Assurance Systems

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Background: Task-shifting and scale-up of HIV testing services in high HIV prevalence countries challenge testing quality. The Zambia National Quality Assurance program was launched in 2009 to monitor HIV testing performance countrywide. This study aimed to evaluate quality of laboratory and non-laboratory HIV testing in Zambia and impact of national quality assurance (QA) systems over time. **Methods:** HIV testing performance was investigated among rural and urban HIV testing sites participating in four annual national HIV proficiency testing (PT) exercises conducted from 2009 to 2012, i.e. 2009 (n=282), 2010 (n=488), 2011 (n=500), 2012 (n=404), including 108 sites participating in all four PT exercises. Testers included lay counselors, nurses, laboratory personnel and others. PT panels consisted of five serum samples conditioned into dry tube specimens issued to test sites by the national reference laboratory. Test site accuracy level was assessed by comparison of reported results to expected results. Non-parametric rank tests and multiple linear regression models were used to assess variation in accuracy between tester groups and to examine factors associated with accuracy respectively. Poor-performing sites were followed-up through supervisory visits in 2009 and 2010 and phone call from 2011 onwards. **Results:** The QA system reached only 30% of registered sites countrywide. Response rates varied by year: 51.3%, 71.8%, 84.5% and 63.0% between 2009 and 2012. The overall accuracy level was 93.1%, 96.9%, 96.0%, 96.2% between 2009 and 2012. Frequency of participation in PT exercises, training, experience and adherence to the national HIV testing algorithm were associated with higher accuracy over time. Differences in accuracy were seen between tester groups in 2009 with laboratory personnel being more accurate than non-laboratory personnel, while from 2010 onwards no differences were seen due to a substantial improvement among non-laboratory tester groups. **Conclusion:** Improvements were seen in overall accuracy level and particularly among lay counselors over time. More improvement is needed and the QA system seems to be useful in this regard. The QA system, however, faces limitations particularly in coverage, follow-up and resources to effectively monitor HIV testing countrywide and needs strengthening.

Board 64. Evaluation of Data Analysis Software Programs for Quantitative Fluorescent Microsphere Immuno Array (FMIA) Validation

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Background: Serological testing of immunoglobulins (IgG) levels serves as a diagnostic tool for assessing individual immune status. Enzyme linked immunosorbent assay (ELISA) is widely used as the gold standard for quantitation of human IgG (hIgG). For validation of quantitative ELISAs, guidelines and free ELISA for Windows software version 2.15 for analysis were made available by the Centers for Disease Control (CDC). However, no such software and guidelines exist for Fluorescent Microsphere Immuno Arrays (FMIAs). In the current study, using total hIgG quantitation as a model, we adapted the CDC ELISA acceptance criteria to validate a FMIA test. Six different software packages were compared for meeting the acceptance criteria set for the validation of

hIgG quantitation. **Methods:** Total hIgG FMIA quantitation was done multiple times by 3 operators on non-consecutive days. Each assay included a quantitative hIgG reference standard (ERM®-DA470k/IFCC reference), 7 unknown sera, 1 negative human IgG quality control (QC) serum and 3 hIgG positive QC sera. Data acquisition was done in a Bio-Plex 200 Suspension Array Reader (Bio-Rad). Data analysis, IgG quantitation and statistical modeling were conducted using six different software programs that included: 1) Bio-Plex Manager 6.1; 2) ELISA for Windows Version 2.15; 3) SigmaPlot 12.5; 4) MasterPlex QT 2.0.079; 5) MILLIPLEX Analyst 5.1; 6) StatLIA 3.2. **Results:** While all software programs produced comparable 4 parameter standard curves, each of the programs had some advantages and limitations. Data analysis using all the software programs gave R^2 value of > 0.99 except Bio-Plex Manager, which only featured fit probability instead of R^2. Overall, Bio-Plex Manager, MasterPlex QT and MILLIPLEX Analyst software programs were easy and user friendly for quantitative data analysis. Comparatively, CDC ELISA for Windows and SigmaPlot software programs required manual data entry, required additional data processing and formatting prior to analysis. Advantages and limitations of each software will be highlighted in a table to be useful to the community. **Conclusions:** Our evaluation of different data analysis software provides valuable information about various features of different software quantitative FMIA test as per CDC validation criteria set-forth for hIgG quantitation.

Host and Microbial Genetics

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Board 65. Host Genetic Susceptibility to Enteric Viruses: A Systematic Review

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Background: Enteric viruses, specifically norovirus and rotavirus, are a leading cause of diarrheal illness. Both viruses recognize and bind to histo-blood group antigens (HBGA), which are expressed by individuals, known as "secretors," who have a functional fucosyltransferase 2 (FUT2) gene. As such, host susceptibility to these viruses may be influenced by polymorphisms in the FUT2 gene. Challenge and observational studies have reported evidence to support a correlation between infection and HBGA phenotypes such as secretor status, Lewis phenotype, and blood type. Here, we aim to systematically describe these associations by conducting a meta-analysis of the rapidly expanding literature. **Methods:** We performed a systematic review of the PubMed database, which included publications with data on norovirus or rotavirus cases and their association with secretor status, Lewis phenotype, or blood type. Nonhuman studies or publications presenting secondary data analysis were excluded. Data were abstracted and compiled for descriptive and meta-analysis. **Results:** Of the 23 publications that met the inclusion criteria, 20 (87%) presented data only on norovirus, two (9%) focused on rotavirus and one (4%) had data on both viruses. Publications included data on a total of 3000 subjects from 13 countries and on age groups ranging from neonates to the elderly. Associations with secretor status were assessed in 20 studies (87%), with blood group in 14 studies (61%), and with Lewis phenotype in nine studies (39%). Of those studies that reported associations, 14 (70%), four (29%), and two (22%) publications reported a significant positive association between infection and secretor status, O blood type, and Lewis epitope. Meta-analysis of 16 studies on norovirus which presented data on associations with secretor status showed that secretors had 2.3 times the odds of infection, compared to non-secretors (95% CI: 1.5 - 3.1). **Conclusions:** Analysis of the existing literature suggests a strong association between norovirus infection and the FUT2 gene. While many studies have assessed genetic susceptibility to norovirus, few publications have focused on the correlation with rotavirus. More data on these associations are needed from observational studies, especially from developing countries and among various ethnicities.

Surveillance for Vaccine-Preventable Diseases

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Board 66. Population-based Incidence of Childhood Pneumonia Associated with Viral Infections in a Tropical Developing Country

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Background: Pneumonia is the leading cause of child mortality worldwide. The role of respiratory viruses as a cause of pneumonia in tropical developing countries is poorly understood. We used population-based respiratory illness surveillance in children <5 years old in an urban area in Dhaka, Bangladesh to characterize these illnesses. **Method:** Longitudinal active prospective surveillance was conducted in children in households selected by stratified cluster sampling. Participants were visited weekly and referred to clinic if febrile or had respiratory symptoms. Standardized clinical data was collected. Nasopharyngeal washes were collected for 1 in 5 children with eligible symptoms; specimens had virus isolation for influenza and reverse transcription polymerase chain reaction for other viruses. Pneumonia was defined as age-specific tachypnea and crepitations on auscultation by study physicians. **Results:** From April 2004 to February 2008, 17,584 children were followed for 21,636 child-years; 6,335 children had 12,499 clinic visits with eligible illnesses. We identified 6,345 pneumonia episodes (incidence of 29 episodes/100 child-years). Annual incidence of pneumonia/100 child-years was 77 for children 0-6 months, 64 for those 6-12 months, 43 for 12-24 months, 25 for 24-36 months, and 10 for 36-60 months. Of 1,248 pneumonia visits with laboratory testing, 803 (64%) were associated with a viral pathogen, including 274 respiratory syncytial virus (RSV) (22% of pneumonia visits with laboratory testing; 6.5 episodes/100 child-years), 244 adenovirus (19%; 5.8 episodes/100 child-years), 198 human metapneumovirus (16%; 4.7 episodes/100 child-years), 174 parainfluenza (14.0%; 4.1 episodes/100 child-years), and 81 influenza (6.5%; 1.9 episodes/100 child years); pathogen distribution varied by age. Multiple viruses were detected in 155 (12%); 19 (1.7%) had concomitant blood cultures positive for bacterial infection. Influenza rates may be underestimated given use of a less sensitive laboratory testing method for this pathogen. **Conclusion:** Viral pathogens contribute to a majority of childhood pneumonia episodes in Bangladesh, a setting with high pneumonia rates, especially in children <2 years old. Developing effective prevention strategies targeting these children is a high priority.

Board 67. Global Role and Burden of Influenza in Adult Respiratory Hospitalizations: A Systematic Analysis

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Background: The global burden of severe respiratory disease is substantial, but the contribution of influenza viruses among adults is not well known. We used published and unpublished surveillance data to estimate the role of influenza in severe acute respiratory infection (SARI) among hospitalized adults worldwide. **Methods:** We searched nine databases to identify articles describing adult inpatients tested for influenza and published during 1996-2012. Eligible articles included original data on hospitalized adults (≥18 years), presented 12 months of continuous testing (≥50 samples), and included number tested and positive for influenza. We supplemented the literature review with unpublished surveillance data among adult SARI inpatients tested for influenza from sentinel hospitals in 26 countries between 2003 and 2012. We compared median proportion positive across key variables (age, diagnostic test, case definition, geographic region, and United Nations country development status) by Kruskal-Wallis test. We then constructed a regression model among the subset of studies that used gold-standard diagnostic testing to estimate the pooled proportion of adults hospitalized with respiratory disease positive for influenza by age group (18-64 and ≥65 years). Data from 2009 were classified as "pandemic" and excluded from pooled estimates. **Results:** Among 55 published and unpublished data sources included in the regression model, influenza was associated with 11% (95% confidence interval (CI): 9-13%) of SARI hospitalizations in all adults, 12% (95% CI: 9-15%) among persons 18-64 years and 10% (95% CI: 10-10%) among persons ≥65 years. Data from developing countries (n=42) had a significantly higher crude median percent positive for influenza than from industrialized countries (n=34) (10% versus 7%, p= 0.03). There was no significant difference in median percent positive for influenza by age group, diagnostic test, case definition, or region. **Conclusions:** Influenza is an important contributor to acute respiratory hospitalizations throughout the world, among both younger and older adults, and particularly in lower-resourced settings. These findings can inform implementation of preventative measures such as vaccination.

Board 68. An Applied Comprehensive Surveillance System Using Human Antibody, Epidemiological, Entomological, and Veterinary Surveillance to Monitor Japanese Encephalitis in Beijing, China

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Background: A low incidence of Japanese Encephalitis (JE) has remained in Beijing since 2000's due to vaccines and improved JE surveillance. This study is to examine the burden of JE and the risk factors based on the integrated system including human antibody, epidemiological, entomological, and veterinary surveillance. **Method:** Healthy residents in 7 districts participated in this study. 5-6 ml of blood was obtained. Plaque Reduction Neutralized Test (PRNT) was used for neutralized antibody. 4 sites were selected, where sera sample from 8-10 piglets were collected and applied PRNT; also mosquito was trapped and PCR was used. In addition, routine epi surveillance data from 2001 to 2013 and vector density data from 2009 to 2012 were used. **Results:** 43 JE cases were reported from 2001 to 2013 including 0 case from 2008 to 2012 with a peak of 13 cases in 2013. The annual incidence rate varied from 0.02 to 0.06/100,000. 28 cases (65.1%) were older than 20 years old, with 20 cases ages 20-49; 34 cases were reported during Sept. to Oct., accounted for 79.1%. The majority of patients (88.4%) did not have JE vaccine history or "unknown". 142 sera sample from 38 piglets were tested. Positive naturalize antibody occurred in 2 districts, in late Aug. and Sept. Mosquito density began to rise in late May, sharply increased in June and peaked in July and Aug., then declined in Sept. and Oct. Culex tritaeniorhynchus (CT) was trapped and 22 specimens collected in 2009, 24 in 2010, 0 in 2011 and 2012, and a peak of 103 in 2013. Collected CT tested positive for virus in only 1 district in 2007. 1676 healthy people tested for antibody presence, 74.8% were positive. <1 year of age had the lowest rate (27.9%), while all other age groups ranged from 70% to 86%. **Conclusion:** Low incidence of JE occurring with adults ages 20 to 49 the main victims. The peak of 13 cases in 2013 related to the increase in CT density. The occurrence were related to seasonality when the piglet positive antibody was detected in late Aug. & Sept., and humans had more exposure to the risk due to outdoor activities. A majority of patients didn't have vaccination. This comprehensive system enhanced surveillance in: A better understanding of disease burden; determine groups at high risk; provide early notification to the public to minimize risk of exposure; recommend a potential vaccination to people at high risk.

Board 69. Measles Outbreak—Northern Lao PDR, January 2013

B. Sengkeopraseuth; Natl. Ctr. for Lab. and Epidemiology (NCLE), Vientiane, Lao People's Democratic Republic

Background: Measles is an acute disease caused by measles virus that is often fatal in developing countries. Measles is vaccine-preventable-disease, which in Lao PDR is given to all children at 9 months of age through the routine immunization program. On 16/1/2013, provincial clinician reported 3 suspected measles adult cases admitted to hospital.

The investigation was carried out to describe the source of the outbreak. **Methods:** Active case finding was done at the affected villages by the investigation team. We defined a suspected case as any person presented with fever and rash with onset after 1/1/2013, and a laboratory-confirmed case when specific-measles IgM was detected. We took samples for serological testing by ELISA. **Results:** A total of 92 suspected cases with no death with the onset of symptoms between 1/1/2013 and 17/2/2013. Attack rate was 13.3%. Most affected age group was adult above 20 years of age (53%) and children <5 (28%). Male:Female ratio was 1.8:1. Eleven out of 34 samples were laboratory confirmed cases (32.3%). The vaccination coverage was 95% for the affected district in 2012. Measles-Rubella Supplementary Immunization Activities (MR-SIA) was conducted in 2011 and some children were received (3.2%). However none of these cases remembered whether they received measles vaccination. Vitamin A and MR were administered together with health education during the outbreak response. **Conclusion:** This measles outbreak indicated that majority of the affected cases are under 5 and over 20 years. Immunization coverage was high in target group of 9 months but older children and adult were not immunized. It is highly recommended that immunization strategy and SIA should be targeting to catch up these missed target groups.

New Vaccines

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Board 70. Global Age Distribution of Pediatric Norovirus Cases

K. Shioda, A. Kambhampati, A. J. Hall, B. A. Lopman; CDC, Atlanta, GA, USA

Background: Norovirus has been increasingly recognized for its predominant role as a cause of acute gastroenteritis (AGE); however, there remains a need for detailed data on the burden of norovirus in specific populations. We describe the global age distribution of pediatric norovirus AGE to investigate differences by income level or disease severity. **Methods:** We performed a systematic review of the Embase, Medline, and Global Health databases for studies published from Jan. 2001 to Aug. 2014 that included age distribution among patients <5 years of age with laboratory-confirmed norovirus AGE. Studies were included if they used PCR to detect norovirus in stool specimens collected from AGE cases, if the study period was at least one year, and if a specific catchment area was defined. We extracted data on the total number of norovirus AGE cases. Data were used to calculate the age distribution of norovirus cases for each study and to construct a weighted and pooled cumulative proportion. We fit linear regression models to assess bivariate associations between the cumulative proportion of pediatric norovirus cases by the age of 12 months with per capita GDP of each country and study settings (e.g. outpatient vs inpatient). **Results:** We identified 35 studies that included the age distribution of norovirus AGE cases. Twenty of them were conducted in the inpatient setting. Overall, of norovirus AGE cases aged <5 years, 13% were in children <6 months, 33% were aged 6-11 months, 36% were aged 12-23 months, and 19% were aged 24-59 months after weighting by study population size. The cumulative proportion of norovirus AGE cases <12 months of age was inversely associated with per capita GDP (-5.9% for every 10,000 USD increase, p<.0001, R^2=0.42). The said cumulative proportion in the inpatient setting (51%) was higher than the outpatient (38%, p=0.02) and community setting (25%, p=0.004). **Conclusions:** Across various settings, the majority of pediatric norovirus cases occurred within the 6-23 month age range. Cases in lower income settings and inpatient cases were generally younger in age. These findings suggest that a norovirus immunization schedule completed by 6 months could potentially prevent ~85% of cases in children <5 years, while a vaccine delivered at one year of age could potentially prevent about 50% of cases in the same age group.

Board 71. Estimating the Impact of Pediatric Non-typhoidal *Salmonella* Vaccination on the Number of Invasive Illnesses Prevented Among Children < 5 Years of Age in the United States

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Background: Invasive non-Typhoidal *Salmonella* (NTS) infections are often severe and can be fatal; young children are at highest risk. Glycoconjugate NTS vaccines provide protection in animal models. We estimated the number of invasive NTS infections that would be averted annually in the United States in children <5 years of age by adding NTS vaccination to the routine immunization schedule of infants aged 2, 4, and 6 months. **Methods:** We defined invasive infections as isolation of NTS from blood. Using mean annual frequency of invasive NTS infections reported to the Laboratory-based Enteric Disease Surveillance (LEDS) system and mean US census data from 1996-2012, we estimated incidence rates among children in the following age groups (months): <2, 2-3, 4-5, 6-11, 12-23, 24-35, 36-47, 48-59. We then simulated the effect of a three-dose vaccine protective against NTS serogroups B, C, and D on mean annual incidence of reported NTS infections. Based on data for the Vi conjugate typhoid vaccine (Vi-rEPA) in children, we assumed a NTS vaccine effectiveness range of 75-90% following 3 doses. We specified the following age group-specific parameters: 1) proportion of invasive NTS infections attributable to serogroup B, C, or D based on LEDS data, 2) population at risk, 3) vaccine coverage, and 4) average time until dose. Real-world coverage and dose timing (accounting for catch-up doses in children up to 3 years of age) were estimated using the 2012 National Immunization Survey. **Results:** Without vaccination, an annual mean of 303 invasive NTS infections per 19,777,485 US children <5 years of age was reported to LEDS. Incidence rates were highest in infants aged <2 months (4.8/100,000 children), 2-3 months (3.0), and 4-5 months (2.6), and lowest in children aged 24-59 months (0.9). With a NTS vaccination program, we estimate 153-193 (51-64%) fewer infections would be reported to LEDS. **Conclusions:** A NTS vaccination program may prevent more than half of the annual invasive NTS infections in US children <5 years, but would not protect infants <2 months of age, the group at highest risk. However, our analysis underestimates the absolute number of invasive NTS infections averted due to underdetection and underreporting. Maternal NTS vaccination may be able to prevent additional pediatric infections.

Board 72. Modeling Norovirus Transmission and Strategies for Vaccination in the United States

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Background: Noroviruses are the leading cause of acute gastroenteritis in the United States. Norovirus vaccine development has progressed rapidly in recent years, but critical questions, including which age groups should be vaccinated to maximize population health impact

remain to be addressed. **Methods:** We developed a deterministic, age-structured compartmental model that tracks norovirus transmission and immunity in the U.S. population. We estimated three age specific transmission parameters using maximum likelihood by fitting the model to age-specific monthly US hospitalizations (1996 and 2007). Assuming that vaccination provides the same duration of protection as natural infection, we simulated two vaccine strategies: routine immunization at birth and individuals turning 65 years old. We assumed vaccine efficacy was 50% and coverage was 50%. **Results:** The model provided a good fit to the U.S. hospitalization data, with the best fit model suggesting that 0-4 year olds were much more important in transmission (R_0=3.38), than 5-64 year olds (R_0=1.86), and ≥65 years (R_0=0.33). The routine infant immunization program at equilibrium, is predicted to avert 17,258 (a 19% reduction) hospitalizations in 0-4 year olds and 12,784 (9%) hospitalizations in the 65 years and older age group over a five year time period. A routine immunization program of individuals turning 65 is predicted to avert 5,341 (4%) hospitalizations in the 65 year and older age group over a five year time period. In considering total population effects, vaccinating 0-4 and 65 years and older is predicted to avert 39 and 6 hospitalizations, respectively, per 10,000 doses administered, with much greater indirect benefits in the infant immunization program. **Conclusion:** This model demonstrates that the potential population-level impacts of norovirus vaccination are maximized by vaccinating infants, due to their importance in transmission and that immunization of infants provides the elderly with better protection from disease than vaccinating 65 year olds. Simulations of other levels of coverage, efficacy and duration of vaccine protection will also be considered along with other outcomes, including illnesses and deaths.

Board 73. Indirect Cohort Analysis of 10-valent Pneumococcal Conjugate Vaccine Effectiveness Against Vaccine-type and Vaccine-related Invasive Pneumococcal Disease

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Background: *Streptococcus pneumoniae* is a leading cause of bacterial pneumonia, meningitis and sepsis worldwide. In March 2010, Brazil introduced a newly available 10-valent pneumococcal conjugate vaccine (PCV10); PCV10 effectiveness against invasive pneumococcal disease (IPD) was demonstrated in a multi-state case-control study. However, case-control studies of vaccine effectiveness can be costly and challenging to carry out. A secondary analysis of case-only data was conducted to evaluate use of IPD surveillance data to measure vaccine effectiveness. **Methods:** We applied the indirect cohort method to estimate effectiveness of 10-valent pneumococcal conjugate vaccine (PCV10) in Brazil. Cases of invasive pneumococcal disease (i.e. S. pnuemoniae detected in a normally sterile fluid) were identified through national laboratory-based surveillance, and classified as vaccine-type (serotypes in PCV10), vaccine-related (same serogroup as a vaccine-type), or non-vaccine types. We estimated vaccine effectiveness using multivariable logistic regression comparing PCV10 vaccination among children with vaccine-type or vaccine-related invasive disease versus children with non-vaccine type disease. **Results:** The adjusted effectiveness of ≥1 doses against vaccine-type IPD was 72.8% (95% confidence interval [CI] 44.1 to 86.7) and against vaccine-related IPD 61.3% (95%CI 14.5 to 82.5).These estimates were similar to those of the case-control study (83.8% [95%CI 65.9 to 92.3] and 77.9% [95%CI 41.0 to 91.7] respectively). One or more doses were significantly protective against vaccine serotypes 14 (75.4%, 95%CI 14.5 to 82.5), 6B (69.7%, 95%CI 16.5 to 89.0), 23F (76.6%, 95%CI 14.6 to 93.6), and 18C (86.6%, 95%CI 30.6 to 97.4), as well as vaccine-related serotype 19A (71.3%, 95%CI 16.6 to 90.1). **Conclusions:** PCV10 protects against invasive pneumococcal disease due to vaccine- and vaccine-related serotype in young children in Brazil. An analysis of case-only data yielded very similar results to more resource-intensive case-control study, and provided additional insight on serotype-specific protection. The indirect cohort is a methodologically sound approach for evaluating pneumococcal conjugate vaccines that leverages existing surveillance and is feasible even in resource-limited settings.

New Challenges for "Old" Vaccines and Vaccine-Preventable Diseases

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Board 74. Seroprevalence to 2011 Swine Variant Influenza A (H3N2v) Among Three Age Groups of US Department of Defense Service Members

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Background: A recent emergence of a novel influenza virus (H3N2v) occurred in 2011, consisting of recombinant genes from swine virus and 2009 pH1N1. Once relatively rare in the U.S., the frequency of human cases increased dramatically between 2011-12 during which over 300 cases were identified, mostly small children exposed to animals at agricultural fairs. Although human-to-human transmission was relatively rare, there is growing concern about the potential mutation that might enhance transmission. To date, there are very few studies that have examined cross-protective immunity against H3N2v between different vaccinated age groups. This study allowed the examination between vaccinated age groups among U.S. DoD service members during the 2011 influenza season. **Methods:** Postvaccination sera collected in 2011 were obtained from the DoD Serum Repository for service members in three different age groups (19-21, 32-33, & 47-48 years of age). In addition, prevaccination matching samples were obtained from the youngest age group, as part of a previous public health study in 2011. All samples were tested using influenza microneutralization assay, quantitatively measuring antibody titers against A/Indiana/11/2011 (H3N2v) and A/Perth/16/2009 (H3N2). **Results:** The youngest age group showed significantly higher geometric mean titer against H3N2v with 165 (95% CI, 105-225) compared with the 32-33 and 47-48 age groups, with geometric mean titers of 68 (95% CI, 55-82) and 46 (95% CI, 24-65), respectively. Similar trends were seen for geometric mean titers against the seasonal H3N2 across all age groups, where the highest antibody titers among he youngest age group. In addition, the proportion of subjects in the youngest age group who seroconverted after vaccination was 12% for H3N2v and 27% for seasonal H3N2. **Conclusion:** Our data were similar to previous studies, where (a) seroprotection to be highest among younger adults and (b) decreasing titers among older adults. In addition, the proportion of young adults seroconverted to both strains after seasonal vaccination was found to be low, supporting previous studies. Improvements in the knowledge of H3N2v immunity across different age groups would allow for better vaccination practices by addressing those at highest risk during vaccine shortages and outbreak situations.

Vaccine-Preventable Diseases

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Board 75. Seroepidemiology of Diphtheria and Pertussis in Beijing, China: A Cross-sectional Study

X. Li, M. Chen, T. Zhang, J. Li, Y. Zeng, L. Lu; Beijing Ctr. for Disease Control and Prevention, Beijing, China

Background: In 2006 combined DTaP replaced DTwP in Beijing. The immunization schedule has included 4 doses at 3, 4, 5, 18-24 months, and one dose of Td at 6 years and 15 years. The reported coverage rate of DTP has been higher than 99% since 1990. The reported cases of pertussis has remained 3-15 cases per year and no diphtheria case has been reported since 1996. However, the outbreaks of the two diseases have been reported in other countries where the coverage of vaccination maintains high. **Methods:** A total of 2147 subjects aged 0-74 years were selected with a random sample of resident population. The information on socio-demographic characteristics were collected by questionnaire. Serum samples were tested for IgG antibodies to DT and PT by using commercial ELISA kits. PT antibody ≥28 IU/ml was seropositive and ≥100 IU/ml was indicated for an acute infection, DT antibody ≥0.1 IU/ml was given for a protection and seropositivity. **Results:** The overall positivity rate of anti-DT IgG was 66.28% with the mean concentration of 2.169 IU/ml. Age stratified data showed that the highest positivity rate of 97.63% was observed in 1-4 years and the rates decreased with age. The positivity rates were only around 50% or below since 25 years. The positivity rate of anti-PT IgG was 12.34% with the mean concentration of 15.163IU/ml. The highest level of positivity rate (22.23%) and antibody level (23.101IU/ml) was seen in 0 year. In subjects older than 10 years, the anti-PT IgG positivity rate was 10.19%-13.51% and concentration was 13.295IU/ml -16.353IU/ml, with no significant differences observed between these groups. The subjects with anti-PT IgG≥100IU/ml were observed in nearly all the groups except for 10-14 age group. The estimated incidences of pertussis infection were higher than 6000/100,000 in the age groups older than 5 years. A sharp increase of immunity level of diphtheria was observed at 1 year and 6 years respectively, which was consistent with the current immunization schedule. But there was no significant increase of immunity to pertussis observed after booster immunization at 18-24 months. **Conclusions:** The adult population was generally lack of protective antibody against diphtheria and all the age groups showed a low immunity to pertussis indicating the potential risk of transmission and outbreaks of the two diseases in Beijing.

Board 76. Sub-optimal Vaccine Effectiveness for the Live Attenuated Influenza Vaccine Among Air Force Children, 2013-14 Season

A. Eick Cost[1], Z. Hu[1], L. Lloyd Soderlund[2], M. Cooper[1]; [1]Armed Forces Hlth. Surveillance Ctr., Silver Spring, MD, USA, [2]US Air Force Sch. of Aerospace Med., Wright-Patterson Air Force Base, OH, USA

Background: Live attenuated influenza vaccines (LAIV) have been licensed for use in the United States since 2003. Since then, many studies have found LAIV to be highly effective among children. However, with ever changing influenza strains and vaccines, it is important to continue to assess influenza vaccine effectiveness (VE) on annual basis. Therefore, we investigated the VE of the 2013-14 influenza vaccines among Air Force children aged 2-17 years. **Methods:** We used a case test-negative control methodology among Air Force dependent children aged 2-17 years. Cases were lab-confirmed influenza (PCR, culture, or rapid assay) patients. Test-negative controls were negative for influenza by PCR or culture. Crude and adjusted odds ratios and VE estimates were calculated overall and by age, vaccine type, and influenza subtype. VE for the 2013-14 influenza season will be presented in additional to VE data for the 2010-11, 2011-12, and 2012-13 seasons. **Results:** We identified 322 cases (24% vaccinated) and 426 test-negative controls (33% vaccinated) for the 2013-14 influenza season. Overall VE was 42 (95% CI: 15, 60). VE by vaccine type was 57 (95% CI: 33, 72) and 5 (95% CI: -60, 40) for inactivated influenza vaccines (IIV) and LAIV, respectively. None of the subtype specific VE estimates reached statistical significance, but point estimates indicated protection for all vaccine types against A/H3 (overall: 25 (95% CI: -125, 75); IIV: 25 (-160, 78); LAIV: 27 (-268, 85)). Non-statistically significant protection against A/H1 was seen only for the IIV (overall: 12 (95% CI: -58, 51); IIV: 45 (-16, 74); LAIV: -69 (95% CI: -259, 21)). **Conclusions:** Moderate VE was found for all vaccines combined and for the IIV among all age groups. However, the LAIV had low to negative, non-statistically significant VE for all age groups. The lack of effectiveness of the LAIV may be related to the predominance of A/H1 circulation this season; a theory supported by the non-statistically significant moderate VE against A/H3, but no effectiveness against A/H1 for LAIV. Comparisons and combining of data from the 2010-11, 2011-12, and 2012-13 may yield additional insights into this finding.

Board 77. Estimated Tetanus Immunity by Multiplex Bead Assay and Double-antigen ELISA in a National Survey of Women Aged 15-39 Years, Cambodia, 2012

C. Gregory[1], M. Bunsoth[2], S. Buth[3], K. Wannemuehler[4], C. Sorensen[5], K. Chheng[3], M. Jenks[6], D. Moss[7], J. Priest[7], S. Soeung[8], L. Quick[1], M. Deming[6], P. Lammie[6], H. Scobie[4]; [1]Div. of Global Hlth. Protection, CGH, CDC, Atlanta, GA, USA, [2]Univ. of Health Sci., Phnom Penh, Cambodia, [3]Natl. Inst. of Publ. Hlth., Phnom Penh, Cambodia, [4]Global Immunization Div., CGH, CDC, Atlanta, GA, USA, [5]Statens Serum Inst., Copenhagen, Denmark, [6]Div. of Parasitic Diseases and Malaria, CGH, CDC, Atlanta, GA, USA, [7]Div. of Foodborne, Waterborne, and Environmental Diseases, CDC, Atlanta, GA, USA, [8]Natl. Immunization Program, Phnom Penh, Cambodia

Background: For evaluating tetanus sero-protection, the double-antigen ELISA (DAE) and toxin binding inhibition test are considered the gold-standard in-vitro assays but are infrequently performed due to their technical complexity and difficulty with easy integration into other disease testing. Recently multiplex bead assays (MBA) have shown promise for use in serosurveys as antibody responses to multiple pathogens can be simultaneously measured using minimal serum volumes. Our study evaluated the suitability of a MBA for measuring tetanus immunity. **Methods:** During November-December 2012, we conducted a nationally representative serosurvey of 2,154 women aged 15-39 years in Cambodia. Tetanus antibodies were measured with DAE and MBA. Antibody concentrations ≥0.01 IU/ml were considered sero-positive for DAE, cut-offs for MBA positivity were determined by receiver-operating characteristic analysis. Sensitivity and specificity with 95% confidence intervals (CI) were calculated for the MBA relative to DAE. **Results:** Estimated tetanus sero-protection among women 15-39 years in Cambodia was 85.987.4% (95% CI: 83.685.1-87.989.4) by MBA and 87.6% (95% CI: 85.6-89.4) by DAE. Estimates from both DAE and MBA were substantially higher than those obtained from vaccination history (87.6% and 85.9% versus 58.4%). Sub-populations noted by DAE to have significantly lower immunity, including parous women aged 15-19 years, nulliparous women, and women living in

western Cambodia, were also identified by MBA. The MBA showed high sensitivity (99.0%; 95% CI: 98.4%-99.4%), and specificity (92.0% (95% CI: 88.3%-94.6%)) compared to DAE. **Conclusion:** MBA appears to be a good alternative for monitoring tetanus immunity in areas where DAE is not an option. Because MBA can detect antibodies to multiple antigens from a minimal sample volume, it may be possible to integrate tetanus elimination monitoring into other planned national surveys.

Board 78. Influenza Vaccine Effectiveness During 2010-2014: Maintained Protection Throughout Duration of Influenza Season Among US Department of Defense Beneficiaries

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Background: Factors such as age, comorbidities, vaccine type, herd immunity, previous influenza (flu) exposure, and antigenic shift may impact the immune response to the flu vaccine, protection against circulating strains, and antibody waning. Evaluating vaccine flu effectiveness (VE) is important for informing timing of vaccine administration and evaluating overall vaccine benefit. **Methods:** VE was assessed using outpatient febrile respiratory illness surveillance among Department of Defense (DoD) non-active duty beneficiaries from flu seasons 2010-2011 through 2013-2014. Respiratory swabs were taken from a convenience sample of participants meeting the case definition and tested by polymerase chain reaction (PCR) for flu viruses. Cases were PCR-positive for flu, and controls were PCR-negative. Vaccine status was assessed by both patient recall and medical record review. VE was calculated using logistic regression and by taking 1 minus the odds ratio of being vaccinated in the cases versus controls and was adjusted for age group, calendar season (spring, summer/fall, winter), and influenza season. Overall VE during 15-180 days post vaccination by flu season were also run. **Results:** This study included 1,522 participants out of whom 55% were female and 75% under 25 years old. VE by flu season ranged from 40% to 69%. We found an adjusted VE that provided significant and fairly consistent protection up to 180 days post vaccination, with 61% (3%-85%) during 0-14 days, 62% (42%-75%) during 15-90 days, and 60% (41%-72%) during 91-180 days post-vaccination. The VE dropped to -11% (95% CI: -102%-39%) beyond 180 days post-vaccination. **Conclusions:** Our study found moderate VE up to 6 months post-vaccination. There was some fluctuation in VE across flu seasons which was adjusted for in our model. Administering flu vaccines closer to the start of flu season may slightly increase effectiveness of the vaccine. However, the flu season starts at different times each year, making optimal timing difficult to predict. Consequently, early flu vaccination may still offer the best overall protection.

Board 79. Prevalence and Factors Associated with Rotavirus Gastroenteritis Among Hospitalized Children Less Than 5 Years of Age in Enugu Metropolis, Nigeria, 2012

C. C. Nwodo[1], O. P. Ossai[2], W. Nwachukwu[3], O. Fagbemiro[1], P. Nguku[1], A. Olayinka[1]; [1]Nigeria Field Epidemiology and Lab. Training Programme, Abuja, Nigeria, [2]Ministry of Hlth., Enugu, Nigeria, [3]Univ. of Nigeria Teaching Hosp., Enugu, Nigeria

Background: Rotavirus is a leading cause of severe dehydrating diarrhea and vomiting among children less than 5years worldwide. Children in developing countries like Nigeria die more from rotavirus due to several factors including poor access to hydration therapy and ignorance. As Nigeria plans to introduce rotavirus vaccines into the routine immunization schedule, we carried out a study to find out the prevalence, associated factors and circulating strains of rotavirus in Enugu, Nigeria. **Methods:** We conducted a cross sectional study among hospitalized children less than 5years who passed ≥ 3 loose stools per day in the last 3 days within 3 study sites in Enugu metropolis from October 2010 to September 2012. We collected information on demography, clinical history and associated factors for infection from caregivers using a semi structured questionnaire. Stool specimens were screened using ELISA technique, strain characterization was performed using PCR technique. We performed data analysis using Epi Info 3.5.1. **Results:** Eighty samples (n = 116) tested positive for rotavirus. Mean age of patients was 10.2 months (SD ± 0.4). Factors associated with the disease were Age less than 24 months (OR=5.0, CI=1.8 - 14.0), Contact with a patient (OR=3.5, CI=1.5 - 8.2), Mothers educational level (OR=2.6, CI=1.0 - 6.5) Dehydration (OR=2.2, CI=0.9 -5.6). Short RNA electropherotypes (55%) were the predominant RNA profiles while G3P6 (36%) was the predominant genotype. **Conclusion:** Rotavirus is a common cause of acute gastroenteritis in children less than 5years in Enugu metropolis. Key factors for transmission were Age less than 24 months and Contact with a patient. Short RNA electropherotypes and G3P6 were the predominant genotypes .We recommend immediate introduction of rotavirus vaccines by the Government into the routine immunization schedule.

Board 80. A Measles Outbreak in a Middle School with High Coverage of Prior Evidence of Immunity, Beijing

R. Ma[1], L. Lu[1], J. Z. Zhang[1], M. Chen[1], L. X. Yu[1], S. F. Wang[2], R. X. Peng[2], J. Wu[1], H. X. Pang[1]; [1]Beijing Ctr. for Disease Control and Prevention, Beijing, China, [2]Shunyi Ctr. for Disease Control and Prevention, Beijing, China

Background: Age-appropriate receipt of 2 or more measles-containing vaccines (MCV) doses has been deemed as evidence of immunity. Measles transmission is rarely reported among such persons. **Methods:** We reported a measles outbreak in a middle school in Beijing with high coverage of 2 or more MCV doses. Previous measles history and immunization documentation were collected for all students. Cases were obtained by passive followed by active surveillance and confirmed by detection of measles-specific immunoglobulin M (IgM) and/or RNA. Clinical presentations and results of ELISA for measles immunoglobulin G (IgG) were also reported for each case. IgG seropositivity was defined as titers ≥200 mIU/mL. **Results:** Of 1245 students, 1172 (94.1%) had ≥2 MCV doses before the outbreak. A total of 13 cases (2 teacher cases and 11 student cases) occurred and had typical clinical presentations. Both the primary case (the first case) and the secondary cases (3 cases) were students. The tertiary cases included 2 teachers and 7 students. All 11 student cases had ≥2 MCV doses. Of the 11 student cases, 4 (36.4%) had negative IgM but positive RNA. Measles IgG titers of 9 (81.8%) student cases reached >2200 mIU/mL 0-7 days after rash onset. For all the secondary cases and 3 of 7 tertiary student cases, IgG titers 30-40 days after rash onset were close with that 0-7 days after rash onset. Among the total 1172 students with ≥2 MCV doses, neither the total number of MCV doses nor the MCV1 immunization age altered measles risk. But the risk was significantly higher when the last MCV was received 5-9 years (RR_{adj}=5.6) or ≥10 years ago (RR_{adj}=6.5), compared with <5 years ago. And the attack rate among students who received the last MCV ≥10 years ago was 3.1%. **Conclusions:** On measles transmission among persons with prior evidence of immunity, this is the second report in the world and the first report in China. Secondary vaccine failure might play an important role. More thorough laboratory surveillance is needed to assess the persistence of vaccine-induced immunity for domestic MCV in China.

Board 81. Assessing the Cocooning Strategy for Preventing Infant Pertussis — United States, 2011

A. Blain[1], M. Lewis[1], E. Banerjee[2], S. Currenti[3], M. Khan[4], K. Kudish[5], J. Liko[6], K. Scherzinger[7], S. Martin[1], T. Skoff[1]; [1]CDC, Atlanta, GA, USA, [2]Minnesota Dept. of Hlth., St. Paul, MN, USA, [3]New York State Dept. of Hlth., Albany, NY, USA, [4]California Emerging Infections Program, Oakland, CA, USA, [5]Connecticut Dept. of Publ. Hlth., Hartford, CT, USA, [6]Oregon Dept. of Human Services, Portland, OR, USA, [7]New Mexico Emerging Infections Program, Albuquerque, NM, USA

Background: Infants are at greatest risk for pertussis morbidity and mortality. The Advisory Committee on Immunization Practices (ACIP) recommended in 2006 that all adolescents and adults, especially those in contact with infants ("cocooning"), be vaccinated with a single dose of Tdap (tetanus toxoid, reduced diphtheria toxoid, and acellular pertussis vaccine). To assess the effectiveness of the cocooning strategy, we conducted a case-control evaluation of infant close contacts. **Methods:** Infants aged <2 months with probable or confirmed pertussis according to the CSTE case definition were identified through surveillance in six Emerging Infections Program Network (EIP) sites. For each case, we recruited three controls from birth certificates and interviewed identified adult cocoon members (CMs) or parents of CMs aged <18 years. Pertussis vaccination status was verified through medical providers and/or immunization registries. CMs of cases with cough onset between 1/1/2011 and 12/31/2011 were included in the analysis for all states except CA; CMs of CA cases with cough onset between 7/1/2011 and 12/31/2011 were included. **Results:** A total of 857 CMs were identified, including 599 adult and 258 non-adult CMs. An average of 5.4 CMs was identified per case and 4.1 CMs per control. 552 (64% of identified) CMs were enrolled, including 371 adult and 182 non-adult CMs. 130 (35% of enrolled) adult CMs had a valid (2 weeks before cough onset), provider-verified Tdap. The proportion of case CMs (32%) and control CMs (35%) with Tdap vaccination were similar (p=.7196). The 599 identified adult CMs comprise 196 infant cocoons. Of these, 9 cocoons were fully vaccinated with every member having received Tdap; however, 5/9 cocoons only included a mother, and 4/9 contained only 2 individuals. There was no difference in the proportion of fully vaccinated case (1/42, 2%) and control (8/154, 5%) cocoons (p=.6870). More than 49% of cocoons contained no adult members with Tdap vaccination; no difference was observed in the proportion of fully unvaccinated case (43%) and control (51%) cocoons (p=.3321). **Conclusions:** The low Tdap coverage observed in adult CMs reinforces the difficulty of implementing the cocooning strategy and the importance of the ACIP recommended strategy of Tdap vaccination during pregnancy to prevent infant pertussis.

Board 82. Vaccine Coverage and Adherence to EPI Schedules in Eight Resource Poor Settings in the Malnutrition and Enteric Disease (MAL-ED) Cohort Study

C. Hoest[1], J. Seidman[1], A. Ali[2], G. Lee[3], J. Platts-Mills[4], M. Paredes[5], P. Bessong[6], R. Chandyo[7], S. Babji[8], V. Raghava[8], D. Mondal[9], M. Mahfuz[9], E. Mduma[10], S. Knobler[1], M. Miller[1], C. Mason[11]; [1]Fogarty Intl. Ctr., NIH, Bethesda, MD, USA, [2]Aga Khan Univ., Naushahroi, Pakistan, [3]Johns Hopkins Univ., Baltimore, MD, USA, [4]Univ. of Virginia, Charlottesville, VA, USA, [5]PRISMA, Iquitos, Peru, [6]Univ. of Venda, Thohoyandou, South Africa, [7]Tribhuvan Univ., Kathmandu, Nepal, [8]Christian Med. Coll., Vellore, India, [9]Intl. Ctr. for Diarrhoeal Diseases Res., Bangladesh (ICDDR,B), Dhaka, Bangladesh, [10]Haydom Lutheran Hosp., Haydom, United Republic of Tanzania, [11]AFRIMS, Bangkok, Thailand

Background: Vaccines are one of the most successful and effective public health measures. The Expanded Program on Immunization (EPI), launched in 1974 against six diseases - polio, diphtheria, pertussis, tetanus, tuberculosis, and measles - revolutionized child health, saving 2-3 million lives annually. The Malnutrition and Enteric Disease (MAL-ED) study is a multi-site cohort study investigating effects of undernutrition and enteric disease on child health, growth, and vaccine response. Here we describe vaccine coverage in the cohort, adherence to country-specific EPI schedules, and socioeconomic factors influencing adherence. **Methods:** Vaccination histories were obtained monthly from vaccination cards, local clinic records and/or caregiver report. Children followed for at least 12 months were included in this descriptive analysis. Children receiving 1 dose of BCG, 3 doses of DPT, 1 dose of measles, and 3-5 doses of polio vaccine were considered fully vaccinated. Individual doses administered within 7 days of the scheduled age were considered on schedule. **Results:** A total of 1872 children were followed for at least 12 months. Coverage rates for EPI vaccines varied between the 8 cohort study sites and by type of vaccine. Coverage was highest at the Nepal and Bangladesh sites where 100% and 94% of children were fully vaccinated, respectively and lower at Brazil and Tanzania sites where 59% and 15% of children were fully vaccinated. The percentage of children completing the polio vaccine regimen at seven sites ranged from 75% in the South Africa site to 100% in the Nepal site; at the Tanzania site only 22% of children received the recommended number of polio doses. Children at the Pakistan site received as many as 19 doses of OPV by 24 months of age. Measles vaccine coverage at the 8 sites ranged from 72% to 100%. Significant delays between the scheduled administration age and actual vaccination date were a concern. BCG was generally administered on schedule while measles had low schedule adherence across all sites. Socioeconomic factors were significantly associated with vaccination status but the results were largely site-specific. **Conclusions:** Our findings suggest a need to improve measles vaccination coverage and reduce the gap between the scheduled and actual date of vaccination to achieve EPI coverage targets.

Board 83. Time Trends in Diarrhea Mortality in Mexican Children Under 5 over Three Decades: Impact of Various Interventions Including Clean Water, Sanitation, and the Rotavirus Vaccine

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Background: Diarrhea is the second leading cause of mortality in children <5 worldwide. Many of these deaths can be prevented by oral rehydration therapy (ORT), clean water/sanitation, and rotavirus vaccine. In Mexico, diarrhea deaths in children <5 have decreased dramatically over the past 3 decades as the country transitioned from lower to upper middle income economy, while introduction of the rotavirus vaccine in 2006 has been found to cut the residual diarrhea mortality in half. Seasonality in diarrhea mortality changed from summer peaks to modest winter peaks that coincide with the timing of rotavirus circulation in Mexico. We quantify the relative impact of various public health interventions on reducing diarrhea mortality and infer the expected impact of the rotavirus vaccine in countries undergoing epidemiologic transitions. **Methods:** This study examines time series of monthly diarrheal deaths from 1979-2010 in Mexican children aged 0-4 years based on national vital statistics (ICD10 code A0-A10). Mortality rates were calculated using census data and mapped with various public health interventions. **Results:** Diarrheal mortality rates in Mexican children <5 decreased 40-fold over the 3 decades. The

annual diarrheal mortality reduction temporally associated with ORT introduction (1984), water/sanitation improvements (1989-1999), and rotavirus immunization (2006) was 58.8/100,000, 30.5/100,000, and 6/100,000, respectively. The rotavirus vaccine contributed only marginally to the total rate reduction in diarrheal mortality. Using Mexico in the 1980s as a proxy for a contemporary low income country, had the vaccine been introduced before the transition from summer to winter mortality, we estimate the vaccine-associated mortality burden reduction to be ~18% or lower. **Conclusions:** The dramatic reduction in diarrheal mortality in Mexico was achieved prior to introduction of the rotavirus vaccine, and can best be explained by public health interventions, improved treatment and fertility reduction. On-going analyses will focus on estimating the state-specific mortality and hospitalization benefits of the rotavirus vaccine. Low- and middle income countries should weight costs and benefits of a vaccine program against what could be achieved with more universal diarrhea reduction strategies.

Board 84. Reminders, Recommendations and Offers for Adult Influenza Vaccination, 2011-2012 Season, United States

K. M. Benedict[1], E. D. Kennedy[2], T. A. Santibanez[2], C. L. Black[2], H. Ding[3], S. B. Graitcer[2], K. E. Kahn[4], L. J. Pabst[2], C. B. Bridges[2]; [1]IHRC, Inc., Atlanta, GA, USA, [2]CDC, NCIRD, ISD, Atlanta, GA, USA, [3]Eagle Med. Services, LLC, San Antonio, TX, USA, [4]Leidos, Atlanta, GA, USA

Background: Reminders, recommendations, and offers for influenza vaccination have been found to improve vaccination coverage in adults. The purpose of this analysis was to investigate associations between influenza vaccination and receipt of reminders, recommendations, and offers for influenza vaccination of adults in the 2011-2012 influenza season. Additionally, differences between demographic groups of adults receiving these interventions were investigated. **Methods:** Responses from the March 2012 National Flu Survey were evaluated. Adults were asked if they had received an influenza vaccination and if they had received a reminder to be vaccinated in the 2011-2012 influenza season. Adults who had visited a doctor since July 1, 2011 were asked if they had received a recommendation for influenza vaccination; those receiving a recommendation were asked if they received an offer to be vaccinated. **Results:** Of the adults interviewed, 45.5% reported receiving an influenza vaccination, 17.2% reported receiving a reminder for influenza vaccination, and 72.8% reported visiting a doctor at least once since July 1, 2011. Of those who reported visiting a doctor, 42.8% reported receiving a recommendation for influenza vaccination. Of those who reported receiving a recommendation, 75.6% reported receiving an offer for vaccination. Adults reporting receipt of reminders, recommendations, and offers for influenza vaccination were more likely to be vaccinated for influenza than adults not receiving them (unadjusted Prevalence Ratios (PR) =1.33, 2.09, and 1.90, respectively). Health care personnel were more likely to report receiving a reminder (PR=1.37) or offer (PR=1.09) for influenza vaccination; those aged 50-64 years were more likely to report receiving a recommendation (PR=1.23) or offer (PR=1.09) than those aged 18-49. **Conclusions:** Influenza reminders, recommendations, and offers are important interventions that can increase influenza vaccination coverage; however, these interventions are under utilized. Efforts are needed to increase implementation of influenza vaccination needs assessment, recommendation and offer into routine clinical practice to reduce disparities in influenza vaccination and improve coverage especially among those at highest risk of influenza-related complications.

Polio Eradication: New Approaches

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Board 85. The Effect of Diarrheal Disease on Bivalent Oral Polio Vaccine (bOPV) Seroconversion in Nepali Children

C. Cardemil[1], C. Estivariz[1], H. Gary[1], L. Shrestha[2], J. Sherchand[2], A. Sharma[2], S. Oberste[1], W. Weldon, III[1], A. Anand[1], O. Mach[1], S. Chu[1]; [1]CDC, Atlanta, GA, USA, [2]Inst. of Med., Tribhuvan Univ., Kathmandu, Nepal

Background: In 2009, the Advisory Committee on Poliomyelitis Eradication recommended using bivalent oral poliovirus vaccine (bOPV) in vaccination campaigns after a clinical trial showed bOPV was more immunogenic than trivalent OPV (tOPV) for poliovirus types 1 and 3. However, the effect of diarrheal disease on the immune response to bOPV is unknown. **Methods:** Nepali infants aged 6 weeks-12 months, who had received <3 doses of OPV, were recruited for participation during visits for mild-moderate diarrhea or other illness not requiring hospitalization at five health facilities in eastern, central and western Nepal. Consented infants were administered one dose of bOPV and neutralizing antibody titers to poliovirus types 1 and 3 were measured before and 28 days after vaccination. Multivariable logistic regression was used to measure the effect of diarrhea, nutritional status, breastfeeding, age, prior OPV doses, and study site on seroconversion (change from seronegative to seropositive) or boosting (4-fold increase) in antibody titers to poliovirus. **Results:** Analysis was conducted in 294 children with diarrhea and 326 children without diarrhea. Seroprevalence (95% confidence interval) after 3 doses of OPV was 84.9% (75.8%-91.0%) for type 1 and 64.5% (56.6%-71.6%) for type 3. Children with diarrhea had reduced response (seroconversion or boosting) to poliovirus type 3 (OR 0.4, 95%CI 0.3-0.7, p<0.001) but not to type 1 (p=0.16). Infants with a higher number of prior OPV doses had a reduced type 1 response (p=0.047). In addition, response rates to both type 1 (p=0.028) and type 3 (p=0.007) in all infants varied by study site. **Conclusions:** Diarrheal disease was associated with a significantly lower type 3 seroconversion among underimmunized infants in Nepal. Supplemental doses of OPV, through routine immunization and OPV campaigns, should be continued to ensure high population immunity against poliovirus in areas with high diarrheal disease incidence, including Nepal.

Global Vaccine Initiatives

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Board 86. Early Findings from an Evaluation of Influenza Vaccination on Birth Outcomes in Lao PDR, 2014

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Background: Studies have demonstrated that seasonal influenza vaccination has been associated with improved birth outcomes, such as reduced risk of preterm delivery. In Mar-Jun 2014, Laos PDR administered 760,000 doses of influenza vaccine to specific target groups, including pregnant women. Analysis of birth outcomes by vaccination status must wait until the desired sample size is attained post influenza season. Here we compare characteristics of women by vaccination. **Methods:** From Apr 2014-Jan 2015, we consented and enrolled pregnant woman who delivered at 2 hospitals in Vientiane Capital Province and 1 in Luang Prabang Province. Women ≥18 years, residing in the region with a singleton birth were included. We collected demographic and clinical information on mother and child. Influenza vaccination status and date was ascertained by vaccine card. **Results:** Between May 3-Oct 9, 2014, 3,304 (92%) of 3,574 women who delivered in the 3 hospitals were enrolled. Of the 1,773 entered in a database, 113 (6.4%) did not meet inclusion criteria and 149 (8.4%) had missing/incorrect vaccination date. Of the 1,511 analyzed, 1,033 (68%) were vaccinated (85% in 3rd trimester). Vaccinated and unvaccinated women were similar with respect to mean age (26.5 vs. 26.8 yrs), distance to hospital, smoking (1.1% vs. 1.5%), household smoker (36% vs. 38%), and hospitalization (2.8% vs. 2.5%) or respiratory illness (8.6% vs. 10%) during pregnancy. Vaccinated women were significantly more likely to be Lao Loum (89% vs. 78%, p<0.01), have completed secondary school (56% vs. 42%, p<0.01), have more mean antenatal visits (5.4 vs. 3.9, p<0.01) and have less underlying disease (0.5% vs. 2.7%, p=0.02). Only in Luang Prabang, vaccinated women had smaller mean household size (5.4 vs. 5.9, p<0.03), smaller mean members <15 years (1.7 vs. 2.2, p<0.01) and were more likely to have a monthly household income of >1M Kip (US$124) (79% vs. 59%, p<0.01). Among all women, there were 59 (3.9%) perinatal deaths (18 stillbirths, 40 miscarriages and 1 after birth). Of 1,452 live births, 100 (6.9%) weighed <2,500g and 131 (9.0%) were born <37 weeks. **Conclusions:** These early data suggest some differences between vaccinated and unvaccinated women that will need to be taken into account, particularly by province, in assessing the effect of vaccination on birth outcomes.

Board 87. Introducing Seasonal Influenza Vaccine in Low Income Countries: An Adverse Events Following Immunization (AEFI) and Acceptability Survey in Lao People's Democratic Republic

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Background: In 2012, Lao PDR introduced seasonal influenza vaccine based on evidence of seasonal influenza occurrence. The vaccine campaign targeted 375,000 persons among four WHO-SAGE (World Health Organization-Strategic Advisory Group of Experts (SAGE) on Immunization)recommended target populations (pregnant women, persons aged ≥50 years, persons with chronic diseases and healthcare personnel) in four provinces and was conducted by the Lao National Immunization Program (NIP). A survey of adverse events following immunization (AEFI) and acceptability in targeted groups was conducted post-vaccination. **Methods:** A multi-stage randomized cluster sample design was used to select survey participants representative of the target populations. Data on demographics, occurrence and type of AEFI, acceptability and awareness of the immunization campaign was collected via in-person interviews. **Results:** Between April and May 2012, 355,902 persons received seasonal influenza vaccine. Of 2,089 persons interviewed, 261 (12.5%) reported one or more AEFI. Among the 261, the most commonly reported AEFI's were local reactions: redness or swelling around injection site (21%), nausea (15%), fever (15%), headache (15%), and general weakness (11%); these frequencies were similar among the four target populations. No hospitalizations or deaths were reported. Sixteen percent (43) sought medical care following their AEFI. Acceptance and awareness of vaccination was high; 99% indicated they would receive the vaccine annually if available, and 72% of survey participants had heard of the vaccine and campaign via awareness activities prior to the campaign. **Conclusions:** Independent (to NIP monitoring) AEFI survey findings highlighted the safety of seasonal influenza vaccine introduction in these recommended target populations. High acceptability of seasonal influenza vaccine by survey participants corresponded with recognized public demand that greatly exceeded supplies. Lao PDR was able to mobilize and leverage resources, setting an example for other low income countries in introducing seasonal influenza vaccine.

Board 88. Seasonal Influenza Vaccine Recommendation: Northern or Southern Hemisphere Formulation? A Challenge in Adoption for Tropical Bangladesh

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Background: Many tropical countries are considering the introduction of seasonal influenza vaccine. Given the complex timing of viral circulation in this region, the adoption of the Northern (NH) or Southern (SH) Hemisphere formulation should be assessed, as the vaccine is most effective when there is good antigenic match between the vaccine and circulating strains and timely vaccine delivery prior to the influenza season. We investigated the optimal vaccine formulation and timing for Bangladesh, to inform the design of possible immunization programs. **Methods:** We performed a secondary analysis on antigenic characterization data generated by the WHO influenza collaborating center at the CDC Influenza Division for specimens (n=1054) submitted by Bangladesh's national influenza surveillance during 2005-2013. Annual recommended NH and SH formulations were obtained from WHO. A retrospective simulation analysis was performed to assess the effectiveness of adopting either formulations and optimal timing of vaccine delivery. Effectiveness was operationally defined as the proportion of antigenic match between strains included in either annual hemispheric vaccine formulations and strains circulating the following 9 months after hypothetical vaccination (Mello et al, 2009). To account for logistical issues with vaccine purchase and delivery, we also quantified matching with scenarios considering up to a 5 months delay from when the vaccine was available globally. **Results:** Peak influenza activity in Bangladesh occurred from April-October. From 2005-2013, the proportion of correct matches between circulating strains and vaccine formulation was similar: 40% for NH and 39% for SH, respectively. When considering a 3 months delay, the proportion of correct matches was 24% for SH and 46% for NH formulation. **Conclusions:** Based

on past data, both hemisphere formulations are predicted to confer equivalent protection against circulating influenza strains in Bangladesh when the vaccines becomes globally available. However, a better match is observed with the NH formulation when a 3 months delay is introduced in the analysis. This would provide the government more flexibility for opportunistic acquisition strategy of vaccine stocks year-round, in case they decide to implement an influenza immunization program.

Late Breakers I

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Grand Hall

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Innovative Strategies to Control and Prevent Healthcare-Associated Infections

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Grand Hall

Board 89. Increasing the Efficiency and Yield of a Tuberculosis Contact Investigation Through Electronic Data Systems Matching—New York City, 2013

J. M. Sanderson[1,2], L. Trieu[1], D. Proops[1], S. D. Ahuja[1]; [1]New York City Dept. of Hlth. and Mental Hygiene, Bureau of Tuberculosis Control, New York, NY, USA, [2]CDC/CSTE Applied Epidemiology Fellowship, Atlanta, GA, USA

Background: Transmission of tuberculosis (TB) in healthcare settings remains a risk to the health of patients and healthcare workers (HCWs). When a person with TB disease exposes others in a healthcare setting, infection preventionists at the facility are expected to lead a contact investigation (CI) to identify contacts. CIs can require extensive resources and record review; therefore, electronic health data can be a useful tool to improve the timeliness and accuracy of healthcare-associated CIs. **Methods:** In 09/2013, the New York City Bureau of TB Control (BTBC) and Hospital A initiated a CI around a HCW with infectious TB who worked in a maternity ward. We employed two data systems in the response: hospital-based electronic health records (EHRs) to identify exposed patients, and an electronic immunization registry (EIR) to obtain contact information for exposed infants and their healthcare providers. During 10 months of follow-up, two matches were conducted with the EIR to capture changes in contact information. To assess the impact of EHRs we calculated the proportion of patients identified as exposed among those in the maternity ward, and to evaluate the EIR we quantified the amount of new information from this registry. **Results:** 954 patients received care in the maternity ward during the HCW's infectious period. Review of EHRs narrowed TB exposure to 145 mothers and 140 infants with ≥30 minutes of HCW interaction (30%). Over 99% of exposed infants were identified in the EIR data matches. The first EIR linkage yielded a new telephone and/or resident address for 49% of infants and a different provider for 52% of infants compared with data obtained from the EHR. Matching with the EIR a second time provided updated provider information for 30% of infants. During 10 months of follow-up, most mothers (59%) and infants (80%) had evaluation results reported to BTBC. **Conclusions:** Electronic data matching improved the efficiency and yield of this CI. Hospital EHRs helped identify patients with direct TB exposure, enabling the concentration of resources on those at greatest risk for TB infection. Also, gathering accurate contact information from the EIR allowed us to successfully locate and notify patients. These findings underscore the importance of exploring how electronic health data can improve epidemiologic investigations.

Board 90. A Hand Sanitizer Intervention to Improve Hand-hygiene Behavior in a Tertiary Care Public Hospital in Bangladesh

S. Parveen[1], R. Sultana[1], N. Amin[1], M. Y. Sharker[1,2], J. Abedin[1], M. Hasan[1], R. K. Babar[1], S. Akter[1], R. J. Nijhum[1], M. U. Bhuiyan[1], F. A. Nizame[1], N. A. Rimi[1], M. Rahman[3], K. Sturm-Ramirez[1,4], S. P. Luby[5], E. S. Gurley[1]; [1]Intl. Ctr. for Diarrhoeal Diseases Res., Bangladesh (ICDDR,B), Dhaka, Bangladesh, [2]Coll. of Publ. Hlth. and Hlth. Professions, Univ. of Florida, Gainesville, FL, USA, [3]Inst. of Epidemiology Disease Control and Res. (IEDCR) & Natl. Influenza Ctr. (NIC), Dhaka, Bangladesh, [4]Natl. Ctr. for Immunization and Respiratory Diseases, CDC, Atlanta, GA, USA, [5]Infectious Diseases and Geographic Med., Stanford Univ., Stanford, CA, USA

Background: Bangladeshi public hospitals often lack handwashing stations and have intermittent water supplies. We deployed a hand sanitizer intervention in a public hospital to improve hand-hygiene behavior among family caregivers (FCG), who provide the majority of nursing care to patients, and healthcare workers (HCW). **Method:** We conducted this pilot study during 2012-2013 in 2 adult medicine and 1 pediatric ward in a tertiary care hospital. We conducted baseline observations for 24 hours to record opportunities for hand-hygiene based on WHO recommended critical times during patient care and the proportion when hand cleaning occurred. We then supplied hand sanitizer on the study wards and communicated messages to rub hands at critical times through repeated verbal counseling, training, posters and cue cards. After 6 months we observed hand-hygiene behavior for 48 hours and compared to baseline results. We conducted 14 exit interviews with FCG and 8 short interviews with HCW to collect feedback on the intervention. **Results:** At baseline, we observed 1959 hand-hygiene opportunities among FCG in which 5 (0.3%) episodes of handwashing with soap occurred. After the intervention, we observed 2057 opportunities, and in 75 (4%) episodes hands were cleaned with soap or sanitizer ($p<0.001$). FCG reported that sanitizer was new to them and they were not aware it was provided on the wards for their use. FCG learned about sanitizer from our posters or staff nurses; they felt motivated to use it when doctors told them to. Among HCW, we observed 1587 opportunities and no handwashing with soap but only 2 (0.1%) episodes of cleaning hands with sanitizer observed at baseline. After the intervention, HCW cleaned hands with sanitizer in 86 out of 2570 (3%) observed opportunities ($p<0.001$); none washed hands with soap. HCW said that they did not have time to clean hands after each task of patient care or between attending patients because of high patient load; so they cleaned hands before starting and after ending each ward round. **Conclusion:** Our intervention significantly increased hand-hygiene among FCG and HCW, although the proportion of opportunities when hands were cleaned remained very low. Further effort is needed to identify effective interventions to improve hand-hygiene behavior in this high risk setting. Given that time was a major constraint, interventions that focus on the riskiest activities should be explored.

Board 91. Targeting Intervention for Healthcare-associated Infections in Tennessee: Methods for Identifying and Communicating Facility-specific Impact on Statewide Standardized Infection Ratios

M. A. Kainer, B. Berger, M. Kanago; Tennessee Dept. of Hlth., Nashville, TN, USA

Introduction: In Tennessee, seven healthcare-associated infection (HAI) events are reportable to the state via the National Healthcare Safety Network (NHSN), and data are regularly provided to the HAI Multidisciplinary Advisory Group (MDAG) to guide prevention efforts. In response to MDAG concern regarding sustaining improvement in the state standardized infection ratio (SIR) for certain HAIs, our aim was to explore methods to identify facilities for targeted intervention, based on their impact on the state SIR, and to communicate this information to infection control staff. **Methods:** Each facility's relative impact (RI) on the state SIR was calculated by determining the percent change in the state SIR when the facility's numerator and denominator data were included in the state calculations (SIR_{TN}) versus when the facility's data were removed (SIR_{NEW}). Additionally, we calculated the number of infections a facility would have needed to prevent (NNTP) in the reporting period of interest in order to meet each HHS National 5-year Prevention Target: NNTP = $Obs_{FACILITY}$ - ($Exp_{FACILITY}$*HHS Goal SIR) Results of each method were presented to the MDAG for feedback before sharing with hospitals. **Results:** Relative impact was displayed on a bubble plot, in which each facility was represented by a circle with size proportional to the facility's relative impact on the state SIR, with number of procedures or device days on the x-axis and SIR on the y-axis. The MDAG used this information to target outlying facilities for intervention. Additionally, a tabular facility-specific Prevention Report Card, which displayed the NNTP and other impact metrics (including whether the facility had a top-5 NNTP) for each reportable HAI, was created and distributed to facilities quarterly. A web-based calculator was posted on the TDH website <http://health.state.tn.us/ceds/HAI/calculator.shtml>, allowing facilities to calculate their NNTP in real time. **Conclusions:** By assessing the impact of each facility's data on the state SIR, we identified facilities for which targeted prevention efforts may have the greatest opportunity to improve statewide metrics. Additionally, providing these metrics directly to infection control staff is an important tool for facilities to implement data-driven prevention efforts.

Board 92. MicroRNAs Regulating Tulane Virus Replication in LLCMK2 Cells: New Targets with Therapeutic Potential

P. Chhabra, T. Cromeans, J. Vinjé; CDC, Atlanta, GA, USA

Background: Human noroviruses are the leading cause of epidemic and sporadic acute gastroenteritis in the United States. While most of the control efforts are focused on prevention of virus transmission, very few studies have looked into treatment strategies that target virus replication. Tulane virus (TV), a recently discovered calicivirus in the stools of rhesus macaques, represents viruses in the tentative new *Recovirus* genus. Recent studies have shown that TV has similar environmental survival characteristics as human norovirus. MicroRNAs (miRNAs) are an important class of ~17- to 24-nt non-coding RNAs that modulate gene regulation at the post-transcriptional level. Viruses use miRNA to inhibit viral or host transcripts and also recruit host miRNAs for viral replication. The expression levels of miRNA change drastically in host cell during cell-viral interactions. In the present study, we report miRNA regulating host-virus interactions of TV replication in LLCMK2 cells. **Methods:** LLC-MK2 cells were infected by Tulane virus at a multiplicity of infection (MOI) of 0.01 plaque-forming units (pfu) per cell. miRNA expression profiling was done by miScript™ miRNA PCR Array system. Anti-miR-143 and anti-miR-93 were transfected into LLCMK2 cells with Oligofectamine. Replication kinetics of TV and miRNA expressions in LLCMK2 cells were measured by SYBR® Green RT-qCPR assay. **Results:** Replication kinetics of TV in LLCMK2 cells as measured by quantitative RT-PCR of TV RNA showed onset of virus replication by 12 hr and peaked at 36 hr post-infection (pi). Cytopathological effect was detected as early as 48h pi. Up-regulation of 4 and down-regulation of 26 miRNAs in LLCMK2 cells was observed in LLCMK2 cells in response to TV infection at 36hr pi of which miR-143 and miR-93 were significantly up and miR-30d was significantly down-regulated. Pretreatment of LLCMCK2 cells with anti-miR -93 and anti-miR-143 not only delayed TV replication but also drastically reduced viral titers at 36hr pi. **Conclusion:** The results indicated a possible correlation between miR-143 and miR-93 with TV replication in LLC-MK2 cells. These observations provide important insights into developing novel miRNA based antiviral strategies against norovirus.

Healthcare Worker Safety/Infection Control

Monday, August 24, 3:30 PM - 4:45 PM

Grand Hall

Board 93. T-Zone Teaching Moment for Healthcare Workers to Prevent Contraction of Virulent Organisms Using Positive Deviance

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Background: Not touching the mucous membranes of the eyes, nose, and mouth (T-Zone) with a bare hand or finger is the most critical step in preventing the perpetuation of infectious disease (e.g. influenza, Ebola) as it prevents the transmission of pathogens by self-inoculation. While not all respiratory pathogens are transmitted via this route, many are. (Bertsch, 2010; Goldman, 2000) While this area has not received the same study as hand hygiene, office workers have been documented to touch their faces at a rate of 16 time per hour, and one in three healthcare workers were documented to pick their nose during the course of a grand rounds meeting, while one in 2.7 rubbed their eyes (Nicas & Best, 2008; Elder, 2014). Other studies have focused on wearing masks for preventing transmission (Hogg & Huston, 2006; Aiello, et al, 2010), and Michael Bell, MD of CDC reiterated the significance of using protective eye wear to prevent the individual from self-inoculation of the conjunctival mucus membranes (APIC webinar May 28, 2014 about MERS-CoV). **Methods:** Two possible ways to approach effecting behavior change include role modeling and the use of operant conditioning tools. Role modeling takes advantage of the non-conscious behavioral mimicry that occurs when we unconsciously mirror the behavior of those around us. Operant conditioning tools modify behavior by applying positive deviance strategies. Tools include- retraining device, freeze hands, "germ potion" lotion, respiratory atomizer, and health shield. The effectiveness of these methods can be increased when incorporated in tandem with "just in time" coaching methodologies to choose additional T-Zone Teaching Moments. **Results:** Increased rates of compliance with appropriate hand behavior leads to reduced colonization and infectious disease events. Given recent events in caring for Ebola patients in the healthcare setting, modifying this behavior is just another example why this has become even more critical. **Conclusions:** More attention needs to be paid to T-Zone cross-contamination in the healthcare setting as it leads to morbidity and mortality of healthcare workers. If we believe health care workers should be on the frontline helping in pandemic efforts, they need better training than the present effort, as evidenced by recent events surrounding Ebola.

Board 94. Incidence of Latent Tuberculosis Infection Among Nursing Students in a Tertiary Care Hospital—Bangladesh, 2011-2013

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Background: Healthcare workers in public hospitals in Bangladesh are at increased risk for latent tuberculosis infection (LTBI) because few infection control measures are employed. Patients with active tuberculosis (TB) often spend several days on the wards before diagnosis and treatment. LTBI incidence among nursing students, who have little prior exposure to hospitals and spend time caring for TB patients, is high. Nursing students in neighboring India have one of the highest incidence rates reported (7.8 per 100 person-years). We estimated LTBI incidence among a cohort of nursing students in Bangladesh. **Methods:** During 2011-2012 (baseline) and 2013 (follow-up), we conducted a prospective cohort study on consenting residential nursing students in a tertiary care public hospital. We performed tuberculin skin tests (TSTs) with a single 10 Tuberculin Unit of PPD using the Mantoux method. A TST result of ≥10 mm induration was considered positive. During the follow-up, we repeated TSTs on students with negative baseline TST results; conversion was defined as a ≥10mm increase from baseline. Incidence and 95% CIs were estimated using Poisson regression. **Results:** Of 288 nursing students enrolled in three year levels, 243 (84%) completed the baseline TST. The median age was 20 years (range 17-27) and 233 (96%) were female. Average time to follow-up was 1.4 years. At baseline, 85 (35%) students had a positive TST. Of the 158 (65%) students with a negative baseline TST, 100 (63%) completed the follow-up TST and of these, 41 (41%) had a positive TST. Overall LTBI incidence was 29 per 100 person-years (95% CI 22, 37), and ranged from 26 (95% CI 17, 39) to 50 (95% CI 27, 93) per 100 person-years (p=0.12) by year level. No outbreaks of active tuberculosis were reported among the students. **Conclusions:** LTBI incidence was higher than in India, suggesting healthcare workers might have high exposure to TB in hospitals in Bangladesh. Not using a two-step TST at baseline might have overestimated incidence. However, booster effect alone, estimated at <15%, likely could not account for the level of incidence seen. Individual and facility-related risk factors for LTBI should be assessed. Once risk factors are identified, TB infection control measures should be implemented to reduce risk of TB transmission in tertiary care hospitals in Bangladesh.

Board 95. Epidemiological Analysis of Microbiological Results of Intrahospital Infections in General Hospital Veles, 2010-2014

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Background: Infections acquired during the hospitalization period of the patient at last 48 hours after reception, and the most 48 hours after living hospital they are nosocomial or intrahospital infections. They are significant problem which brings to complication in the hospital treatment, increased mortality and costs of treatment. **Methods:** Descriptive and analytical metod has been used to show the epidemiological condition in the hospital departments based on microbilogical results of taken materials. **Results:** Between 2010-2014year, 2515 test has been taken. In 2010, 183 test has been taken , from which 5,4% are isolated patogen results , or in 30 materials. In 2011, 550 test has been taken from which 4,4% are isolated patogen results or in 24 materials. In 2012, 607 test has been taken from which 6,8% are isolated patogen results or in 41 materials. In 2013, 422 test has been taken from which 7,6% are isolated patogen results or in 32 materials. In 2014, 379 test has been taken from which 3,7% are isolated patogen results or in 14 materials. The percentage of isolated patogen results in whole five year period is 5,6% from the total number of taken materials.From patogen bacteria mostly are isolated staphilococcus aureus-MRSA with 104 isolates, koliformes bacterials with 25 isolates, klebsiella with 3 isolates, pseudomonas aeruginosa with 2 isolates, proteus with 2 isolates, and with one isolat escherichia colli, enterobacter, enterococcus and akinetobacter.The patogen bacteria, mostly are isolated from the department of surgery, ginecology, neuropsychiatry, intern medicine and sterilisation . Mostly isolated patogen bacteria are from common use objects, working surface, and from employees. **Conclusion:** Based on the conducted analisys we conclude that the percentage of the isolated patogen bacteria is increasing. The employees and the behaviour in the hospital environment are key factor for its contamination. The percentage of isolated patogen bacteria is decreasing with improving of the sanitary-hygienic condition in the hospital, with continuous desinfection of the hospital area, and the object for common use, also with imroving of the hygienic habbits of the employees. Although book of regulation exists, intrahospital infections are rarely reported, therefore bigger awareness and responsibility at the medical personal is nececarry, for its discovering and reporting.

Board 96. Biosafety Cabinets Testing, Calibration, and Certification Problems in the Armenian Ministry of Health Laboratories, 2013

N. Bakunts, L. Avetisyan, A. Vanyan; Natl. Ctr. for Disease Control and Prevention, State Noncommercial Organization, Ministry of Hlth., Yerevan, Armenia

Background: Ensuring biosafety in laboratories is an important capacity required by some international documents, including International Health Regulations. Biosafety cabinets (BSC) are one of the components to ensure it. International performance specifications have been established (NSF/ANSI Standard 49), and BSCs must be certified annually by accredited personnel to ensure the cabinet is operating at a standard level. The Republic of Armenia Ministry of Health, with the United States Defense Threat Reduction Agency's Cooperative Biological Engagement Program in Armenia, conducted a program to inventory BSCs in the public health state laboratories and determine compliance with international performance standards. The local legislation was also examined for regulations pertaining to BSCs. **Methods:** Armenian legislation related to laboratory safety programs was reviewed and acts/regulations on BSCs identified. The public health laboratories in Armenia were inventoried for BSCs. Investigators tested each BSC according to seven indicators. Measurements and a smoke test were also carried out, and the results were compared with international criteria and manufacturer's specification. Three standards were used. **Results:** Armenia has four legislative acts regulating BSCs. Attestation of BSCs is required only after initial installation and if the cabinet is moved or repaired. Only BSC type verification is done without calibration. There are no NSF certified companies or professionals in Armenia. There were 13 BSCs in the public health state laboratories that were included in this study. Five of the BSCs (38.4%) passed the international performance tests and were certified. The other eight BSCs failed the performance testing. Six (75%) cabinets displayed problems with air inflow and HEPA filter leakage; one (12.5%) had problems only with air inflow; and one (12.5%) had a faulty HEPA filter gasket. **Conclusions:** The current legislation in Armenia does not correspond to international criteria on BSC performance. There are no in-country resources for calibration and certification. Over half (61.6%) of the BSCs in the public health state laboratories are not in compliance

with international standards. We suggest defining requirements for BSCs testing, calibration and certification, corresponding to international standards, and developing appropriate resources and capacities for their implementation.

Board 97. Ebola Virus Disease—Gaps in Knowledge and Practices of Health-care Workers in Lagos State, Nigeria, August 2014

A. M. Oladimeji; African Field Epidemiology Network (AFENET)-Nigeria Field Epidemiology and Lab. Training Programme, Abuja, Nigeria

Background: Health-care workers (HCWs) play pivotal roles in outbreak responses. Ebola Virus Disease (EVD) outbreak spread to Lagos, Nigeria in July 2014, infecting 11 HCWs (case fatality rate of 45%). This study was conducted during the outbreak to assess HCWs EVD-related knowledge and practices. **Methods:** A health facility based cross-sectional study was conducted among HCWs across Lagos State using stratified sampling technique. Interviewer-administered questionnaire was administered to elicit respondents' socio-demographic characteristics, knowledge and practices. A checklist assessing health facility's level of preparedness and HCWs' EVD-related training was employed. HCWs' knowledge and practices were scored and, classified as either good or poor. Multivariate analysis was done with confidence interval set at 95%. **Results:** A total of 112 health facilities with 637 HCWs were recruited. Mean age of respondents was 40.1±10.9 years. Overall, 462 (72.5%) HCWs had good knowledge, highest prevalence was among doctors, 131 (92.9%). However, only 29 (4.5%) HCWs reported good practices. One hundred and six (16.6%) reported been trained in identifying suspected EVD patient(s) while 78 (12.2%) had a triaging area for febrile patients in their facilities. Higher proportions of HCWs with good knowledge [28 (6.1%) vs 1 (0.6%), p=0.003] and, training [14 (13.2%) vs 15 (2.8%), p<0.001] reported good practices. HCWs with EVD-related training were three times more likely to adopt good practices [OR = 3.3 (95%CI 1.5 - 7.1]. **Conclusion:** Lagos State HCWs had good knowledge of EVD, without a corresponding level of good practices. Training was found as a predictor of good practices. We developed Standard Operating Procedures (SOPs) for EVD active surveillance and patient management. EVD-related Information, Education and Communication (IEC) materials were also developed and used in training the HCWs in infection prevention and control towards containing the outbreak.

Board 98. Barriers to Implementation of Optimal Laboratory Biosafety Practices in Pakistan

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Background: National Biosafety Rules and Guidelines in Pakistan are focused toward preventing undesirable effects of genetically modified organisms (GMOs) in agriculture, veterinary settings and public health. However, hospitals, biomedical research institutions, and biomedical laboratories in Pakistan are not governed by regulatory agencies and they are not held under any regulatory laws pertaining to healthcare biosafety. Consequently, employers are not legally bound to facilitate optimal biosafety practices in laboratories and institutions. **Methods:** In an effort to create awareness of good laboratory practices and appropriate biosafety practices, 2 workshops were organized under aegis of the Pakistan Biological Safety Association and sponsored by NIH-Fogarty grant. Questionnaires were designed to be administered to workshop participants at the end of each workshop to evaluate perceived barriers to biosafe practice. This tool was developed by modifying the BARRIERS scale (Funk et al, 1987) where evaluators are required to rate each specific barrier based on the extent to which it is operant in their workplace. Nineteen of the original 29 perceived barriers were included. In addition, respondents were also asked to rank the three greatest barriers as perceived by them. **Results:** Two full-day workshops were conducted each in Karachi and Lahore in February 2015. Each workshop was attended by 35 participants, and included senior-level laboratory technologists, laboratory physicians and microbiologists (academic and research). Over 80% of respondents identified the following perceived barriers affected implementation to a great extent: administrators not allowing for implementation (80%), lack of staff authorization to change practice (90%), and insufficient time on the job to implement new practices (90%). Participants' responses were heterogeneous for the 3 greatest barriers. The BARRIERS scale was informally evaluated by participants to be difficult to understand and rate. **Conclusions:** Based on perceived barriers, substantial improvement in work environment, worker facilitation, and enabling is required for enhancement of optimal biosafety practices in Pakistan.

Board 99. Serological Monitoring of Leptospirosis Among Laboratory Animals

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Background: Leptospirosis is an infectious natural focal zoonotic disease. Rodents are the sources of leptospirosis pathogens in which the strains of Icterohaemorrhagiae, Grippothyphosa and Pomona serogroups are detected more often. They secrete infectious agents into the environment, contaminating it by which there is a threat of infection for other animals and human. As in researches scientists often have to contact with laboratory animals it is necessary to control leptospirosis infection in these animals. Thus, we decided to examine the laboratory animals from Kyiv vivariums for leptospirosis and to identify the most common serogroups of Leptospira. **Methods:** Sera of laboratory animals from 4 vivariums were taken for the research: vivarium #1: 10 samples from white mice and rats evenly; vivarium #2: 40 samples from white mice and rats evenly; vivarium #3: 20 samples from rats; vivarium #4: 56 samples from hamsters. In total 70 samples from rats, 50 samples from mice and 56 samples from hamsters. Sera were tested with microagglutination test using antigens of 19 Leptospira serovars. **Results:** 40 (57.1%) of 70 rat's sera samples were positive in titers 1:50 and 1:100. 12 samples (30.0%) were positive in monoreaction, and 28 (70.0%) have shown polyreaction. The most often registered serovars are Icterohaemorrhagiae - 17.8%, Grippotyphosa - 16.8%, Cynopteri - 11.6%. There were also a small number of positive reactions to other serogroups of leptospira they are Mini and Sejroe. 20 (40%) of 50 mice sera samples were positive in titers 1:50 and 1:100. 10 (50%) samples have shown monoreaction and 10 (50%) samples have shown polyreaction. Dominated serovars are Canicola, Grippotyphosa, Icterohaemorrhagiae (15.6% each). There were also detected few other serovars Cynopteri and Hebdomadis. 17 (30.4%) of 56 hamster's sera samples were positive. Monoreaction was registered in 41.2% of cases and polyreaction in 58.8%. Pomona serovar have been registered more often (21.1%). Significantly fewer cases were detected with Canicola, Australis and Cynopteri serogroups. **Conclusions:** Established the circulation of leptospirosis among laboratory animals: rats 57.1% of cases, mice in 40.0%, in hamsters in 30.4% of cases. Serovars Icterohaemorrhagiae and Grippotyphosa were dominated in rats and mice, and Pomona in hamsters.

Tracking and Preventing Healthcare-Associated Infections

Monday, August 24, 3:30 PM - 4:45 PM
Grand Hall

Board 100. 124 Acute Care Hospitals and Point-prevalence Survey of Health Care-associated Infections in a Certain Area of East China in 2014

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Background: By analyzing the results and impact factors relating to the point prevalence of health care associated infections in acute care hospitals in a certain area of east China, this study will provide evidence for hospitals of different scales in different regions to conduct hospital infection monitoring. **Methods:** Epidemiology cross-sectional survey method was used to investigate the point prevalence rate of health care associated by consulting cases and bedside surveying conducted by fulltime and parttime infection management personnel. **Results:** Surveys were conducted in 124 hospitals. Of 61908 patients, 1294 had 1 or more healthcare associated infections (2.1%; 95% confidence interval, 1.6 to 2.4). The prevalence rate of health care associated infections for ICU was 14.5%, followed by internal medicine (2.3%) and surgery (2.0%) with the lowest for the Department of Otorhinolaryngology (0.3%). Lower respiratory tract, urinary tract, respiratory tract, blood and superficial incision are the top five sites of infection, accounted for 78% of all infections. Of the 1389 hospital infection cases, the top five pathogens were Pseudomonas aeruginosa, Bauman Acinetobacter, Escherichia coli, Klebsiella pneumonia and Staphylococcus aureus. Of the 61908 cases, there were more men than women and the average age were 53.90±22.12 years old. Cases from internal medicine department were in majority and cases in tertiary acute care hospitals were greater in number than secondary acute care hospitals.Arteriovenous intubation rate, urinary tract intubation rate and ventilator use rates were 9.9%, 12.4% and 3.8%, respectively. 23.7% patients in the day of investigation or from admission to the day of investigation received surgery. The antibacterial drug usage rate was 33.1%. **Conclusions:** In areas with limited human and material resources and information lagging behind, regular investigation of point prevalence rate of health care associated infections can be carried out to replace comprehensive monitoring of hospitals infections that requires more manpower and resources, so as to understand risk factors and disease burdens that are associated with hospital infections and finally provide data to support the implementation of best practices for the prevent and control of health care associated infections.

Board 101. Role of Personal Clothing in Transmission of Respiratory Infection Within the Neonatal Intensive Care Unit (NICU)

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Background: RSV continues to be the main cause of childhood respiratory hospitalization, especially in preterm neonates. We conducted a prospective longitudinal study to identify potential sources for transmission of respiratory infections within the NICU. **Methods:** During May-June 2014 (peak RSV season) once weekly, nasal swabs were collected from every third admitted neonate. Three swab specimens were collected from the nose, hand and personal clothing of visitors to NICU and all health care workers (HCWs). Once during the study period environmental swabs were also collected from patients' beds, adjacent chairs, counter tops and computers and desks in nurses' and doctors' stations. Each specimen was tested for RSV using real time RT-PCR. **Results:** There were 81 nasal swab specimens collected from 55 neonates. The median gestational age of the babies was 32 weeks and median birth weight was 1820 gm. One of the neonates (1%) was positive for RSV infection. There were109 swabs (327 total) collected from each of nose, hand and dress specimens from 80 visitors. The median age of participants was 33 years IQR 28-39 years), median number of household residents was 3 (IQR 2-3) and 12% had school aged children at home. Participants reported they washed their hands a median of 10 mins (IQR 5-35) before they were sampled. There was 1 nasal swab (1%) and 4 dress specimens (4%) from visitors positive for RSV, with 1visitor with both dress and nasal specimens collected on the same day. A total of 173 (total 519) of each of nose, hand and dress swabs from 84 HCWs were collected. The median age was 35 years (IQR 29-43 years). Only 6% HCWs reported any cold symptoms and 9% reported household members with cold symptoms in the 3 days prior to sample collection. Reported median duration since last handwashing was 5 (IQR 3-20) mins. Nasal swab from one HCW (1%) was positive for RSV. Swab specimens from nurses' computer and the bed rail and adjacent chair of the one of the neonates was positive for RSV. **Conclusion:** Although detection of RSV was infrequent, the intimate contact between preterm neonates and visitors means personal clothing may play a role in RSV transmission within the NICU.

Board 102. Forty Percent Attack Rate of Multi-strain *Staphylococcus aureus* Skin Infection Among Neonates in an International Private Hospital in Bangkok, July 2013

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Background: On 27 July 2013, the Bureau of Epidemiology, Thailand Ministry of Public Health was notified from a private hospital in Bangkok about abnormal increase of neonatal *Staphylococcus aureus* skin infection in July 2013. An investigation was conducted to determine source of infection and risk factors. **Methods:** Medical records of 101 neonates born during 29 June to 31 August 2013 were reviewed. The workplaces including the delivery and operating room, the nursery ward and washing area were inspected. Clinical and environmental samples were obtained and examined for bacterial culture with pulse field gel electrophoresis. **Results:** The baseline monthly rate of neonatal skin infection was 4 - 10% during January and June. Since 29 June until 31 August, forty neonates (39.6%) had skin lesion of pustules, vesicles, abscess or exfoliation on any part of the body or diagnosed as pyoderma, bullous impetigo, furunculosis, Staphylococcal Scalded Skin Syndrome (SSSS) or bacterial skin infection. Methicillin susceptible *S. aureus* (MSSA) was isolated from 7 (87.5%) samples of the 8 neonate cases and 3 (10.7%) nasal swabs of 28 healthcare personnel. Multiple PFGE pattern were identified in the outbreak. Matched PFGE but different drug resistant pattern was shown in one pair of patients and healthcare personnel. Association between male sex and infection was found. The outbreak rapidly curtailed to zero after implementing strong contact precaution among healthcare personnel, isolation of cases, carriers

treatment, improvement of hospital environment and mother preparing before returning to communities. **Conclusions:** The multi-strain MSSA skin infection outbreak among neonates probably caused by nosocomial transmission, although community infection cannot be excluded. Nasal carriers of healthcare worker could transmit the organism through environmental equipment. The number of case markedly decreased after implementing massive control measures.

Board 103. Latent Tuberculosis Infection Among Health Care Workers in Tuberculosis Specialty Hospitals, Bangladesh, 2012-2013: Putting Infection Control Into Context

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Background: Bangladesh has the sixth highest tuberculosis (TB) burden in the world. TB specialty hospitals admit and treat pulmonary TB patients regularly. Health care workers (HCWs) at TB specialty hospitals with limited TB infection control practices are at increased risk for TB. To assist focusing on highest risks groups to implement TB infection control interventions, we estimated the prevalence of latent TB infection (LTBI) among these HCWs in Bangladesh. **Methods:** Between 2012 and 2013, we conducted a cross sectional study in four TB specialty hospitals. After obtaining informed consent, each HCW completed a questionnaire and was given a two-step tuberculin skin test (TST). A medical technologist read the TST at 48-72 hours after placement; induration ≥ 10 mm was considered positive and the HCW was deemed to have LTBI. We estimated prevalence ratio (PR) with 95% CI to determine factors associated with LTBI and age-adjusted PR using a generalized linear model. We excluded HCWs with prior history of TB from this analysis. **Results:** A total of 636 HCWs (56% male) with a median age of 43 years (range 17-70) consented to and completed a TST. The overall prevalence of LTBI among HCWs was 55% (CI 51%-59%) which was highest among lab workers 74% (CI 54%-88%) and lowest among doctors 52% (CI 38%-65%). Eighty one percent of HCWs reported BCG vaccine receipt. Among HCWs with LTBI, 87% reported no prior exposure to pulmonary TB patients at home. The prevalence of LTBI among nurses increased by 1.02 (95% CI 1.01-1.04) and among lab workers by 1.01 (95% CI 1.01-1.02) with each additional year spent in areas where pulmonary TB patients are cared for. For doctors and support staff, the prevalence of LTBI increased by 1.22 (95% CI 1.13-1.33) and 1.05 (95% CI 1.01- 1.09) with each additional hour spent per day with pulmonary TB patients. **Conclusions:** More than half of HCWs from all occupational groups had LTBI. The independent increase in prevalence of LTBI with years spent with TB patients after controlling for age suggests healthcare-associated TB infection occurs regularly, underscoring the urgent need for improved TB infection control policies and procedures in TB specialty hospitals. These findings can assist the national TB control program to prioritize areas and populations to target for infection control.

Board 104. Impact of Monthly Data Quality Checks for Facilities on Surgical Site Infection (SSI) Data

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Background: Surgical site infections (SSI) following colon (COLO) and abdominal hysterectomy (HYST) are reported to the Tennessee Department of Health (TDH) via the National Healthcare Safety Network (NHSN). Because resources are not sufficient to conduct onsite validation of SSI data in all Tennessee facilities, we developed quality checks to identify potential SSI reporting errors and provide each facility with a list of errors to correct. We sought to quantify the impact of these automated quality assurance measures on SSI data in Tennessee hospitals. **Methods:** Data quality checks were developed using SAS 9.3 which check SSI event and procedure data for completeness. Checks also include potential data entry errors. Special focus was placed on identifying procedures with missing or outlier values for variables required for risk adjustment. Errors identified through these checks are included in existing quality reports sent to facilities on a monthly basis. Support is provided to facilities that need assistance addressing errors and follow-up is conducted for facilities with errors that have not been corrected. **Results:** Of 96 facilities reporting COLO and HYST procedures to TDH between January 2012 and September 2013, 70 facilities (73%) had at least one error. Of the 29,808 COLO and HYST procedures performed during the same time period, 151 procedures (0.5%) were excluded from SIR calculations. 95 procedures were excluded from the SIR because of missing or incomplete values for one or more variables required for risk adjustment. 56 procedures were excluded because procedure time was missing, less than 5 minutes or an outlier. Of the 70 facilities with errors, 38 (54%) had procedures excluded from their SIR and 4 facilities had 10 or more excluded procedures. **Conclusions:** Running automated data quality checks each month and providing the results to facilities provides an opportunity to identify and correct errors that have a direct impact on facilities' publically reported SSI data. While the 151 procedures identified as being excluded from SIR calculations represent a small proportion of the procedures performed statewide, the potential impact on facility-level SIRs is significant. These quality checks can be modified and shared with other states to improve the quality of their facilities' SSI data.

Board 105. Trends in the Incidence of *Clostridium difficile* Infection in Monroe County, New York, from 2010-2014

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Background: *Clostridium difficile* infection (CDI) is a common healthcare-associated infection and is increasingly recognized in the community. CDI is a significant burden in vulnerable elderly and nursing home residents. We performed population-based surveillance to describe the trends in CDI over a five year time period. **Methods:** We conducted population and laboratory based surveillance for CDI between 2010 and 2014 in Monroe County, NY as a part of the CDC Emerging Infections Program. An incident CDI case was defined as a positive *C. difficile* stool specimen greater than 8 weeks after the previous positive stool specimen. Recurrent cases were defined as a positive stool specimen between 2 and 8 weeks after the last positive specimen. CDI cases were classified as Community Associated (CA), Community Onset Healthcare Facility Associated (COHCFA), Hospital Onset (HO), or Nursing Home Onset (NHO) based on location of stool collection, residence 4 days prior to stool collection, and healthcare exposures in the previous 12 weeks. A convenience sample of stool specimens underwent molecular characterization. **Results:** During 2010-2014, 8,075 incident CDI cases were identified in 6,668 individuals. Most cases were white (50%), female (62%), and over 65 years of age (55%). Thirty-six percent of the cases were CA, 24% HO, 20% NHO, and 20% COHCFA. In 2010, CDI incidence was 213 per 100,000 population and in 2011 it increased to 241 after implementation of nucleic acid amplification

testing by all labs. The incidence subsequently decreased to 193 per 100,000 population in 2014. Most of this reduction is attributed to the decreasing incidence in elderly NHO CDI cases (56% reduction). Seventeen percent of CDI cases had at least one recurrence, 7% had severe disease requiring ICU admission or colectomy, 178 (4%) cases died, of which 76% were 65 or older. Nine-hundred eighty-one stool samples underwent molecular characterization, NAP1/027 was the predominant strain (26%) followed by NAP4/014/020 (12%) and NAP11/106 (9%). **Conclusions:** The incidence of CDI in Monroe County, NY has decreased since 2010, mostly due to a reduction in NHO cases and in patients aged 65 years and older. The reasons for this trend need further evaluation.

Board 106. Risk Factors of MDR Gram-negative Bacteremia Among Hospitalized Patients

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Background: Over the past decade, the numbers of bloodstream infections caused by multidrug-resistant (MDR) Gram-negative bacteria have risen sharply. MDR Gram-negative bacteremia increases not only mortality, but also patient morbidity, length of treatment and hospitalization costs. It is important to identify risk factors of MDR Gram-negative bacteremia among hospitalized patients to prevent these risk factors and to lower the incidence of MDR Gram-negative bacteremia. **Method:** Risk factors were identified by a case-control study. Data was collected from inpatients medical record that had positive blood cultures of Gram negative bacteria from 2008-2013. The case group was subjects who had MDR Gram-negative bacteremia, and the control group was subjects who had non-MDR Gram negative bacteremia. All variables that had a value of p <0.25 on bivariate analysis were included in multivariate analysis using logistic regression. **Result:** During the study period, there were 131 patients fulfilled the criteria: 42 patients who had MDR Gram-negative pathogen bacteremia (case) and 89 patients who had non-MDR Gram-negative pathogen bacteremia (control group). Based on the bivariate analysis, two variables were statistically significance: history of treatment in ICU / HCU (p=0.003) and history of ventilator (p=0.030). Further multivariate analysis showed that there was one variable statistically significance, which was history of treatment in ICU / HCU (OR: 3.118; CI 95% : 1.443 - 6.736; p=0,004). **Conclusion:** History of treatment in ICU/HCU was risk factor of MDR Gram negative bacteremia among hospitalized patients.

Detecting Emerging Threats in Healthcare

Monday, August 24, 3:30 PM - 4:45 PM

Grand Hall

Board 107. Surveillance for Recent Animal Contact Among Patients with Febrile Illness in Bangladesh Hospitals to Identify Emerging Zoonoses

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Background: Bangladesh is a hot spot for the emergence of new zoonotic diseases. The Institute of Epidemiology, Disease Control and Research (IEDCR), Bangladesh and ICDDR,B conduct hospital based surveillance for patients admitted with fever and acute respiratory illness or meningoencephalitis. We aimed to identify patients captured through these surveillance activities who were most likely infected with zoonotic pathogens to focus resource intensive laboratory diagnostics. **Methods:** We added 5 screening questions to ongoing surveillance questionnaires in 16 public and private tertiary care surveillance hospitals distributed throughout Bangladesh. Questions included high risk occupations (veterinarian, butcher, skinner or zoo worker), consumption of raw or fermented date palm sap which might be contaminated by infected bat's saliva/urine, recent slaughtering or eating sick domestic or wild animals, or receiving bites or scratches from wild animals within 21 days prior to illness. Study physicians recorded detailed exposure histories using tablet computers and uploaded data to the central server for real-time monitoring. Collected specimens (serum, throat swab, oral swab and cerebrospinal fluid) were tested in the laboratories at ICDDR,B and IEDCR to detect evidence of Nipah and common respiratory viruses. **Results:** From September 2013 to August 2014, hospital staff screened 1,085 encephalitis and 1,648 respiratory illness patients for recent zoonotic exposure. 93 patients (3.4%) reported animal exposures. The majority (56%) consumed raw date palm sap; 38% slaughtered, prepared, or consumed meat form sick domestic animals and 5% reported bitten/scratched by wild animal or consumed wild animal. Case fatality was 13% (12/93). Laboratory testing detected 1 patient with adenovirus and 7 patients with Nipah virus infection. More than 91% of cases remain undiagnosed and require further investigation. **Conclusion:** Integrating animal exposure questions into existing surveillance identified patients with a recent zoonotic exposure and no current etiologic diagnosis. Method of collecting real-time data from multiple sites and providing appropriate feedback on prioritization of sample testing could be used in other settings at high risk for zoonotic disease emergence to focus diagnostic efforts.

Board 108. Chikungunya: First Time Identified in Dhaka City, Bangladesh

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Background: Chikungunya is a mosquito borne viral disease caused by Chikungunya (Chik) virus. Main vectors of Chik in Asia are Aedes Aegypti and Aedes Albopictus mosquitoes. Chik infection characterized by sudden onset of fever, severe multiple small and large joint pain. The first Chik outbreak in the World recorded in Tanzania in 1952. In India, first reported Chik outbreak was in 1963, and re-emerge in 2005. Chik first identified through an outbreak in 2008 in north-western part of Bangladesh, after that four reported outbreak occurred in Bangladesh and all in rural area. We conducted household survey to find out the serological prevalence of Chikungunya infection and to measure entomological indices of its vector in Dhaka, capital city of Bangladesh. **Methods:** We conducted household survey in September 2013 in Dhaka. We conducted study in four sites (Sutrapur, Dhanmondi, Motijheel and Mohakhali) of Dhaka city. Interviewer and specimen collector visited every 10th household and interviewed people 15-60 years of ages residing the house using structured questionnaire. From each participant 5ml of blood drawn, serum separated for testing Anti-Chik IgM and IgG by Enzyme-Linked Immunosorbent Assay. Larvae collected from natural and artificial wet container of interviewed households and their surroundings. **Results:** We interviewed 621 participants having mean age 32 years

(Median, 30years), 344 (55%) were female. 341 (55%) participants usually don't use mosquito net at night. During data collection 65 (10%) were suffering from fever. We found 207 (33%) specimen positive for Chik IgM and 16 (3%) positive for IgG. We inspected 640 households for larvae collection, 1780 larvae collected from 1584 containers. Among those larvae 1725 (97%) were Aedes Aegypti, 29 (2%) were Armigeres spp. and 16 (1%) were Culex spp. We found 4.6% water holding container infested with larvae, 7.8% household found positive with larvae. **Conclusions:** This is the first time Chikungunya identified in Dhaka. A. Aegypti identified as the possible vector. In all previous outbreaks main vectors were A. Albopictus. Regular cleaning of vector breeding places is necessary to control the infection in Dhaka city with more than 15 million people. Periodic sero and vector surveillance is necessary to monitor the disease.

Board 109. An Outbreak of *Salmonella* Paratyphi A Infection in Shenzhen, China

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Background: In Southeast of Asia, *Salmonella* Paratyphi A is an emerging infection and increasingly this decade. During October 2013-November 2013, an outbreak in *S.* Paratyphi A infection was noted in Shenzhen, China. **Methods:** The field epidemiological investigation and sample testing were applied to trace the infection resource of an outbreak of *Salmonella* Paratyphi A infection. Descriptive epidemiological analysis was used to study the three distribution process of the outbreak. Multiple RT-PCR including the homo-tag assisted non-dimer (HAND) system and modified molecular beacons were established for rapid detection of *Salmonella enterica* serovars Typhi, Paratyphi A, B and C in one tube. Multiple RT-PCR methods and bacterial culture were combined applied to screen 250 specimens which collected from patients, food handler's stools and environment or food samples. The strains isolated were further detected via pulsed-field gel electrophoresis (PFGE) analysis and antimicrobial susceptibility testing. **Results:** *Salmonella* Paratyphi A was verified positive in 15 samples (13 patients stool, 1 food handler stool and 1 toilet swab) via multiple RT-PCR and traditional bacterial isolation. All 15 isolates had an identical pattern on PFGE, and all were nalidixic acid resistant. **Conclusions:** "Paratyphoid Mary-like" food handler who sold meals every night and had the typical syndrome of typhoid one month before was identified as the source of this outbreak. The established multiple RT-PCR assays could increase the speed of detection and differentiation of pathogens in a diagnostic setting, which can make the early detection and enhance the sensitivity of blood culture and bacterial isolation. PFGE can be used to track the source of the epidemic of typhoid.

Board 110. 12 Acute Measles Encephalitis Cases Without Rash

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Background: Measles outbreaks occur in some countries and regions, hindering the goal of eliminating measles set by WHO recently. Encephalitis is the most common cause of death and disability in measles patients. A typical measles-like rash is an important symptom for the clinical diagnosis of measles. Acute measles encephalitis without rash has rarely been reported. **Methods:** Patients who were hospitalized for acute viral encephalitis in the pediatric center of the Hunan Provincial People's Hospital were enrolled from October 2011 to July 2013. Cerebrospinal fluid (CSF) samples and serum samples were collected. CSF samples were tested by real time-PCR to detect 11 types of viruses including mumps virus (MuV), Epstein-Barr virus (EBV), human Parechovirus (HPeV), herpes simplex virus type 1 (HSV-1), herpes simplex virus type 2 (HSV-2), adenovirus (ADV), human herpesvirus-6 (HHV-6), enterovirus (EV), varicella zoster virus (VZV), Japanese encephalitis virus (JEV), and measles virus (MeV). RT-PCR and sequencing were performed in the MeV positive samples for genotyping. IgG and IgM against measles were tested by ELISA in all CSF and a few serum samples. Demographic and clinical information were collected. **Results:** 71 of 161 CSF samples were tested positive for at least 1 type of virus. 12 samples were positive for MeV, among which 7 samples were genotyped with 5 cases were H1 and 2 cases were B3. IgM against measles were positive in one CSF sample but negative in all serum samples. IgG against measles were positive in 3 serum samples but negative in all CSF samples. The average age of the 12 MeV cases was 41.67 ± 7.96 months. The male to female ratio was 1:1. All the MeV cases have no typical measles symptoms such as rashes, mucous measles spots and conjunctival hyperemia except fever. The main clinical characteristics of the cases were symptoms relevant to encephalitis as headache, altered consciousness, drowsiness and convulsions. Among all the 12 cases, 2 cases never received any measles vaccine, 8 cases were vaccinated for 1 dose and 2 cases were vaccinated for 2 doses. **Conclusions:** Our study indicates acute measles encephalitis can have no typical measles symptoms, which may be related to no fully vaccination of measles vaccine. Measles screening in viral encephalitis children is necessary to monitor, control and prevent measles.

Board 111. Development of a 16-plex PCR Assay Based on the GeXP Principle for the Detection of Diarrhea Pathogens

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Background: Diarrhea caused by bacterial infections is a major health problem in developing countries. A rapid, sensitive, specific, and cost-effective diagnostic method which can detect multiple pathogens simultaneously would be highly preferred for routine laboratory testing. The GenomeLab Gene Expression Profiler (GeXP) analyzer is a multiplex gene-expression profiling analysis platform, normally used in identifying virus infections. But GeXP multiplex assay was seldom developed for the identification of bacterial infections. **Methods:** A 16-plex PCR assay was designed based on the principle of GeXP multiplex amplification assay and the PCR products were analyzed by Qiacel capillary electrophoresis. The assay identifies the 12 most common bacterial pathogens associated with diarrhea in a single PCR reaction. Targeted pathogens included diarrheagenic *Escherichia coli (DEC)* (EHEC, ETEC, EPEC, EAEC, and EIEC), *Shigella*, *Salmonella*, *Yersinia enterocolitica*, *Campylobacter jejuni*, *Campylobacter coli*, *Vibrio cholerae* and *Vibrio parahaemolyticus*. An internal control was amplified in each reaction to monitor the system. The detection limits of the assay were evaluated by performing the assay on serial dilutions of recombinant plasmids. The analytical specificity was examined with 279 strains. Diagnostic specificity and sensitivity were evaluated with 243 stool samples. **Results:** The low detection limits of the assay were 500 - 5,000 copies/reaction for each target. The assay gave specific bands when pure cultured strains were detected, and no cross reaction was found. When stool samples were detected, the sensitivities of the targets were STh 15/16, *elt* 5/9, *eaeA* 7/7, *aggR* 4/5, *stx1* 3/3, *virA* 3/3, *ompC* of *Salmonella* 1/4, *hipO* of *C. jejuni* 2/2, and *ompW* of *V.*

cholearae 0/1. Targets *toxR* of *V. parahaemolyticus*, *stx2*, *bfpA*, STp, and *ail* of *Y. enterocolitica* were not detected in these samples. **Conclusions:** The multiplex assay is sensitive and specific for the simultaneous detection of enteric bacteria. It showed good performance especially when DEC exists.

Board 112. Middle East Respiratory Syndrome and Severe Acute Respiratory Syndrome—an Epidemiological Comparison

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Background: Middle East Respiratory Syndrome (MERS-CoV) and Severe Acute Respiratory Syndrome (SARS-CoV) are closely related in the phylogenetic tree of novel coronaviruses that have generated infections in humans. While case and death counts for MERS follow an almost continuous uptick trend in the Arabian Peninsula since June 2012, our basic epidemiological understanding of MERS is limited, extending into unknown areas such as transmission mechanisms, dynamics of human spillover events, natural animal reservoirs and its potential to generate a pandemic. **Methods:** The SARS dataset consisted of 8,422 cases were obtained through the World Health Organization database covering cases from November 2002 through August 2003. Similarly, the MERS dataset covering cases from March 2012-March 2014 comprised 528 cases. For each case, age, gender, mode of transmission, health outcome and location was obtained from a line list. Data points were only collected from the confirmed cases as of March 2014. The data for each transmission period was split geographically into three waves: the initial, secondary and tertiary outbreaks. Once these wave periods were controlled for, percentages of male to female, age, recovery vs. fatality and health care worker transmissions were determined for each wave and then compared against the corresponding wave of the other virus. Analysis was based on a strict percentage basis of all recorded cases during the previously stated time periods. **Results:** Our results indicate that MERS-CoV affects a disproportionate number of males between 40-50 years old particularly those with comorbidities. Health care worker incidents increased the risk of infection in both diseases. The case fatality rate for MERS-CoV cases ranged from 46 to 60% compared with a case fatality rate at 9.6% for SARS-CoV. **Conclusions:** There is the potential that while MERS-CoV is not currently a pandemic, the risk remains that if its virulence rises to be equal to that of SARS-CoV, we will see a much higher fatality rate among infected individuals. Based on this epidemiological analysis, MERS-CoV could prove to be a worse pandemic than SARS-CoV if continuing on its development towards a higher virulence.

Board 113. Novel Technology Combats an Old Foe: WGST Utilized to Investigate the Origin of *Sarocladium kiliense* in a Multi-national Outbreak

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Background: Small-scale molecular genotyping provides an epidemiologic tool for determining genetic relationships among strains in outbreak investigations. However, for many fungal pathogens, such methods are either incomplete or non-existent. Whole genome sequence typing (WGST) has been proposed as a method of interrogating genetic relationships among pathogens. We describe the use of whole genome single nucleotide polymorphism (SNP) typing of *Sarocladium kiliense* (formerly *Acremonium kiliense*) implicated as the etiologic agent of blood stream infections associated with receiving contaminated medication among pediatric oncology patients in Colombia and Chile. **Methods:** A total of 22 patient isolates (15 Colombians, 7 Chileans), 7 isolates from the contaminated medication, and 16 control isolates were subjected to whole genome phylogenetic SNP analysis in order to elucidate a common source. **Results:** WGST analysis indicated that all outbreak isolates were nearly indistinguishable (0-4 SNPs), while greater than 483 SNPs were identified from the control isolates of *S. kiliense* not related to this outbreak. **Conclusion:** These results suggest a single origin of this outbreak and link human infections that occurred in two countries to the contaminated medication and highlight the utility of WGST for outbreak investigation caused by eukaryotic pathogens without existing genotyping methods or reference genomes.

Board 114. Human Parvovirus B19 Infections Have Emerged but Given a Back Seat: A Pioneer Work from a Single Centre in India Indicates a High Disease Burden

J. Kishore; Sanjay Gandhi Post Graduate Inst. of Med. Sci., Lucknow, India

Background: Parvovirus B19 (B19), family parvoviridae (discovered 1975) was listed as newly emerging virus (1981-1987) but could not gain importance due to asymptomatic/self-limiting besides unknown disease burden. **Methods:** Hence in-house methods of DNA extraction from serum, PCR, nested-PCR, IgM and IgG ELISA were standardised by us. **Results:** *Seroprevalence* of B19 was 39.9% among 1000 blood donors; rendering 60% of Indian population (1.2 billion) at risk of B19 infections. Cases of B19 induced *pure red cell aplasia* and *thrombocytopenia* and death occurred. Study on 69 children with *juvenile rheumatoid arthropathy* found B19 infection in over 27.5%. *Feto-pathogenic* association done on 372 women found that among 116 women with recurrent spontaneous abortions 19.8% had anti-B19 IgM antibodies in contrast to 11% among 136 pregnant-women and 5% of 120 non-pregnant women further in 60 high-risk pregnant women with BOH and/or polyhydramnios, oligohydramnios, intrauterine growth retardation anti-B19 IgM positivity was 13.6%. In 35 *paediatric haematological malignancies* B19 infection was seen in 17.1% (5 ALL, 1 NHL) and two had B19 DNA/giant pronormoblasts (lantern cells). Of 90 *multitransfused beta-thalassemia major* patients had B19 seropositivity in 81% and anti-B19 IgM positivity in 41% besides transmission through donor units. Novel clinical associations like a*megakaryocytic thrombocytopenia, myositis* as a complication of erythema infectiosum in a 9 yr female and recently *non-occlusive ischemic gangrene* of stomach and bowel were reported. **Conclusions:** Our limited work denotes high/alarming situation of B19 infections, hence B19 be looked/recognised and prevented by a licensed B19 vaccine.

Board 115. Profile of *Candida* Infections in HIV Seropositive Patients from a Tertiary Care Hospital in New Delhi

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Background: Candida infection is a common opportunistic infection during the course of Human immunodeficiency virus (HIV) disease progression. Changes in the clinical severity of candidiasis and the type of Candida species profile may be a reflection of immunological changes in HIV positive patients. The aim of this study was to document the

Candida species profile of HIV positive patients for future reference. **Methods:** One hundred and twenty HIV seropositive subjects were recruited. Clinical specimens including blood, oral swabs, expectorated or induced sputum/ bronchoalveolar lavage specimens and urine were collected depending on the patient's symptoms. **Results:** A total of 128 Candida isolates were obtained from 88 cases and 7 different Candida species were identified. *C.albicans* (50%) was the most common species isolated followed by *C.glabrata* (17%) and *C. dubliniensis* (12.5%). Other species isolated were *C.parapsilosis* (7.8%), *C.krusei*, *C.tropicalis* (4.6% each) and *C.kefyr* (3%). **Conclusions:** The proportion of Candida infections caused by C. albicans in HIV seropositive individuals has fallen and there is a shift in the distribution of Candida species in HIV positive patients towards the non albicans Candida species which tend to be less susceptible to antifungal agents and this has accounted for their emergence as a significant pathogen. Recurrent fungal infections due to the immunocompromised state and repeated exposure to antifungal agents are responsible for this shift in the spectrum in HIV positive cases. Consequently more focus should be placed on the accurate diagnosis and treatment of Candida species other than the Candida albicans.

Board 116. Japanese Encephalitis Virus Detected in Non-encephalitic Illnesses from West Java

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Background: Japanese encephalitis virus (JEV) is the most common vaccine-preventable cause of encephalitis in Asia. Clinical symptoms vary from a mild non-specific febrile illness to severe encephalitis. However, the majority of JEV infections are asymptomatic, meaning most remain undetected. In Indonesia, JEV is presumed to be endemic in several provinces, but limited disease surveillance means no clinical case has ever been recorded in West Java. JEV surveillance is therefore critical for characterizing epidemiology, measuring disease burden, and documenting the impact of control measures. **Methods:** Archived specimens were gathered from previous studies in West Java on hospitalized patients suspected of hantavirus infection (n = 406), and cases of suspected dengue from a cohort of adult factory workers (n = 737) and community clusters (n = 143). All available paired samples (n = 236) from non-dengue febrile cases were tested for anti-JE IgM using immunoglobulin M antibody capture ELISA (MAC-ELISA). Case definition for JE was relatively conservative, based on detection of IgM antibodies in convalescent sera samples (seroconversion) using a CDC reference assay. **Results:** Preliminary testing of 253 samples showed 2 JEV-positive cases, one adult and one child. Both cases were from systemic febrile illnesses with fever and headache but no neurological manifestations. Cell culture and RT-PCR were also attempted without positive results. The acute sera (day 2) of both cases were negative but both convalescent sera (day 11) tested positive for JE IgM. Hematological investigations showed no hemoconcentration, thrombocytopenia or leucopenia. **Conclusions:** Although there are a number of laboratory tests to diagnose JEV infection, virus detection assays are not useful for diagnostic purposes due to low-level, transient viremia. We may have documented more seroconversions if there were more appropriately timed convalescent samples. This is the first reported case of JEV as the cause of non-encephalitic illness in Java, as JE is not usually in the diagnostic algorithm for febrile illnesses. Our study also suggests that JE surveillance in non-encephalitic cases might contribute towards the true epidemiology of JE disease in humans, which is based primarily on acute encephalitis syndrome.

Antimicrobial Use and Resistance

Monday, August 24, 3:30 PM - 4:45 PM

Grand Hall

Board 117. *Staphylococcus aureus* Bacteremia and Methicillin Resistance in Two Rural Provinces in Thailand, 2006-2013

D. Jaganath, P. Jorakate, S. Makprasert, T. Akarachotpong, O. Sangwichian, S. Thamthitiwat, T. Defries, H. C. Baggett, T. Whistler, C. Gregory, J. Rhodes; Thailand Ministry of Publ. Hlth.–US CDC Collaboration, Nonthaburi, Thailand

Background: *Staphylococcus aureus* is a common cause of bloodstream infection, and methicillin resistant *S. aureus* (MRSA) is a growing threat globally. There are limited data on the incidence of invasive *S. aureus* infections, including MRSA, in Thailand and Southeast Asia. **Methods:** Blood cultures were collected as clinically indicated from hospitalized patients at all 20 hospitals in two rural Thai provinces and processed using an automated blood culture system. Susceptibility to oxacillin/ cefoxitin (to define MRSA) and other antibiotics were determined by disk diffusion. Vancomycin susceptibility among MRSA isolates was evaluated by E-test. Infections were classified as community-onset when blood cultures were obtained ≤2 days after hospital admission. **Results:** From >125,000 blood cultures performed on >90,000 hospitalized patients from 2006 - 2013, we identified 790 cases of *S. aureus* bacteremia in 770 individuals. Annual incidence increased from 6.5 per 100,000 population in 2006 to 8.7 in 2013. The highest age-specific incidence (per 100,000) and largest increase over time occurred in patients aged ≥50 years, from 12.9 over years 2006-2007 to 23.6 in 2012-2013. Of 790 S. aureus bacteremia cases, 79 (10%) were MRSA, and overall MRSA incidence was 0.9 per 100,000 without clear trend over time. The majority (66.2%) of MRSA cases were community-onset infections; however, among cases with available data, 54.9% were hospitalized in the last year or had a recorded healthcare-associated risk factor. Methicillin resistance was highest in neonates (11.5%) and adults aged ≥50 years (12.4%). *S. aureus* bacteremia cases at provincial hospitals were more frequently methicillin resistant than those at district level hospitals (12.2% vs. 5.8%, p=0.004). MRSA was more frequently resistant to other antibiotics (erythromycin, clindamycin, gentamicin, co-trimoxazole, and fosfomycin, p<0.001 for all) than was methicillin susceptible *S. aureus*. No cases were vancomycin resistant. **Conclusions:** MRSA incidence remained stable in two rural Thai provinces despite increasing overall *S. aureus* bacteremia incidence between 2006 and 2013. The high proportion of MRSA cases that were community-onset, had co-resistance, and occurred in vulnerable groups, such as neonates and older adults, calls for increased surveillance and stronger antimicrobial stewardship efforts in rural Thailand.

Board 118. Lessons Learned from an Annual Kids' Art Competition to Promote Antimicrobial Stewardship

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Background: Despite the growing threat of antimicrobial resistance, children with acute respiratory viral illnesses are frequently prescribed antibiotics. In partnership with the CDC Get Smart: Know When Antibiotics Work Program and academic partners, Pennsylvania recently

created a website (Knowwhentosayno.org) to promote appropriate antibiotic use among healthy children and parents. The site includes an annual kids' art competition. Little is known regarding strategies to motivate targeted audiences to access online resources. **Methods:** We used participation records from the kids' art competitions during 2013-2014 and Google Analytics data on visits to the site for the same period to assess use of this approach to increase use of the website. The competition guidelines directed participants to the *Kids' Hangout* section of the site for ideas and sample entries. Various methods were used to create awareness about the competition including emails, flyers, announcements in print and online, and newsletters directed to childcare facilities. Flyers were distributed to multiple venues including pediatric clinics, libraries, farmers markets, and welcome centers on interstate highways. Winners were announced during the annual Get Smart About Antibiotics Week. **Results:** In 2013, 388 entries were received from children in 31% (21 of 67) of counties in Pennsylvania. Of these 24% were from children ≤4, 36% from 5-6, and 40% were by 7-8 year olds. A winner from each category was declared and their entries were posted on the website. After the announcement, 81.4% of the 1,839 unique visitors who visited the site were new. Google Analytics trends showed bounces in activity that correlated with competition announcement in September, October, and November 2013 and when winners received prizes from the state's Physician General in February 2014. Eighty percent of the 2,213 new sessions in 2014 are new and increased activities show a similar trend. **Conclusion:** Increases in website traffic for an appropriate antibiotic use program correlated with drawing competition announcements, suggesting this approach could be used to engage children and parents in online public health interventions. More research is needed on ways to sustain interest in online resources over time.

Board 119. Antimicrobial Resistance Among *Shigella* Isolates from Rural Western Kenya: 2006-2014

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Background: In developing countries, where unrestricted use of antibiotics is common, therapeutic options are becoming limited due to increasing bacterial resistance. The aim of this study was to describe the antibiotic resistance patterns among *Shigella* serogroups isolated from individuals with diarrhea in western Kenya. **Methods:** We collected stool samples from 1st September 2006 to 31st August 2014 from patients presenting with diarrhea to Lwak mission hospital in rural Asembo, western Kenya. *Shigella* spp. isolated from these samples were tested for susceptibility to 12 antimicrobial agents. Cochran-Armitage was used to test for trends of antimicrobial resistance pattern across the years. **Results:** From a total of 1,571 stool samples collected, 375 (23.9 %) tested positive for *Shigella which* included; *S. flexneri* (219, 58.4%), *S. dysentery* (53, 14.1%), *S. sonnei* (40, 10.7 %), *S. boydii* (34, 9.1 %) and *Shigella* spp non-typable (29, 7.7%). *Shigella* isolates regardless of species, were most commonly resistant to; tetracycline (88.3%), streptomycin (77.4%), sulfisoxazole (77.3%), trimethoprim-sulfamethoxazole (76.8%), ampicillin (52.8%) and amoxicillin/clavulanic acid (41.6%). The isolates were most susceptible to ciprofloxacin (100%), gentamicin (98.9%), ceftriaxone (98.1%) [(with 1/33 (3%), 3/23 (13%) and 0/34 (0%) of resistant strains from 2012, 2013 and 2014 respectively)], nalidixic acid (98.0%), kanamycin (89.9%) and chloramphenicol (67.6%). Resistance increased over time for a few such as amoxicillin/clavulanic acid (1.9% in 2009 and 22% in 2012; p=0.0098), streptomycin (22.6% in 2009 and 100% in 2013; p=0.0009), sulfisoxazole (16.7% in 2009 and 98% in 2011; p=0.0004), trimethoprim-sulfamethoxazole (22.6% in 2009 and 100% in 2014; p=0.0003) while resistance decreased for chloramphenicol (64.1% in 2007 and 6.5% in 2009; p=0.035) and tetracycline (90.6% in 2007 and 79.4% in 2014; p=0.024). **Conclusions:** The wide spread increase in antimicrobial resistance for *Shigella* isolated in Kenya, with potential emerging resistance to ceftriaxone, highlights the risk for decreased effective treatment options. Continued monitoring for drug resistance and promotion of judicious use of antibacterial drugs in this setting are urgently needed.

Board 120. The Prevalence of MRSA and ESBL Producing *Escherichia coli* and *Klebsiella pneumonia:* Tawam Hospital, 2004-2013

W. Tariq, A. A. Hassanein; Tawam Hosp., Al Ain, United Arab Emirates

Background: This study aims at studying the prevalence of MRSA and ESBL producing isolates of *Escherichia coli* and *Klebsiella pneumonia*. The study will cover the period from 2004 until 2013.The prevalence of MRSA has increased worldwide in both healthcare and community settings. MRSA infections have high impact on the patient mortality, hospital stay, and costs. Extended-spectrum beta-lactamases (ESBL) confer resistance to beta lactam agents. Plasmids that carry ESBLs typically carry other resistance genes as well so these organisms are frequently multidrug resistant. **Methods:** Retrospective Study was held in Tawam hospital, Al Ain, United Arab Emirates. The data analyzed covers 10 years for the interval 92004-2013). **Results:** MRSA rates were 6.1%, 6.0%, 7.3%, 9.0%, 15.6%, 21.5%, 27.2%, 31.4%, 32.6%, and 26.9 %. The number of MRSA isolates increased steadily from 6.1% in 2004 to 21.5% in 2009. The increase was significant (p<0.05). During the period 2010 until 2013, there was no significant increase. For *Escherichia coli* (ESBL):The rates of *Escherichia coli* (ESBL) were 7.0%, 7.4%, 11.4%, 16.2%, 22.3%, 22.0%, 23.1%, 26.1%, 18.9%, 26.9%, and 29.7%.The number of *Escherichia coli* (ESBL) isolates increased steadily from 7.0% in 2004 to 22.3 % in 2008. The increase was significant (p<0.05). During the period 2009 until 2013, there was no significant increase. As for *Klebsiella pneumoniae* (ESBL): The rates of *Klebsiella pneumoniae* (ESBL) were: 9.3%, 8.2%, 6.5%, 8.2%, 16.4%, 13.7%, 13.8%, 15.1%, 15.3%, 23.9%. The number of *Klebsiella pneumoniae* (ESBL) isolates increased significantly during 2008 and again during 2013(p<0.05). There were two peaks, two fold rise during 2008 and another in 2013. **Conclusions:** The Prevalence of MRSA and an ESBL producing Escherichia coli and Klebsiella pneumonia has increased significantly,in Tawam Hospital, during the period 2004-2013.

Board 121. Antimicrobial Resistance in *Escherichia coli* O157 Isolates from Humans, United States, 1996-2012

J. Grass, K. Joyce, F. Medalla; CDC, Atlanta, GA, USA

Background: *Escherichia coli* O157 (O157) produces Shiga toxin, which can lead to hemolytic uremic syndrome, a major cause of acute renal failure in children. Although antimicrobial treatment is not recommended, O157 isolates are received at public health laboratories for confirmation, and thus are available for susceptibility testing by the National Antimicrobial Resistance Monitoring System (NARMS) at CDC. Antimicrobial use in food animals may cause selective pressure for resistance in the intestinal flora, including O157, producing a reservoir of resistance genes. Some resistance genes may be transferable to other bacteria or cause human infections by direct contact with animals or via the food production chain. **Methods:** Participating public health

laboratories submitted every 5th (1996-2002) or 20th (2003-2012) O157 isolate from humans to NARMS. Minimum inhibitory concentrations of antimicrobial agents representing 9 classes were determined by broth microdilution and interpreted using Clinical and Laboratory Standards Institute criteria when available. We examined resistance and its distribution and prevalence by patient age and sex, specimen source, region, and month of collection. **Results:** During 1996-2012, 3,843 isolates were tested; 3,499 (91.0%) were susceptible to all classes, and 344 (9%) were resistant to at least one. We found the highest resistance to folate pathway inhibitors (5.4%), tetracyclines (4.8%), aminoglycosides (3.0%), and penicillins (2.3%); 115 (3.0%) were resistant to ≥3 classes. Resistance to the quinolone nalidixic acid was first observed as 0.7% (2/291) in 1999 and increased to 2.4% (4/166) in 2012. Ciprofloxacin resistance was first observed in 2006 and overall in 4 (0.1%) isolates. Third-generation cephalosporin resistance was first observed at 1.0 % (4/407) in 2000. Resistance to azithromycin (tested since 2011) was observed in one isolate in 2012. Resistance was highest among isolates from blood, from patients in the Midwest, and from isolates collected in the first 4 months of the year. **Conclusion:** Most O157 isolates were susceptible to all agents tested; however, resistance to important agents may be emerging. Monitoring resistance in O157 is a useful approach to detecting emerging resistance genes that may be transferable to other bacteria.

Board 122. Molecular and Clinical Characteristics of Methicillin-resistant *Staphylococcus aureus* Infections in Nine Sentinel Hospitals Across Shenzhen City, China

Q. Hu[1,2], Y. Li[1], L. Hu[1], Y. Lu[1], X. Shi[1], Y. Qiu[1], Y. Lin[1], M. Jiang[1], Q. Chen[1], R. Zhang[1], H. Ma[1], J. Cheng[1]; [1]Shenzhen Ctr. for Disease Control and Prevention, Shenzhen, China, [2]Sch. of Life Sci., Shenzhen Univ., Shenzhen, China

Background: To investigate the clinical characteristics and determine the molecular epidemiology of methicillin-resistant *Staphylococcus aureus* (MRSA) in Shenzhen city,China **Methods:** MRSA strains were isolated and identified from patients with infectious diseases in nine sentinel hospitals and epidemiological information of the patients was collected using the questionnaire. Community-associated MRSA (CA-MRSA) infections, health care-associated, community onset (HACO), hospital-associated MRSA (HA-MRSA) infections and colonization were confirmed based on epidemiological data and *mecA* result, according to US-CDC MRSA case definition. Antimicrobial susceptibility test was analyzed and virulence factors, including *pvl*, accessory gene regulator (*agr*) I-IV and sixteen enterotoxin genes (*sea-see and seg-seq*) and genotyping including SCCmec typing, spa typing, multi locus sequence typing (MLST) and pulsed-field gel electrophoresis (PFGE) typing were carried. **Results:** A total of 209 MRSA cases were identified between October 2013 and December 2014. The proportion of MRSA in CA, HACO, HA and colonization isolates were 33.49% (70/209), 32.54% (68/209), 21.53% (45/209) and 12.44% (26/209), respectively. The clinically significant difference included skin and soft-tissue infection (P<0.001), surgical site infection (P=0.002), traumatic wound infection (P=0.002) and respiratory tract infection (P<0.001) was showed in CA, HA, HACO and colonization. There were no significant differences in leukocyte counts among the four categories, while the significant difference in neutrophile granulocyte counts of HA was showed. HA-MRSA isolates showed higher antibiotic resistance rate to gentamicin, ciprofloxacin, SXT and tetracycline than other three types of MRSA. Among 209 strains, 51.67% (108/209) were *pvl*-positive, 78.47% (164/209) were *agr* I and 94.74% (198/209) were *seb*, respectively. SCCmec IV, spa types t437 and CC59 were identified as the predominant types in four categories. PFGE patterns of the 209 isolates had no identity with USA100-USA1200. **Conclusions:** The major predominant clone was CC59-SCCmecIV-t437-pvl (+) - seb-agrI in MRSA. There was no significant difference in the molecular characteristics among CA, HACO, HA and colonization. Less expensive antimicrobial drugs were suggested to cure HA MRSA.

Board 123. Ciprofloxacin-resistant *Salmonella enterica* ser. Kentucky from Imported Foods

C. Kabera; US Food and Drug Admin., Laurel, MD, USA

Background: Ciprofloxacin resistant (Cip^R) *Salmonella enterica* ser. Kentucky multilocus sequence type 198 (ST198) recently emerged rapidly across the globe as a bacteria of concern due to limited treatment options. In the U.S. and Canada, *Salmonella* ser. Kentucky ST198 infections have been associated with travel to India, Africa, and the Middle East. In African countries, poultry is thought to be an important vehicle for this strain. Although Kentucky is a predominant *Salmonella* serotype in chickens in the U.S., ciprofloxacin resistant strains have not been found in retail chicken products collected through the National Antimicrobial Resistance Monitoring System (NARMS) at FDA. It has been hypothesized that imported spices, produce, or aquaculture may be potential food vehicles in the U.S. and other countries. Here we report findings from surveillance for Cip^R *Salmonella* ser. Kentucky isolates from imported foods collected at FDA. **Methods:** Imported foods and feedstuffs were collected between 2003 and 2013 through sampling assignments and other directives issued to the FDA Office of Regulatory Affairs. *Salmonella* were isolated and serotyped according to published methods. Minimum inhibitory concentrations were determined for 15 antimicrobials and interpreted using Clinical and Laboratory Standards Institute criteria, when available. **Results:** Between 2003 and 2013, the FDA Office of Regulatory Affairs isolated over 5527 *Salmonella* from environmental samples and imported foods and feedstuffs. One percent (53/5527) of the isolates were serotype Kentucky. Nineteen percent (10/53) of *Salmonella* ser. Kentucky isolates were Cip^R. Although 40% (21/53) of the *Salmonella* ser. Kentucky isolates were collected from spices and herbs, all of the Cip^R *Salmonella* ser. Kentucky isolates were recovered from spices and herbs that had been imported from Canada, France, Africa, and the Middle East. Cip^R *Salmonella* ser. Kentucky isolates were resistant to other antibiotics but all were susceptible to ceftriaxone. **Conclusion:** This study provides evidence that imported spices are a potential source for domestic Cip^R *Salmonella* ser. Kentucky infections that are not associated with international travel.

Board 124. Surveillance of Antimicrobial Suceptibility in *Salmonella* in Tawam Hospital

W. Tariq, A. A. Hassanein; Tawam Hosp., Al Ain, United Arab Emirates

Background: Salmonellosis is associated with foodborne infections. It can cause invasive illness. Outbreaks have been reported worldwide. Outbreaks due to *Salmonella* will result in more hospitalizations and deaths more than any other foodborne pathogen. The aim of this study is to monitor antimicrobial resistance during the period 2010 until 2013. **Methods:** *Salmonella* bacteria were isolated and identified by conventional methods. The antibiotic susceptibility rates were detected by minimal inhibitory concentration (MIC). Retrospective study was held in Tawam hospital, Al Ain, United Arab Emirates. The data was taken from the Cerner which is the hospital information system. **Results:**

Antimicrobial susceptibility includes the following, during the period 2010 until 2013 respectively: for Ampicillin the percentage susceptible are 72.5%, 77.4%, 84.3%, 82.7%. for Cefotaxime susceptibility was 97.0%, 98.4%, 100.0%, 93.8%. There was no significant change in susceptibility to ampicillin and cefotaxime during the study. On the other hand, the susceptibility to Ciprofloxacin and Trimethoprim/ Sulfamethoxazole dropped significantly ($p< 0.05$). Ciprofloxacin susceptibility dropped continuously (61.3%, 55.9%, 54.9%, 46.9%). Trimethoprim/ Sulfamethoxazole decreased as well (84.5%, 74.6%, 91.2%, 88.5%). Nalidixic acid, which can serve as a marker for decreased susceptibility to fluoroquinolones, has shown a significant decrease in susceptibility in 2011: (62.4%, 49.2%, 63.4%,72.0%). The isolates continued to show high susceptibility to cefotaxime (97.0%, 98.4%, 100.0%, and 93.8%). The isolates did not show Mutidrug resistance. **Conclusions:** Salmonella showed decreased susceptibility to fluoroquinolones and Trimethoprim/ Sulfamethoxazole. Cefotaxime resistance has not yet developed.

Board 125. A Collaborative Approach to Promote Appropriate Antibiotic Use with Practical Considerations for Sick-child Exclusion Policies in Pennsylvania

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Background: Widespread antibiotic use drives escalating antimicrobial resistance. Misuse of sick-childcare exclusion policies can promote unnecessary pediatric antibiotic use. However, childcare facilities do not always apply evidence-based exclusion requirements. **Methods:** During 2012-2014, we facilitated an advisory group to address misuse of sick-childcare exclusion policies, required in ~8,000 licensed facilities serving ~24200 Pennsylvania children. The group included pediatricians, childcare directors, public health officials, and a pediatric dermatologist. We surveyed directors of a random sample of 904 licensed facilities regarding exclusion policies. With 2 meetings and several telephone discussions, the group reviewed survey data, American Academy of Pediatrics (AAP) Model Child Care Exclusion Policies, public health guidelines, state regulations, and vignettes posed by childcare directors. **Results:** 25% (226) of directors responded. While 95% (215) of facilities had written exclusion policies, only 70% (158) were based on a model policy. Although respondents referred to various resources, 70% (158) relied on state requirements and 45% (102) consulted AAP recommendations. The most common conditions related to unnecessary exclusions were fever, diarrhea, rhinorrhea, conjunctivitis, skin infections and scabies. Staff and child immunization requirements were not always clear. The advisory group produced a document: *Practical Considerations*, to clarify key current recommended exclusion criteria: 1) children <6 months with fever without behavior change do not need exclusion, 2) most children with green nasal discharge or conjunctivitis do not need antibiotics, 3) children with mild diarrhea or under medical treatment for skin infections do not need exclusion, 4) all staff and children should receive recommended immunizations. With state agency approval, *Practical Considerations* is now disseminated as part of the CDC Get Smart efforts to reduce demand for antibiotics. **Conclusions:** A collaborative approach including key stakeholders has the potential for addressing unnecessary demand for antibiotics. Primary prevention through vaccination and infection control practices can strengthen community-based activities that promote appropriate antibiotic use.

Board 126. Antimicrobial Resistance in ICU, Tawam Hospital, Al Ain, UAE

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Background: Intensive Care Unit (ICU) patients are critically ill. Treatment with invasive procedures will expose patients to infections and subsequent use of antimicrobial drugs. *cinetobacter baumannii* and *Pseudomonas aeruginosa* are the major cause of infections in ICU. The present study aims at evaluating the trend of antimicrobial resistance and emergence of Multi drug resistance in ICU. **Methods:** Retrospective study was conducted in Tawam Hospital, Al Ain, and United Arab Emirates during the period 2010-2013. **Results:** *Acinetobacter baumannii* resistance has increased significantly ($p< 0.05$) to third generation cephalosporins (cefotaxime: 13.25, 2.2%, 0%, 0%) and Ceftazidime (24.5%, 6.5%, 14%, 0%). The number of isolates and the percentage of Multidrug resistant strains of *Acinetobacter baumannii* have decreased significantly: (77%, 94%, 91%, 0%).*Pseudomonas aeruginosa* resistance has increased significantly ($p < 0.05$) to piperacillin (% 61.7, 70.3%, 48.6%, 30.9%) , piperaciilin/ Tazobactam (67.6%, 73.3%, 65.7%, 44.6%) and Ceftazidime (52.8%, 68.4%, 55.1%, 44.9%). The percentage of Multidrug resistant strains did not show significant increase: (57%, 47%, 46%, and 51.7%). **Conclusions:** There is a rise in the rate of resistance among isolates recovered in ICU. Judicious antimicrobial utilization and hospital stewardship program can decrease selective pressure that leads to emergence of resistant bacterial isolates.

Board 127. Improving Antibiotic Use in Tennessee: The Tennessee Department of Health's Collaborative Approach

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Background: According to the Centers for Disease Control and Prevention, Tennessee has the third highest outpatient antibiotic prescribing rate among US states, and the highest prevalence of inpatient antibiotic use among 10 participating states in a 2011 prevalence survey. Additionally, TN has high incidence of invasive methicillin-resistant *Staphylococcus aureus*, non-susceptible *Streptococcus pneumonia*, and an increasing incidence of *Clostridium difficile* infections. Currently, no hospitals report antimicrobial use data to the National Healthcare Safety Network (NHSN) Antimicrobial Use (AU) Module due to limited information technology infrastructure. **Methods:** In 2013, TDH began an antimicrobial stewardship collaborative to improve antimicrobial use in TN hospitals. TDH offered educational webinars and conducted a point prevalence survey that collected the number of patients with an active order for selected antibiotics during a 24-hour period. **Results:** In total, 15 hospitals completed at least one facility-wide survey during the first quarter of 2014 and 16 during the second quarter of 2014. Various sized facilities participated and the median census was 112 patients per day and 99 patients per day for Q1 and Q2, respectively. During both quarters about 50% of patients were on any antibiotic in participating TN facilities. Specifically for Q1, 16.3% (Range: 0-45.1%) were on fluoroquinolones, 12.5% (Range: 0 - 19.4%) were on 3rd generation cephalosporin, 10.5% (Range: 0 - 27.8%) were on IV Vancomycin, and 4.7% (Range: 0 - 13.9%) were on carbapenems. During Q2, 15% (Range: 2-46.4%) were on fluoroquinolones, 10.3% (Range: 2.5 - 32.1%) were on 3rd generation cephalosporin, 11.8% (Range: 2 - 29%) were on IV Vancomycin, and 3.6% (Range: 0 - 20%) were on carbapenems. Educational webinars are provided monthly by antimicrobial stewardship experts. **Conclusion:** Antibiotic use varied across facilities, including in similar sized facilities. Hospitals received facility specific reports plus anonymous results of

other facilities for comparison purposes. The survey will be repeated at least quarterly in participating facilities, allowing TDH to monitor antimicrobial use trends over time and target high use facilities with interventions.

Board 128. Detection and Molecular Characterization of Antibiotic Resistant *Staphylococcus aureus* from Milk in the North-West Province, South Africa

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Background: The aim of this study was to investigate the occurrence, antibiotic susceptibility profiles, virulence genes determinants and the genetic relationships of *S. aureus* isolated from milk obtained from retail outlets and some farms in the North-West Province, South Africa. **Methods:** A total of 200 raw, bulk and pasteurised milk samples were collected and analysed using Mannitol Salt agar and 380 potential *S. aureus* isolates were subjected to Gram staining, DNase, catalase, haemolysis, rapid slide agglutination test, MALDI-TOF mass spectrometry and *nuc* specific PCR assays to determine their identities. The antimicrobial resistance profiles of isolates against a panel of 11 antimicrobial agents were determined. Isolates were screened using a serological assay for the presence of an altered PBP2a that confers resistance to methicillin and beta-lactam antibiotics. The presence of virulence genes encoding enterotoxins, exfoilative toxins and collagen adhesins were also screened using PCR. RAPD-PCR and ERIC-PCR fingerprints were generated using PCR analysis and dendrograms were used to access the genetic relationships of the isolates from different stations and milk types. **Results:** Thirty out of the 40 (75%), 25 of 85 (29%) and 10 of 75 (13%) of the raw, bulk and pasteurised milk samples, were positive for *S. aureus*. In general, 156 *S. aureus* isolates were positively identified using *nuc* PCR analysis. Large proportions (60-100%) of these isolates were resistant to penicillin G, ampicillin, oxacillin, vancomycin, teicoplanin and erythromycin. On the contrary, low level resistance (8.3 to 40%) was observed against gentamycin, kanamycin and sulphamethoxazole. Methicillin resistant *S. aureus* (MRSA) was detected in 59% of the multidrug resistant isolates and this was a cause for concern. However, only a small proportion (20.6%) of the MRSA isolates possessed the PBP2a. In addition, 32.7% of isolates possessed the *sec* virulence gene whereas the *sea, seb sed, see, cna, eta, etb* genes were not detected in any isolate. A total of 18 and 9 RAPD and ERIC-PCR banding patterns respectively were generated from 74 randomly selected isolates. There was generally a high level similarity between isolates from different milk types and sample areas. **Conclusions:** In the present study toxigenic and multi-drug resistant *S. aureus* strains were detected in milk samples analysed and this therefore amplifies the need for strict control measures.

Board 129. A Significant Positive Correlation Between Antibiotic Resistance and Biofilm Forming Ability of *Salmonella* Typhimurium

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Background: An increase in the prevalence of multidrug resistance among non-typhoidal *Salmonella* has been reported in many countries, but little is known about the correlation between biofilm formation and multiple antibiotic resistance (MAR) in complex serotype. Another unresolved question is whether the most common clinical isolates are selected by unfavorable factors, thereby conferring improved adaptation and evolution for MAR strains, or whether biofilm formation is accompanied by the acquisition of resistance mutations that would afford bacteria many advantages. **Methods:** A collection of 893 non-typhoid *Salmonella* clinical isolates was tested for susceptibility to 18 antimicrobials. The biofilm formation of 51 isolates that were all resistant to at least 12 antibiotics (MAR ≥ 0.67) belonging to 14 serotypes and 139 *S.* Typhimurium strains with different MAR index were tested. In addition, *S.* Typhimurium strains with high MAR index were analyzed for the biofilm-related phenotypic characteristics, and the expression of biofilm-related genes. Then streptomycin (STR)-resistant mutants were obtained in vitro from susceptible clinical isolates to further determine whether biofilm production was linked to antibiotic resistance. Biofilm formation and expression of biofilm-related genes for STR-resistant mutant strains were tested. **Results:** A proportion (52.6%) of isolates showed resistance to at least four antimicrobial drugs (MAR > 0.2). Importantly, a proportion (96.7%) of *S.* Typhimurium (MAR ≥ 0.67) was formed biofilm. The rate of biofilm formation also increased significantly over MAR index in *S.* Typhimurium ($P < 0.01$); combined with increased biofilm-forming ability ($P < 0.01$) due to highly elevated *csgB* and *csgD* expression. Acquisition of STR-resistant mutation leads to enhanced biofilm formation in *S.* Typhimurium with increased expression of *csgB* and the occurrence of rdar (red, dry and rough) morphotype. **Conclusions:** In summary, the acquisition of streptomycin resistance in *S.* Typhimurium would be associated with increased production of biofilm, with the result that multiple antibiotic resistance was significantly positive correlated with biofilm forming for *S.* Typhimurium.

Board 130. Antimicrobial Resistant Non-typhoidal *Salmonella* Among Human and Retail Food Isolates, Tennessee, 2010-2013

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Background: Over 100,000 antimicrobial resistant (AR) non-typhoidal *Salmonella* (NTS) infections are reported in the US annually. Resistance to clinically important antimicrobials (CIAs), such as ceftriaxone and quinolones, pose public health risks. Food animals are reservoirs of AR NTS that infect humans. The National Antimicrobial Resistance Monitoring System (NARMS) monitors human, retail meat, and food animal enteric bacteria AR. We reviewed recent NARMS data to compare AR among NTS isolated from humans and retail meats samples. **Methods:** Tennessee submits to NARMS every 20th human NTS isolate detected statewide and all NTS isolates from retail meat purchased from 4 counties. Broth microdilution is performed to determine minimum inhibitory concentrations for 14 antimicrobials (8 classes). Resistance patterns among human isolates were compared to those in retail meats. Analysis was done using Epi Info 7. **Results:** From 2010 through 2013, 179 sporadic NTS human isolates and 76 NTS retail meat isolates were tested. Twenty-two (12%) NTS human isolates and 54 (71%) NTS retail meat isolates demonstrated AR. AR to ≥ 3 classes was detected in 13 (7%) NTS human isolates, 6 (18%) chicken breast isolates, and 14 (45%) ground turkey. Four (2%) human isolates were resistant only to ampicillin, chloramphenicol, sulfisoxazole, streptomycin, and tetracycline (ACSSuT); all were serotype Typhimurium. Resistance to quinolones was detected in 2 (1%) human isolates; serotypes Typhimurium and Litchfield. Only 1 (0.6%) of NTS human isolates was resistant to ceftriaxone compared to 2 (6%) and 5 (16%) from chicken breast and ground turkey isolates, respectively. Ceftriaxone-resistant human, chicken, and turkey isolates were differing serotypes and two of them also demonstrated ACSSuT resistance. No retail meat isolates were quinolone resistant. **Conclusions:** AR is a public health concern.

In Tennessee, AR NTS human isolates occurred less commonly than some national estimates, particularly AR to CIAs. Retail meat isolates demonstrated AR more frequently than human NTS with ground turkey isolate AR being more common than chicken. Serotypes varied among AR isolates from all 3 sources. Expansion of NARMS sampling statewide could provide a better understanding of attribution of human AR NTS infections to their source.

Board 131. Use of Carbapenems in an Intensive Care Unit and the Effect of Educational Intervention in Rationalizing Its Use at a Tertiary Hospital

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Background: Global increase in antibiotic resistance promoted by the widespread use of broad-spectrum antibiotics is a big challenge for effective treatment of life threatening infections. Preserving the existing antibiotics is important as no new antibacterial agents have been developed in the last few decades. Carbapenems are the most potent agents for treatment of multidrug resistant gram negative infections. However, the increasing resistance to carbapenems is of concern in our hospital. We therefore, undertook this study as part of the Indian Council of Medical Research (ICMR's) country-wide study on the usage of carbapenems in the ICUs and followed this by educational interventions for the clinicians on the rational use of carbapenems. We also monitored the usage of carbapenems using the defined daily dosage parameters. **Methods:** This prospective study was conducted from September 2012 to January 2014 and comprised of 8 months each of pre-intervention and post-intervention periods with one month of educational intervention to the ICU physicians. The patients who were newly administered only carbapenems were included for this study. Educational intervention included conduct of CMEs on antibiotic stewardship for all the clinicians of the ICU. During the HICC meetings, emphasis was given on careful selection of appropriate antimicrobial agents, de-escalation based on culture reports and that carbapenems were to be prescribed only by a senior consultant. Published literature on appropriate usage of Carbapenem were disseminated through the PIMS intranet to all the ICU physicians. **Results:** The pre-intervention and post-intervention periods included 75 patients each. In the post-intervention group, there was a significant increase in the authorisation of carbapenem use by a senior consultant. The proportion of patients for whom de-escalation was done increased from 16% before intervention to 21.3% after intervention. The DDD of carbapenems per 100 bed-days showed slight decrease following intervention. There was no significant difference in the choice of carbapenem after intervention. **Conclusion:** Various strategies have been employed by different organizations for regulation of antimicrobial use. Education based approach combined with a hospital antibiotic stewardship program could control the indiscriminate use of carbapenems.

Board 132. Detection of Genes Codifying for Metallo-beta-lactamase Among Imipenem Resistant *Pseudomonas aeruginosa* Isolated in Egypt

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Background: *Pseudomonas aeruginosa* continues to be an important pathogen in nosocomial infection due to its innate and acquired resistance to antimicrobial agents. Carbapenems are used as a last resort to treat serious infections caused by multidrug resistant *Pseudomonas aeruginosa*. Acquired metallo-beta-lactamases in Pseudomonas have emerged as one of the most disturbing resistance mechanism due to their capacity to hydrolyze beta-lactam antibiotics including carbapenems. Thus, our study was undertaken to investigate the prevalence of metallo-beta-lactamase and to detect the genes codifying for metallo-beta-lactamases among carbapenem resistant *Pseudomonas aeruginosa* in Egypt. **Methods:** One hundred and fifty four clinical *Pseudomonas aeruginosa* strains were used. The antimicrobial susceptibility test was performed using disk diffusion method. Metallo-beta-lactamase production by *Pseudomonas aeruginosa* was suspected when the strain found resistant to imipenem. All imipinem resistant isolates were tested for metallo-beta-lactamase enzyme. Detection of metallo-beta-lactamase producing *Pseudomonas aeruginosa* was performed by the Imipenem-EDTA disk potentiation test. Polymerase chain reaction was carried out to detect the bla_{IMP} bla_{VIM} bla_{GIM} bla_{SPM} and bla_{NDM} genes among imipenem resistance strains. bla_{VIM} amplified products were subjected to sequencing. **Results:** The resistance rate to imipenem was 22% (34/154) and 14% (22/154) were found to be metallo-beta-lactamase producers. Among metallo-beta-lactamase strains, 10 (64%) strains carried bla_{VIM}, 8 (36%) strains carried bla_{GIM}, 4 (18%) strains carried bla_{NDM} and 2 (1%) strains carried bla_{IMP}, while, no strain found to carry bla_{SPM}. Two strains were positive genotypically for bla_{VIM} gene but were negative phenotypically. bla_{VIM} was concomitant with bla_{IMP}, bla_{GIM} or bla_{NDM}. Only one strain harbored both bla_{VIM} and bla_{NDM}; 2 strains both harbored bla_{VIM} and bla_{IMP} while 7 straines carried both bla_{VIM} and bla_{GIM}. **Conclusions:** Imipenem resistance in *Pseudomonas aeruginosa* is mainly mediated by metallo-beta-lactamase production. Thus proper antibiotic policy should be taken to minimize the emergence of this beta-lactamase producing pathogens. bla_{VIM} gene was the most prevalent gene in *Pseudomonas aeruginosa* in this study.

Board 133. A Novel Class of Chikungunya Virus Inhibitors Targets the Enzymatic Activity of the Viral Capping Enzyme NsP1

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Background: The last decade, chikungunya virus (CHIKV) re-emerged in many parts of Africa and Asia, and recently also for the first time in Central and South America. The global re-emergence of this virus and its high morbidity rate emphasize the need for potent antivirals for treatment. We recently identified MADTP_314, a [1,2,3]triazolo[4,5-d] pyrimidin-7(6H)-one, as a potent inhibitor of CHIKV replication with no toxicity to the host cells. The antiviral activity of this molecule was confirmed against several clinical isolates of CHIKV, including the Caribbean St-Martin strain. **Methods:** To identify the viral protein(s) involved in the mechanism of action of MADTP_314, drug-resistant CHIKV variants were isolated and their pheno- and genotypes were characterized. The contribution of identified mutations to the resistant phenotype was determined by reverse-engineering. Enzymatic assays using the nsP1 of Venezuelan equine encephalitis virus (VEEV) were performed to evaluate the activity of MADTP_314 on the capping functions. **Results:** In all independently-selected drug-resistant isolates, a single mutation was identified in the CHIKV nsP1 coding sequence that resulted in a P34S amino acid substitution. Reverse-engineering corroborated the link between this mutation and the compound-resistant phenotype. NsP1 is the central enzyme for the viral mRNA capping and interestingly, the proline at position 34 is located near the conserved histidine (H38) in a region involved in methyltransferase/guanylyltransferase functions. Enzymatic assays with VEEV nsP1 showed that MADTP_314 did not, or

poorly, interfered with the N7 methylation of GTP performed by nsP1 but rather inhibited the covalent binding of N7-GMP on H38 of nsP1. Interestingly, analogues of MADTP_314 with more potent anti-CHIKV activity did not only inhibit the guanylyltransferase activity but also the methyltransferase activity of nsP1. Moreover, the corresponding resistance mutation on VEEV nsP1 (D34S) abrogated the inhibitory effect of MADTP compounds on nsP1 capping functions. **Conclusions:** A novel class of CHIKV inhibitors targeting the viral capping machinery was discovered. This research was funded by the European Union FP7 Program under SILVER grant agreement n° 260644. Leen Delang is funded by the Research Foundation Flanders (FWO).

Board 134. Battling Antimicrobial Resistance: Antimicrobial Resistance Surveillance in the DoD Global Emerging Infections Surveillance and Response System (GEIS) Partner Network

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Background: Since its inception, the Armed Forces Health Surveillance Center Global Emerging Infections Surveillance and Response System (AFHSC-GEIS) has performed global surveillance for infectious diseases that pose a threat to the Department of Defense (DoD) forces throughout the world. GEIS provides direction, funding, and oversight to a network of partners worldwide. These surveillance efforts focus on antimicrobial resistant (AMR), enteric, febrile and vector-borne, respiratory, and sexually-transmitted infections. **Methods:** The goal of the GEIS AMR program is to facilitate global surveillance for antibiotic resistant (AR) pathogens to provide force health protection information, data for public health authorities to identify and respond to resistance threats, clinicians interested in therapy recommendations, and researchers involved in product development. The objectives of the program are to conduct surveillance and evaluate the burden of highly resistant AR pathogens in DoD members and their beneficiaries, and in food-producing animal populations of interest, and to enhance an integrated healthcare-associated infection surveillance network to monitor, characterize, and track the spread of resistant strains as they contribute to emergence of further resistance. **Results:** The mission of GEIS is accomplished through its network of globally situated laboratories that conduct surveillance among DoD members and beneficiaries, foreign military and civilian populations. The AMR program extends to eight countries, and nine laboratories worldwide. Recent accomplishments include discovery of a correlation between inpatient consumption of fluoroquinolones and carbapenem resistance in *E. coli*; discovery of a virulent and highly AR clone of *Acinetobacter baumannii* associated with fatal infections; confirmation of a MRSA outbreak attributable to local spa practices in an overseas setting; estimation of nasal colonization rates with *S. aureus* and MRSA in the Peruvian Air Force; and discovery of plasmid transfer between strains and novel MLST profiles in *E. coli*. **Conclusions:** Through its extensive partner network, GEIS is uniquely poised to conduct surveillance of AMR pathogens, contributing to enhanced Force Health Protection and improved global health security.

Board 135. Comparative Study of the Antiviral Activity of Broad-spectrum and Enterovirus-specific Inhibitors Against Clinical Isolates of Enterovirus-D68

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Background: Enterovirus-D68 was isolated for the first time in California in 1962 in children with pneumonia and bronchiolitis. Until 2008, the detection of EV-D68 infections has been very rare. Since 2008 EV-D68 got increased attention with different clusters of infections worldwide. In a recent epidemic in the United States, 1.153 people were confirmed with respiratory illness caused by EV-D68, mostly children with asthma or a history of wheezing. The virus also has been associated occasionally with polio-like illness (muscle weakness or paralysis). Moreover, EV-D68 was detected in specimens from 14 patients who died. EV-D68 thus emerged as a considerable global health threat, requiring the development of effective antiviral treatment. **Methods:** To assess the activity of antiviral molecules against EV-D68 a panel of 7 clinical isolates was selected consisting of representative strains of the three major genogroups. The following inhibitors were included in this study: (i) two capsid-binding compounds, pleconaril and pirodavir; (ii) the protease inhibitor rupintrivir; (iii) the host cell-targeting compound enviroxime; and (iv) the broad-spectrum antivirals favipiravir (T-705) and arbidol. **Results:** Our preliminary results with the 7 clinical isolates reveal that pleconaril and rupintrivir efficiently inhibited *in vitro* EV-D68 replication. Favipiravir (recently approved in Japan to treat influenza virus infections) and enviroxime also resulted in a clear antiviral effect. On the other hand, pirodavir and arbidol resulted only in a modest inhibitory effect on EV-D68 replication. We will present data on the *in vitro* anti-EV-D68 activity of this compound-panel against the wider panel of recent EV-D68 isolates. **Conclusion:** The enterovirus-specific inhibitors pleconaril, rupintrivir and enviroxime are able to efficiently inhibit the *in vitro* replication of EV-D68 clinical isolates of the three major genogroups. Also treatment with favipiravir inhibits EV-D68 replication in cells. LS is funded by the Chinese Scholarship Council. LD is funded by the Research Foundation of Flanders (FWO).

Board 136. When "Germs Don't Get Killed and They Attack Again and Again": Knowledge and Attitudes About Antibiotic Resistance Among Laypersons and Health Care Providers in Karachi, Pakistan

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Background: In South Asia, where diarrhea is common and antibiotics are widely accessible without a prescription, multidrug-resistant enteropathogens are an emerging problem. However, beliefs and behaviors related to antimicrobial resistance (AR) are poorly understood. Such information can inform community-based strategies to address this serious public health problem. **Methods:** We sought to understand laypersons' and healthcare providers' (HCP) awareness and attitudes about AR in the context of treatment for adult diarrheal disease in Karachi, Pakistan. In-depth, semi-structured open-ended interviews were conducted with 40 laypersons and 45 HCPs (15 general practitioners, 15 pharmacists, and 15 unlicensed providers) in a lower-middle class urban neighborhood. Audiotaped interviews in Urdu were transcribed, translated into English, and coded by a team of qualitative researchers using applied thematic analysis techniques. **Results:** Laypersons were familiar with the term "antibiotic" but frequently confused antimicrobials with antidiarrheal medications. Slightly over half of laypersons and three quarters of HCPs were aware that antimicrobials could lose effectiveness, but misperceptions were common. Both laypersons and HCPs often believed that "the body becomes immune" or "bacteria attack more strongly" if medications are taken "improperly." Another prevalent theme was that causes and effects of AR are limited to the individual taking the antimicrobials and to the specific diarrheal episode. When

asked about the causes of AR, participants often cited patient behavior in terms of taking antimicrobials improperly; HCP behavior was rarely discussed. Less than half of the HCPs were aware of treatment guidelines. In terms of prevention, laypersons and HCPs described the importance of following prescriptions and only using antimicrobials when necessary. **Conclusions:** Outreach campaigns on appropriate antimicrobial use and HCP prescribing practice may be community-supported strategies for combating AR in urban Pakistan. Targets of such campaigns can include consumers as well as HCPs, including pharmacists. To enhance motivation for behavior change, intervention messages can emphasize that AR causes and impacts are both collective and individual.

Board 137. Shared Antibiotic Stewardship and "One Health" Surveillance for Antibiotic Resistance: The Washington State Experience

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Background: Increasing emergence of antibiotic resistance has been linked to use of antibiotics in human health care as well as animal agriculture and veterinary medicine. At the same time, there have been few attempts to harmonize efforts across human and animal health to promote stewardship of antibiotics and prevent and reduce resistance. Furthermore, the role of the environment in antibiotic resistance is often overlooked. The President's Report on Combatting Antibiotic Resistance has called for a "One Health" approach to address antibiotic resistance in a coordinated way between human and animal health. **Methods:** We report on an effort in Washington State to form a multidisciplinary working group to develop a model of "shared antibiotic stewardship" across human, animal, and environmental health. We also report on the conceptual model of data sharing for surveillance of antibiotic resistance simultaneously in human, animal, and environmental sectors. **Results:** The experience to date of work group activities will be presented, including the framework for harmonizing stewardship activities and a model for integrating antibiotic resistance data. **Conclusion:** While integrating activities for antibiotic stewardship and surveillance across human, animal, and environmental sectors poses logistical and organizational challenges, it provides a unique opportunity to coordinate efforts and detect emergence of resistance.

Board 138. Improved Malaria SYBR Green I-based Fluorescence Assay Detection Limit in Field Samples with Varied Parasitemia and Hematocrit

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Background: The Malaria SYBR Green I-based Fluorescence (MSF) assay is used for profiling in vitro drug susceptibility of *Plasmodium falciparum* (Pf) in many research laboratories. While the MSF assay is a fast and inexpensive drug screening tool for Pf laboratory and field samples, the sensitivity of the assay in accurately determining 50% inhibition concentration (IC_{50}) values is debated. This study examined a modified version of the MSF assay for its sensitivity and ability to accurately determine IC_{50} values in samples with ranging parasitemia. **Methods:** Pf laboratory strains (D6) and field isolates were subjected to a dose-range of antimalarials, including chloroquine, mefloquine, artemisinin, and atovaquone, over a range of initial parasitemia. Parasitemias were adjusted to the following percentages for drug testing by MSF: 0.6, 0.3, 0.15, 0.075, 0.038, 0.018, 0.009, 0.0044 and 0.0023. At each dilution, ten replicates of the MSF were performed for both the D6 strains in order to assess the efficiency of the assay at different parasitemia. For the field isolate, four replicates were assayed. The assay success rate was determined by the proportion of successful replicate assays at each dilution which were used to compute the IC_{50} at each dilution. **Results:** At higher parasitemia levels, most of the replicates were successful and were used in computing the IC_{50}s. For the D6, parasitemia dilutions through 0.038% produced 10/10 successful replicates. As the level of parasitemia reduced, the number of successful replicates reduced with only 4 successful replicates at 0.0023% parasitemia. For the field isolate, the IC_{50}s also decreased as the parasitemia level was reduced from 1% to 0.3%. Interestingly however, with the field isolates, the IC_{50}s remained constant from 0.3% to 0.075% and then changed. The final two dilutions did not produce any IC_{50}s. **Conclusions:** The IC_{50}s obtained at these ranges of parasitemia were comparable to 0.0375% for D6 and 0.075% for the field samples. Our findings show that the MSF assay allows for drug testing of malaria samples within a wide range of initial parasitemia. The limit of detection of the new MSF assay closely approximates that of the well-characterized malaria HRP-2 ELISA.

Board 139. Temporal Trends in Prevalence of *Plasmodium falciparum* Molecular Markers Selected for by Artemether-lumefantrine Treatment in Pre-ACT and Post-ACT Parasites in Western Kenya

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Background: Artemether-lumefantrine (AL) has been the first line treatment for uncomplicated malaria in Kenya since 2006. Studies have shown AL selects for Single Nucleotide Polymorphisms (SNPs) in *pfcrt* and *pfmdr1* genes in recurring parasites compared to the baseline infections. The genotypes associated with AL selection are K76 in *pfcrt* and N86, 184F and D1246 in *pfmdr1*. To assess the temporal change of these genotypes in western Kenya, parasites collected before (pre-ACT) and after (post-ACT) introduction of AL were analyzed. In addition, the associations of parasite haplotype against the IC_{50} of artemether and lumefantrine and clearance rates were determined. **Methods:** Genomic DNA of parasites collected between 1995 and 2014 was analyzed by Sanger sequencing or PCR-based single-base extension on Sequenom MassARRAY. IC_{50}s were determined for a subset of the samples. Some of the samples from 2013-2014 were from an efficacy trial with clearance half-lives. **Results:** Data revealed there was significant difference between pre-ACT (1995-2003) and post-ACT (2008-2014) genotypes at the four codons (chi-square analysis; $p < 0.0001$). The prevalence of *pfcrt* K76 and N86 increased from 6.4% in 1995-1996 to 93.2% in 2014 and 0% in 2002-2003 to 92.4% in 2014 respectively. Analysis of parasites carrying pure alleles of K+NFD or T+YYY haplotypes revealed that 100% of the pre-ACT parasites carried the T+YYY and 99.3% of post-ACT parasites carried K+NFD. There was significant correlation ($p = 0.036$) between lumefantrine IC_{50} and polymorphism at *pfmdr1* codon 184. There was no difference in parasite clearance half-lives based on genetic haplotype profiles. **Conclusions:** This study shows there is significant change in parasite genotype, with key molecular determinants of AL selection almost reaching saturation. The implications of these findings are not clear since AL is still highly efficacious. However, there is need to closely monitor parasite genotypic, phenotypic and clinical dynamics in response to continued use of AL in western Kenya.

Board 140. Antimicrobial Resistance of Treated Wool Samples with Madder

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Background: Recently, the potentiality of using natural dyes in textile colouration as anti-UV and anti-microbial has been reported. Reviews on the use of natural dyes in food and in textile colouration have been published. In the past decade, investigations about possible uses of natural dyes in textile dyeing processes have been performed by various research groups, on account of their high compatibility with environment, relatively low toxicity, allergic reactions and various natural coloring sources. Before the turn of the century natural dyes were the only source of color available and, therefore, they were widely used and traded, providing a major source of wealth creation around the globe. Madder is widely distributed in southern and southeastern Europe, in the Mediterranean area, and in Asia. It is a main source of a natural dye producing a variety of anthraquinone pigments in its roots and rhizomes. Madder is an old and famous dye for dyeing wool, silk and cotton fibers. In Asian workshops, the dyers have used Somagh and Madder for dyeing of wool. This research work aims to study the antimicrobial resistance of wool samples which treated with Somagh and dyed with Madder. **Methods:** *Mordanting* Somagh was selected as a natural mordant for this study. The mordanting bath keeping 45 min at 90°C . *Dye extraction* Dye extraction was carried out in 100 ml distillated water at pH=7 and 90°C using 1 g dye powder in 100 mL water for 120 min. *Dyeing* Dyeing of wool samples were carried out for 90 min at 90 °C in a dye bath containing 25 ^{cc} dye extracted solution. The dyed samples were rinsed with cold water and finally dried at ambient temperature. *Evaluation of antimicrobial resistance* The wool samples were subjected to soil burial test as per AATCC Test Method 30-2004. **Results:** The results show that treatment of wool samples with Somagh and Madder leads to enhance the resistance of wool towards microbial attack when measured in terms of loss in breaking load of untreated control samples were reduced due to bacterial damage during soil burial test whereas Madder treated sample could not only protect the sample against bacterial attack but also improved its strength. **Conclusions:** In this research, the antimicrobial resistance of treated wool with Somagh and Madder was evaluated. The results indicated that using madder as a natural dye and Somagh as a natural mordant leads to create a good potential in wool.

Blood, Organ, and Other Tissue Safety

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Grand Hall

Board 141. *Babesia* Sero-epidemiology in Australian Blood Donors

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Background: The first case of locally acquired human babesiosis in Australia, a fatality associated with *Babesia microti* infection, was reported in 2012. This has possible implications for the safety of Australia's blood supply, as transfusion transmitted babesiosis has been documented in other countries, such as the USA. *B. microti* is the most common species associated with human disease in the USA, and this is the species implicated in the Australian case. This study aimed to investigate the seroprevalence of antibodies to *B. microti* in a cohort of Australian blood donors considered at local risk to exposure to this pathogen. **Methods:** Plasma samples (n=7,000; 48% female) were collected from donors at risk of *B.microti*. This risk was defined as those donors who resided in eastern Australia in areas within the distribution of the most common and medically relevant ticks. Demographic information for each donor was obtained, which included age, sex, state of residence, postcode, and previous overseas travel. All samples were tested for *B. microti* IgG by Immunofluorescence Assay (IFA). Samples with a titre of ≥64 were reported as positive and were tested for *B. microti* IgG and IgM by Immunoblot. **Results:** Five donors (0.07% 95% CI: 0.01-0.13%) were positive for *B. microti* IgG by IFA. All were negative for *B. microti* IgG by immunoblot, with one positive for *B. microti* IgM. Four of the five *B. microti* IgG IFA positive donors were female, and their average age was 56 years (range 44-66 years). All of these donors had reported travel outside of Australia. **Conclusions:** This study demonstrates seroprevalence of antibodies to *B. microti* in 0.07% of Australian blood donors considered possibly at local risk of exposure to *B. microti*. However, all donors with *B. microti* antibody had reported travel outside Australia. As exposure status before and after departure is unknown, the exact place of exposure cannot be determined. Investigation of potential assay cross reactivity in our population is currently underway. Given that the majority of samples did not display serological evidence of previous exposure to *B. microti*, despite their being collected from donors considered at local risk for exposure, these data indicate that past exposure to *B. microti* is uncommon in the Australian blood donor population.

Board 142. Emergence of Australian WNV_{KUN} Strains: What Does This Mean for Blood Safety?

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Background: West Nile Virus (WNV) poses a threat to transfusion safety given its capacity to cause neuroinvasive disease and that transfusion transmission has been recorded. A virulent strain of WNV, termed $WNV_{NSW2011}$, was identified in horses in eastern Australia in 2011. Although similar to WNV Kunjin strain (WNV_{KUN}), which is enzootic in northern Australia and rarely causes disease in humans, this strain possessed two known markers of WNV virulence that are not seen in $WNV_{KUN.}$ Surprisingly, there was no increase in the number of human WNV_{KUN} notifications in this region at this time, and, based on a small cohort of samples; seroprevalence to WNV_{KUN} did not increase after the outbreak period, suggesting that humans are still vulnerable to WNV infection. Therefore, this poses questions in relation to transfusion safety with respect to these different strains of WNV_{KUN} circulating in Australia. This study aimed to investigate whether a commercially available WNV blood screening assay can detect RNA of different strains of WNV_{KUN}, including the more virulent $WNV_{NSW2011}$. **Methods:** Human plasma that tested negative for WNV neutralizing antibodies was spiked with four different strains of WNV_{KUN}, as well a prototype WNV strain, at high, medium and low viral loads. Spiked samples were tested with the Procleix® WNV Assay on the Panther system - a Transcription Mediated

Amplification (TMA) blood screening assay, and reactivity determined based on the manufacturer's instructions. **Results:** All spiked samples were positive for WNV by TMA. **Conclusions:** This study demonstrates experimentally that RNA from different strains of WNV_{KUN}, including one with enhanced virulence, can be detected by a commercially available WNV blood screening assay using TMA. As WNV is transfusion-transmissible, it is essential to confirm that blood screening tests can detect emergent strains to ensure ongoing transfusion safety.

Board 143. Blood Transfusion Safety Among Blood Donors and Recipients in Minna—North-Central Nigeria, 2014

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Background: Transfusion usually is a life-saving therapeutic intervention, however many preventable errors may make it hazardous for donors or recipients. Ensuring supply of safe blood is a key intervention in reducing mortality and morbidity attributable to blood transfusion. We conducted a descriptive, coss-sectional study among blood donors to assess blood donor safety in Minna, north-Central Nigeria. **Methods:** We recruited consecutively, all consenting, HIV, hepatitis B and C and anaemia screened blood donors between September, 2013 and January, 2014. We screened all subjects for cytomegalovirus (CMV) antibodies (IgM and IgG) and haematological indices using ELISA kit (DIALAB® Austria) and a haematological analyzer (*Abacus analyzer* 2.75, Diatron® U.S.A) respectively. We administered structured questionnaires to obtain socio-demographic and socio-economic characteristics and practices. Data was subjected to descriptive and analytical statistical analyses using Epi Info version 3.5.4. Significant associations were presumed if $p<0.05$. **Results:** A total of 345 subjects were recruited, 336 (97.4%) males. Mean age ± SD was 32.4± 8.5 years. Monthly earnings ranged from $109 to $212 136(40.6%). The prevalence of anti-CMV IgG and IgM antibodies were 96.2% and 2.6% respectively. Majority of the blood donors 195 (56.5%) were anaemic (PCV<36, Hb<12g/dl), 158 (81.0%) of which were for purpose of family replacement. Strata of the blood donors were family replacement 274 (79.4), voluntary 60 (17.4), commercial interest 11 (3.2%). Those with positive CMV were more likely to be of high income level (P=0.04). **Conclusions:** The seroprevalence of CMV is high with a significant proportion capable of transmitting to potentially immunosurpressed blood recipients. Majority of the blood donors were anaemic. Prospective blood donors for immunocompromised patients should be screened for CMV. The quality of routine donor screening for anaemia should be improved. **Keywords:** Cytomegalovirus, Transfusion, Blood donors, Safety, Nigeria

Risk Assessment

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Board 144. Ultrasonography-assisted Liposuction for an HIV Patient with Severe Respiratory Failure and Associated Cervical Lipohypertrophy

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Background: Lipohtpertrophy is a known complication of long-term HIV infection and aggressive antiviral therapy. Although lipohypertrophy was the first morphological change ascribed to combination HIV therapy, it has been considerably less understood regarding the etiology, complications, and clinical management. Here we report an HIV-infected patient with sever lipohypertrophy combined with respiratory failure was treated by ultrasonography-Assisted Liposuction. **Case report:** A 57-year-old woman comes to the ER with complaints of worsening shortness of breath for past 3 weeks. Immediate arterial blood gas revealed pH 7.26 PO2 79.5 PCO2 55 HCO3 30.5 with Sa02 87% on 6L O2. There was a prominent massive fat pad around her neck. CTA performed did not show pulmonary embolism. Her past medical history is significant for HIV infection of 15 years. She has been taking HAART medications ritonavir, darunavir and emtricitabine/tenofovir. The patient was subsequently intubated. Over the subsequent days, her dyspnea was due to liperhypertrophy around her neck. Plastic surgeons evaluated the patient and performed an UAL of her neck and back, removing 14 liters of fat. Patient tolerated the operation and weaned from ventilator over a couple of days. **Discussion:** HIV associated lipohypertrophy is a syndrome of peripheral lipodystrophy, hyperlipidemia and insulin resistance associated with antiretroviral (ART) use in HIV-infection patients. Several theories regarding the pathogenesis underlying regional fat accumulation have been proposed including abnormalities in levels of adiponectin, growth hormone, and proinflammatory cytokines have been associated with lipohypertrophy, but whether they are a cause or consequence of fat accumulation remains unclear. The patients with lipohypertrophy may present central fat accumulation. UAL is a relatively new procedure that offers several safety advantages over traditional liposuction and allows body contouring of fibrous areas and other body areas that are not amenable to traditional liposuction. However, more than 10 liters of fat was removed under UAL for HIV-related lipohypertrophy has been less reported. **Conclusion:** Our case suggests that UAL represents a well-tolerated and effective treatment modality for HIV-related severe lipohypertrophy.

Board 145. The Assessment for Severe Fever with Thrombocytopenia Syndrome Surveillance in Hubei Province, China

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Background: Severe fever with thrombocytopenia syndrome (SFTS) is an emerging disease that is caused by a novel bunya virus, as referred to as SFTS virus (SFTSV). Because fever with thrombocytopenia is common in most countries, one would expect a higher rate of suspected cases requiring investigation. To estimate the number of hospitalized patients with fever and thrombocytopenia in at-risk areas and compared it with that of surveillance reports in the same periods. **Methods:** We used step by step probability to estimate the probability of surveillance to detect SFTS cases upon hospital admission in Hubei province, China. This model is based on three input parameters which were determined from hospital-based survey and National Disease Report Information Management System (NIDRIS) data: (1) proportion of hospitals that can test for platelets and leukocytes count; (2) proportion of testing for SFTSV among suspected SFTS cases; (3) probability of suspected and confirmed cases that were reported to NIDRIS. **Results:** A hospital survey conducted between Jan 2011 and May 2012 showed that (1) 98% (39/40) of surveyed had laboratory capacity for platelets and leukocytes counts. About 5,800 patients were admitted with acute fever, of which 7% (n=410) had thrombocytopenia and leukopenia. (2) Only 6.3% (12/190) of tested cases were SFTS diagnosed cases which were actually entered into the

NIDRIS database. All the diagnosed cases were from at-risk areas. (3) All the diagnosed SFTS cases were confirmed cases which were tested SFTSV. Taken together the model yielded an estimated probability of 6.1% SFTS reporting when an SFTS case attends a hospital in Hubei province. There were a significant surveillance sensitivity difference between at-risk and no-case areas (6.9% vs. 0%, p<0.01, respectively). **Conclusions:** It is likely that awareness about SFTS is lower among clinicians of these plain areas as training on SFTS surveillance focused on clinicians working in mountainous areas, a so-called at-risk area. Strengthening of surveillance via clinicians training among other things should be encouraged beyond the mountainous areas. This is particularly relevant when it comes to further our knowledge on an emerging and fatal disease.

Board 146. Pertussis Infection in US Pregnant Women, 2012-2014

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Background: Little is known about the characteristics and effects of pertussis in women during pregnancy. We used CDC's Emerging Infections Program Network's (EIP) Enhanced Pertussis Surveillance (EPS) to compare pertussis infection in pregnant and non-pregnant women. **Methods:** CSTE confirmed or probable pertussis cases in women of childbearing age (15-44 yrs) were identified through surveillance in 7 EPS sites from 1/1/2012 - 8/20/2014. Pregnancy status and trimester were collected from patient or provider interview. The population of pregnant women was estimated using previously published methods. Population and fertility rate data were obtained from the National Center for Health Statistics. Incidence rates were calculated by dividing the number of pregnant cases by the estimated population of pregnant women within the EPS catchment by year. χ^2 was used to compare proportions. **Results:** A total of 1,555 pertussis cases occurred among women aged 15-44 yrs; 54 (3.5%) were pregnant at cough onset. Overall incidence in women of childbearing age during 2012 and 2013 was 28.1/100,000 and 12.2/100,000, respectively. Estimated incidence among pregnant women was 19.4/100,000 in 2012 and 12.1/100,000 in 2013. Median age was 26 yrs (range: 16-43) for pregnant case-patients (CP) and 20 yrs (range: 15-44) for non-pregnant CP. The majority of pregnant and non-pregnant CP was white (75% vs. 88%) and non-Hispanic (69% vs. 79%). Of pregnant CP with complete information (n = 40), 90% reported cough onset during the second (37%) or third (53%) trimester. Pregnant CP were more likely than non-pregnant CP to report whoop, post-tussive vomiting and apnea (p<0.05 for all). Although not significantly different, reported receipt of Tdap ≥ 2 weeks prior to cough onset was more common among non-pregnant CP (52%) than pregnant CP (41%) (p=0.1). **Conclusions:** To our knowledge, this is the first descriptive analysis of pertussis among pregnant women in the U.S. Although rates varied by year, our findings show that pregnant women experience similar rates of disease compared with non-pregnant women. Pregnant women more frequently reported classic pertussis symptoms, possibly due to physiologic changes during pregnancy. Continued surveillance will better define the impact of pertussis on pregnant women and their newborns.

Board 147. Clinical Case Definitions for Influenza-associated Outpatient Consultations in Rural North India

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Background: Data on performance of various case definitions for influenza in lower-resourced outpatient settings is lacking. We assessed case definitions among outpatients during Jan-Dec 2011 in 28 villages in north India. **Methods:** Patients presenting with any acute medical illness (onset within previous 3 days) were enrolled. Data on demographics, clinical history and symptoms were gathered and combined nasal/ throat swabs collected and tested for influenza viruses using real-time reverse transcription polymerase chain reaction. Sensitivity, specificity, and area under the curve (AUC) were calculated for the following case definitions: World Health Organization's recommended Influenza Like Illness (WHO ILI, measured temperature > 38°C with cough); modified WHO ILI (reported fever with cough); classical ILI (measured temperature > 38°C plus cough or sore throat); acute respiratory illness (ARI, ≥ 1 of cough, cold, sore throat, difficulty breathing). **Results:** We enrolled 2465 patients, 328 (13%) were aged < 5years, 1400 (57%) were female, and 152 (6%) had influenza (87 A/H3N2, 64 B). Participants with influenza were more likely than those without to have self-reported fever (92% vs 67%, p<0.01), measured temperature >38 degrees C (30% vs 14%, p=0.01), cough (90% vs 82%, p=0.01), nasal stuffiness/discharge (65% vs 51%, p< 0.01), headache (59% vs 43%, p < 0.01) or seizures (3% vs 0.3%, p< 0.01). Participants with influenza were less likely to report difficulty breathing (11% vs 23%, p< 0.01) or abdominal pain (11% vs 20%, p< 0.01). Of 278 patients without any respiratory symptom, 10 (4%) had influenza. ARI had the highest sensitivity (95%) but lowest specificity (9%), whereas WHO ILI had lowest sensitivity (26%) but highest specificity (89%). The modified WHO ILI (reported fever) was 83% sensitive and 45% specific. Modified WHO ILI had the highest Area-Under-the-Curve (AUC) of 64% compared to WHO ILI (58%) and classical ILI (58%). **Conclusions:** Use of reported fever rather than measured temperature, increased the sensitivity of the WHO-ILI case definition in outpatient surveillance more than three-fold. Surveillance objectives should guide choice of case definition. This study was supported in part by cooperative agreements U01 IP000206 from the Centers for Disease Control and Prevention, Atlanta, USA.

Board 148. *Mycobacterium bovis* Bacillus Calmette-Guérin (BCG) Osteomyelitis of the Fibular After Intravesical BCG Therapy for Bladder Cancer

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Background: Mycobacterium Bovis BCG is a live-attenuated strain that is commonly used for immunization against Tuberculosis and in the treatment of in situ/ micro invasive transitional cell bladder cancer. We report a case of BCG related osteomyelitis of the fibular, after 10 years of initial treatment with intravesical BCG therapy for bladder cancer. **Case report:** An 83-year-old Caucasian man visited an outpatient clinic with a complaint of right ankle pain and swelling for the past 4 months. The patient had a history of bladder cancer with transurethral resection followed by BCG immunotherapy. His past medical history consists of stable coronary artery disease, diabetes mellitus with no trauma to the lower extremity and no history of pulmonary or extra

pulmonary tuberculosis. Physical exam showed pitting edema, redness, and tenderness on palpation in the right ankle. X-ray of the tibia showed cystic lesions and bone scan revealed a lucent area in the metaphysis with mild periostitis. Bone biopsy confirms chronic osteomyelitis with foci of necrosis and granulomas. Grocott's Methenamine Silver stain revealed no fungal element and AFB stain showed a few acid-fast bacilli. The confirmatory test was PCR despite negative blood cultures. The patient was treated with isoniazid, ethambutol and rifampin for 9 months and showed improvement. **Discussion:** BCG was given through a trans-urethral catheter into the urinary bladder. The Bacteria disrupts uroepithelial cells, spreads via lymphatic's/ blood and triggers an immune response which include induction of CD4 T cells/ Macrophages and increasing in interleukins & IFN Gamma in bladder. Hypersensitivity hypothesis is supported by TH1 mediated granuloma formation, absence of AFB despite high clinical suspicion, and positive response to steroids. Current literature review showed that the complication of BCG Immunotherpy is sepsis, hepatitis, pneumonitis, arthritis, and vertebral osteomyleitis, but osteomyelitis of the long bone has rarely been reported. **Conclusion:** We report a case of fibular osteomyelitis 10 years after intravesical BCG immunotherapy for bladder cancer.

Board 149. Relevance of Morbidity Markers in Community Diagnosis of Urinary Schistosomiasis in a Resource Constrained Environment, Nigeria, 2012

O. P. Ossai, Sr.[1], R. Dankoli, Sr.[1], N. E. Ossai, Sr.[2], G. O. Eze, Sr.[3], C. C, Nwodo, Sr.[4], O. C. Ekwueme[5], D. Nwagbo[5], G. Abonyi[6], D. Ogbuabor[6]; [1]Nigerian FELTP(2009), Abuja, Nigeria, [2]Enugu State Univ. of Sci. and Technology, Enugu, Nigeria, [3]Enugu State Univ. Teaching Hosp., Enugu, Nigeria, [4]Nigerian FELTP, Abuja, Nigeria, [5]Univ. of Nigeria Teaching Hosp., Enugu, Nigeria, [6]Univ. of Nigeria, Enugu, Nigeria

Background: Urinary schistosomiasis infection is one of the major public health problems facing developing countries with school age children at greatest risk. It is common in rural areas particularly where people depend on streams and rivers for their water. In such setting, the issue of diagnosis is a challenge due to poverty and inadequate or poorly equipped health facilities for microscopy (the gold standard). We assessed the continued relevance of morbidity markers in community diagnosis of urinary schistosomiasis. **Methods:** We carried out a cross-sectional survey of primary school children aged 5-15years, using WHO guidelines. Urine samples were collected between 10.00am and 2.00pm and examined for visible haematuria and turbidity. Each sample was subjected to a commercial reagent strip-Multistix 8 SG reagent strip (Siemens Lot 04200746) to check for the specific gravity (SG), haematuria, leucocyturia, and proteinuria. For urine SG, values greater than 1.020 were considered significant. Leucocyturia was considered significant when greater than 5 leucocyturic eosinophils/hpf. Thereafter, samples were filtered, stained and subjected to microscopy. The number of S. haematobium eggs were counted and expressed as ova/10 ml of urine. Intensity was reported as the number of ova per 10mls of urine and categorized as light when less than 50ova/10mls and heavy when greater than 50ova/10mls of urine. **Results:** Of 842 pupils sampled, 50.6% were females. Prevalence of urinary schistosomiasis 34.1% (287/842). Infection rate was higher(52.8%) among 13-15 years(Prevalence Ratio=2.45, 95% Confidence Interval 1.63-3.69).Heavy infections 62.7% and egg count/10mls urine ranged from 21-1138.Sensitivity, specificity, positive predictive value(PPV) and negative predictive value(NPV) was 83%, 94%, 88% 91%, respectively for haematuria and 73%, 83%, 69%, 86% respectively for proteinuria. For turbidity, sensitivity, specificity, PPV and NPV were 44%, 89%, 68%, and 76% respectively while they were 47%, 92%, 74% and 77% for SP. Leucocyturia had a sensitivity of 98%, specificity of 79%, PPV 71% and NPV of 99%. **Conclusion/Recommendation:** Considering the significant levels of specificity, PPV and NPV the use of morbidity markers which is simple, practical and inexpensive is still relevant in community diagnosis

Board 150. Prevalence of Influenza Viruses in Asymptomatic Persons

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Background: Molecular-based assays of upper respiratory tract specimens are a mainstay of influenza infection diagnosis--yet sparse data on the frequency of influenza virus detection exist in well persons. **Methods:** We searched PubMed for articles published from January 1995 through June 2013 containing data on asymptomatic persons tested for influenza. Articles were eligible if they were 1) in English, 2) published in or after 1995, 3) reported the number of asymptomatic persons tested for influenza viruses and the number or percent who tested positive, and, 4) reported use of RT-PCR for laboratory testing of specimens. The Wilcoxon rank sum test was used to compare medians. Household transmission studies were excluded. **Results:** Overall, a median of 0.7% of asymptomatic persons tested positive for influenza (45 studies, IQR=0.0% to 2.1%). 26 studies of children <18 years had higher positivity than 11 studies of adults (median 0.7% versus 0.4%) although the difference was not statistically significant (p-value=0.25). Some variability in percent positive was observed among WHO Regions. The 5 articles from the African Region reported a statistically higher percent positivity (median=3.7%; IQR=2.2% to 4.3%) than all the 40 studies from other Regions (median=0.3%; IQR=0.0%-1.5%) (p-value<0.01). Compared to studies in industrialized countries (34 studies, median=0.2%; IQR=0.0% to 1.8%), studies in developing countries had a higher median proportion of asymptomatic controls testing positive for influenza (11 studies, median=1.4%; IQR=0.4%-2.9%) (p-value=0.22). The median proportion of asymptomatic controls testing positive for influenza was highest among outpatients (median=0.9%; IQR=0.0% to 3.4%) compared to persons in the community (median=0.7%; IQR=0.0% to 1.7%) and inpatient hospital wards (median=0.0%; IQR=0.0% to 0.0%). **Conclusions:** Nasopharyngeal detection of influenza viruses in asymptomatic persons is uncommon (median=0.7%) and does not vary significantly across age groups. Detection was highest among those living in sub-Saharan Africa, but these differences may be due to study-specific factors rather than population differences.

Board 151. Case Definitions Used in Severe Respiratory Disease Surveillance. What Do They Mean? An Evaluation of Data from Western Kenya

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Background: The Integrated Management of Childhood Illness (IMCI) pneumonia case definitions were developed for clinical management, but are often used for respiratory disease surveillance. The case definitions incorporate clinician-observed and parent-reported signs and symptoms. However, due to subjectivity in interpretation of signs and symptoms there may be variability to which some signs and symptoms actually measure severity. We describe how reported or observed signs and symptoms used in IMCI may influence estimates of severe pneumonia in children, and proportion caused by influenza or RSV. **Methods:** Between January 2008

and December 2012, we conducted respiratory disease surveillance at Lwak Mission Hospital. We identified children under 5 years old with IMCI pneumonia (cough or difficulty breathing with tachypnea), severe pneumonia (cough or difficulty in breathing plus clinician-observed chest in-drawing) and very severe pneumonia (cough or difficulty in breathing and at least one danger sign: vomiting everything, lethargy, unconsciousness or convulsions). Nasopharyngeal and oropharyngeal swabs were collected and tested for influenza (entire study period) and RSV (through February 2011) by RT-PCR. We examined the frequency and care seeking for severe and very severe pneumonia, as well as the proportion of each testing positive for influenza or RSV. **Results:** Among 4314 patients with pneumonia, 98 (2%) were classified as severe pneumonia and 345 (8%) as very severe pneumonia. Among the 345 with very severe pneumonia, the most commonly reported danger signs were lethargy (n=180, 52%) and convulsions (n=173, 50%). Of the 98 patients with severe pneumonia, 78 (80%) were hospitalized while 236 (68%) of those with very severe pneumonia were admitted. Of the patients with influenza and RSV results, influenza was detected in 5% (4/80) of severe pneumonia and 7% (8/108) of very severe pneumonia cases; RSV was detected in 29% (20/68) and 18% (15/85), respectively. **Conclusions:** We observed a burden of very severe pneumonia that was over three times that of severe pneumonia. Fewer patients with very severe pneumonia were hospitalized. Relying on subjective signs and symptoms may overestimate the burden of very severe pneumonia and hence influence interpretation.

Board 152. Increase in Vibriosis in New York State: How Can We Improve Surveillance and Outbreak Identification?

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Background: Vibriosis accounts for an estimated 80,000 illnesses, 500 hospitalizations and 100 deaths each year in the United States. FoodNet estimated the incidence of *Vibrio* infection was 75% higher in 2013 compared with 2006-2008. All *Vibrio* cases are reported to CDC as part of the Cholera and Other Vibrio Illness Surveillance (COVIS) system. Information reported to COVIS for V*ibrio* cases with shellfish consumption is shared with other State and Federal agencies to assist with source identification. Members of those agencies, and industry, participate in the Interstate Shellfish Sanitation Conference (ISSC) and the National Shellfish Sanitation Program (NSSP) through a federal/state cooperative program. **Methods:** In 2014, the New York State Department of Health began a review of the *Vibrio* surveillance process and how outbreaks were defined both within the State and nationally. Case and outbreak data was extracted from our Communicable Disease Electronic Surveillance System and Foodborne Disease Surveillance System, respectively. Analysis was conducted using Statistical Analysis Software (SAS), v 9.3 and Microsoft Excel. **Results:** The incidence of *Vibrio* infection in New York State (NYS), excluding New York City, was 159% higher in 2013 compared with 2006-2008. For 2013, 73% of the *Vibrio* cases reported seafood consumption. A review of key elements in the reporting process identified no guidance document available for completing the COVIS form and outbreak definitions used by the ISSC and NSSP are not consistent with the CDC definition of a foodborne outbreak. The lack of a guidance document and use of inconsistent outbreak definitions leads to misclassification of source information for contaminated shellfish, which could affect water closures and recalls, and leads to the misclassification and underreporting of outbreaks. **Conclusions:** Vibriosis has increased significantly nationally and within NYS. Several agencies are involved when a *Vibrio* case is identified with reported shellfish consumption. These agencies need to adhere to the same standards and principles to be effective and prevent future illness and outbreaks. Guidance regarding completion of the COVIS form and use of a standard outbreak definition could clarify and streamline the process.

Board 153. Aetiology of Acute Febrile Illness (AFI) Cases in a Primary Care Hospital in the Western Ghat Region of India

H. Maity[1], J. A. Majeed[1], C. Akhil[1], S. G. Prabhu[1], A. Aithal[1], G. R. D'Souza[1], G. Arunkumar[1], S. Hossain[2], G. Prabhakar[3], S. Girisha[3]; [1]Manipal Ctr. for Virus Res., Manipal Univ., Manipal, Udupi, Karnataka, India, [2]Global Disease Detection Program, CDC, New Delhi, India, [3]JC Hosp., Thirthahalli, Shimoga, India

Background: Acute Febrile Illness (AFI) is caused by a variety of infectious agents, including viruses, bacteria, and parasites. A retrospective analysis of hospital admission data from a primary care hospital in the western ghat region of India- a unique biodiversity showed that, AFI is a significant cause of hospital admissions. However, limited availability of diagnostic facilities and similarity in clinical presentation did not allow definitive diagnosis in most of the cases. Hence we have initiated a laboratory supported hospital based sentinel surveillance of AFI in a secondary care hospital in the region to decipher the aetiology and epidemiology. **Methods:** A long term hospital based AFI surveillance was initiated in June 2014 at the JC Hospital Thirthahally, Shimoga district, Karnataka, India a Primary care hospital in the western ghat region of India. AFI cases admitted to this hospital and belonging to 5-65 years of age were recruited. Epidemiological and clinical data was obtained using a standard questionnaire and clinical samples including blood and throat swabs were collected by a trained technician. Clinical samples were subjected to an array to diagnostic assays using Real Time PCR or ELISA as appropriate. Generally, every case was tested for Leptospirosis, Dengue, Scrub typhus, Malaria, Kyasanur Forest Disease (KFD) etc. Data collected upto 19 October 2014 were analysed for this report. **Results:** A total of 466 AFI cases were recruited during the study period from amongst the hospitalized cases of Fever. The median age was 31 years (IQR) and Male to Female ratio 1:1.1. Of the 446 cases a laboratory confirmed aetiology could be reached in 208 (44%) cases. The most common aetiology was Leptospirosis (19.5%) followed by Influenza A(H3N2) (9%), Influenza A (H1N1)Pdm09 (5.8%), Influenza B (5%), Dengue (3.6%), Scrub Typhus (1.3%), Malaria (1.1%), Brucella (0.7%) and KFD (0.7%). **Conclusion:** This report describes a model of hospital based AFI surveillance for primary care hospital and detected multiple etiologies of AFI in the region. Continuation of this surveillance will have a significant influence on evidence based patient care as well as public health action in the region. Also, the study results give us important disease epidemiology and transmission pattern and a rough estimate of local burden of disease.

Board 154. Study of Adverse Drug Reactions and Treatment Outcome in MDR-TB Patients Registered at DOTS-PLUS Site, in a Tertiary Care Teaching Hospital, Gujarat, India

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Background: Increasing incidence of multidrug resistant tuberculosis (MDR-TB), is a major concern for TB control programs worldwide. Treatment of MDR-TB is extremely expensive, toxic, arduous and often unsuccessful. The objective of the present study is to analyze

adverse drug reactions and treatment outcome in MDR-TB patients registered at DOTS-PLUS site, of a tertiary care teaching hospital in Gujarat, India. **Methods:** In the present retrospective observational study, culturally proven MDR-TB cases who had started with Category IV Anti-tubercular therapy at DOTS-Plus site of the hospital, from 1st April 2010 to 31st March 2012 were included in the study. **Results:** Total 323 patients were included in the study with mean age of 30.2 years. 7% of the enrolled patients were new cases while 93% had prior exposure to antitubercular treatment. Total 64 different ADRs were recorded which needed medical assistance. Out of which, 33% ADRs needed drug withdrawal and 35% needed dose reduction or modification while 32% ADRs needed symptomatic treatment. Out of 323 patients enrolled in the study only 31% were declared cured and 6.5% completed treatment while 21.3% patients defaulted and 8% had failure of treatment. 28% patients died during treatment period. **Conclusion:** The overall success rate of treatment of MDR-TB regimen still remains very poor. Well designed studies may be planned to evaluate influence of various microbiological as well as clinical factors in deciding outcome of the disease.

Board 155. Factors Associated with Tuberculosis Treatment Outcomes in Bangladesh—Results from 2012 National Surveillance Data

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Background: Tuberculosis (TB) treatment outcome is an important indicator of the effectiveness of a National TB Control Programme (NTP). Understanding reasons for poor treatment outcomes can help improve TB control efforts. We assessed factors associated with unfavorable treatment outcomes among persons with smear-positive pulmonary TB in Bangladesh. **Methods:** We conducted a cross-sectional study using TB treatment outcome data from January-December 2012 reported to the NTP. The NTP categorizes outcomes into six types: 1) cured (test results negative after full treatment course), 2) treatment completed (test results not available after treatment completion), 3) failed (test results positive at the end of treatment), 4) defaulted (treatment interrupted for ≥2 consecutive months), 5) died, and 6) lost to follow up. We considered cured and treatment completed outcomes as favorable and all other outcomes as unfavorable. We used univariate logistic regression to assess association of demographic and treatment delivery factors with unfavorable outcomes. We entered factors with p ≤0.10 into a multivariable logistic regression model and retained factors with p ≤0.05 and those identified as risk factors in prior studies. **Results:** Among 98,932 patients with outcome data, 65,458 (66%) were male and 7,956 (8%) patients had unfavorable outcomes. Of these, 3,737 (47%) died, 1,641 (21%) defaulted, and 1,599 (20%) were lost to follow up. In univariate analysis, unfavorable outcome was associated with being male (p<.001), treatment at a chest disease hospital (p<.001), treatment at a metropolitan health facility (p<.001), and urban residence (p<.001). In multivariable analysis, factors associated with an unfavorable outcome were male sex (adjusted odds ratio [aOR] 1.41; 95% confidence interval [CI] 1.34-1.49) and treatment at a chest disease hospital (aOR 1.44; 95% CI 1.25-1.66). **Conclusions:** The association between male sex and unfavorable outcomes has been found in other studies in Asia in which a possible link with smoking has been suggested. The association of treatment at a chest disease hospital with unfavorable outcomes may be because in Bangladesh, complicated cases (e.g., TB associated with other diseases) are typically treated in these settings. A case-control study assessing these and other factors could further confirm and explain these findings.

Foodborne and Waterborne Infections

Monday, August 24, 3:30 PM - 4:45 PM

Grand Hall

Board 156. Evidence for Non-foodborne Transmission in Some Cases of Neonatal Listeriosis

K. A. Jackson, B. J. Silk, B. E. Mahon; CDC, Atlanta, GA, USA

Background: Neonatal listeriosis is generally attributed to maternal consumption of contaminated food followed by vertical transmission; neonatal illness is usually severe, while maternal symptoms range from mild to severe. Though infection due to exposure after delivery has been documented, little information is available about the frequency of postnatal transmission. Neonatal cases associated with a foodborne outbreak are definitively of maternal origin, whereas sporadic and late-onset cases might not be. **Methods:** We analyzed pregnancy-associated listeriosis cases reported to CDC's *Listeria* Initiative, which collects clinical, demographic, exposure, and microbiological data submitted by health departments. Cases were considered to be of definite maternal origin if the case was associated with an illness cluster or a foodborne outbreak, if *Listeria* was isolated from the mother, or if a neonatal isolate was collected within ≤ 1 day. Cases of possible non-maternal origin included sporadic illnesses in which the isolate was collected ≥ 7 days after birth. Odds ratios (ORs) were calculated to describe associations between maternal symptoms and mode of transmission. The time from mother's onset to delivery or fetal loss was calculated for cases of maternal origin. **Results:** During 2004-2012, 439 pregnancy outcomes were reported, of which 348 (79%) were of definite maternal origin (80 outbreak or cluster associated, 194 sporadic cases with isolates of maternal origin, and 74 sporadic neonatal isolates collected within ≤ 1 day), 80 (18%) were of possible non-maternal origin, and 11 (3%) were unclassifiable. Fever and chills occurred more frequently among mothers in cases classified as definitely maternal (80% and 62%, respectively) than among those classified as non-maternal (38% and 2%) (OR= 6.5, 95% CI: 3.3-12.8 and OR=71.9, 95% CI: 11.9->999.9). Among cases of definite maternal origin, 72% had symptoms within 7 days of delivery or fetal loss. **Conclusions:** Mothers of neonates with listeriosis of definite maternal origin are usually symptomatic. A significant minority of neonatal listeriosis cases may not be acquired from contaminated food. Further investigation of possible non-foodborne sources of late-onset neonatal listeriosis may reveal postnatal sources of exposure.

Board 157. Exposure Routes in Vibriosis in the United States, 1988-2013

A. E. Newton, B. E. Mahon, R. K. Mody; CDC, Atlanta, GA, USA

Background: In the United States, vibriosis, defined as infection with a species from the family *Vibrionaceae* (other than toxigenic *V. cholerae* O1 or O139) is estimated to cause 80,000 illnesses annually. Assessment of routes of vibriosis transmission (i.e., foodborne [from consumption of seafood] or non-foodborne [from skin exposure to saltwater or seafood drippings]) may help guide optimal prevention measures. **Methods:** State Health Departments report vibriosis cases to the Cholera and Other *Vibrio* Illness Surveillance system at the Centers for Disease Control and Prevention. Reporting began in 1988, and most states were reporting by the early 2000s. We analyzed all cases reported through 2013. Transmission was categorized as foodborne, non-foodborne, or unknown based on clinical source and reported exposures. Persons reporting foreign travel

in the seven days before illness onset were excluded. Crude incidence rates (per million) were calculated using US Census Bureau estimates. **Results:** Between 1988 and 2013, 11,341 cases of domestically-acquired vibriosis were reported, with incidence increasing three-folddoubling from 1.6 in 1988 to 3.5 in 2013. Most cases (57%) were categorized as foodborne (range by year, 41%-75%); 33% were non-foodborne (17%-44%), and the route could not be determined for 11% (6%-22%). *V. parahaemolyticus* (43%), *V. vulnificus* (19%), *V. alginolyticus* (13%), and *V. cholerae* (other than toxigenic *V. cholerae* O1 and O139) (9%) were most frequently reported. *V. parahaemolyticus* incidence increased from 0.2 in 1988 to 1.5 in 2013, primarily driven by a five-fold increase in the incidence of foodborne cases (non-foodborne cases tripled). *V. alginolyticus* incidence increased from 0.03 in 1988 to 0.5 in 2013, driven by a large increase in the incidence of non-foodborne cases. The overall and transmission route-specific incidence of *V. vulnificus* and *V. cholerae* infections remained relatively stable. **Conclusion:** Vibriosis incidence has increased in the United States, primarily driven by an increase in foodborne *V. parahaemolyticus* and non-foodborne *V. alginolyticus* infections. To reduce incidence of vibriosis, effective prevention measures are needed to target both foodborne and non-foodborne transmission routes.

Board 158. Increase of *Vibrio alginolyticus* in the United States, 1988-2012

K. M. Jacobs Slifka, A. E. Newton, B. E. Mahon; CDC, Atlanta, GA, USA

Background: *Vibrio alginolyticus*, a halophilic bacterium, can cause gastrointestinal and severe soft tissue infections, especially of the ear. Little systematically collected clinical and epidemiological information about *V. alginolyticus* infection is available. **Methods:** *Vibrio* infections became nationally notifiable in 2007 and are reported to the Cholera and Other *Vibrio* Illness Surveillance (COVIS) system. COVIS data for *V. alginolyticus* was used to categorize specimen site as blood, ear, gastrointestinal, other non-sterile site, and skin and soft tissue (SST). Transmission route (non-foodborne or foodborne) was determined using specimen site and exposure history. We analyzed demographic and clinical characteristics of cases reported from 1988-2012 and calculated crude incidence using US Census Bureau estimates from 2007-2012. **Results:** Of 1,331 *V. alginolyticus* infections reported during 1988-2012, the highest numbers were from Gulf Coast states (40%); however, Hawaii had the largest incidence (1.7 infections per 100,000 population in 2012). Since *V. alginolyticus* infection became nationally notifiable, incidence has increased in all coastal regions; the Gulf Coast increased most—from 0.04 infections per 100,000 population in 2007 to 0.13 in 2012. Non-foodborne infections accounted for 86%. Of patients with non-foodborne infection, 74% reported exposure to a body of water, and 67% had a pre-existing wound or sustained a wound during this water exposure. SST was most frequently reported site (50%) (specifically, lower extremity [34%]), followed by ear (33%). Hospitalization was required by 20% of patients, and 12 died (1%). Fever (20%) and cellulitis (39%) were the most common clinical findings. Complications were described in 60 non-foodborne infections, including debridement (28%), amputation (13%), skin grafting (12%), and hearing loss (3%). **Conclusions:** *V. alginolyticus* infections are increasing throughout the coastal United States. Prevention efforts should target non-foodborne infections, which are usually associated with injury and/or wounds present during water exposure and which account for most infections. Understanding the clinical presentation and associated exposures may help improve early recognition and treatment and prevent severe consequences.

Board 159. Incidence of Norovirus Among Kaiser Permanente Member Populations in the United States, 2012-2013

S. Grytdal; CDC, Atlanta, GA, USA

Background: Noroviruses are increasingly recognized as a frequent cause of acute gastroenteritis (AGE). However, few laboratory-based data are available on the incidence of norovirus AGE in the U.S. This study examined the proportion of norovirus-positive stool specimens submitted for routine clinical diagnostics from patients enrolled in Kaiser Permanente (KP) health plans in metro Portland, OR, and the Baltimore/District of Columbia metro areas and estimated age group-specific estimates of norovirus disease incidence in these populations from 2012-2013. **Methods:** Participating laboratories randomly selected stools submitted for routine clinical diagnostics for inclusion in the study along with accompanying demographic and clinical data. Stool aliquots were tested for norovirus using a standardized real-time RT-PCR protocol. Each KP site provided administrative data which were used to extrapolate pathogen detection rates into population-based incidence rates. **Results:** A total of 1,099 specimens collected during September 2012 to September 2013 were included. Mean age of patients providing stool specimens was 46 years (range: 0-98 years) of age. Six percent (n=63) of specimens were positive for norovirus; 87% were classified as genogroup II. Incidence of norovirus-associated outpatient visits was 5.6 per 1,000 person-years; incidence of norovirus disease in the community was estimated to be 60.8 per 1,000 person-years. Norovirus incidence was highest among patients <5 years of age (outpatient incidence=25.6 per 1,000 person-years; community incidence=152.2 per 1,000 person-years), followed by patients aged >65 years (outpatient incidence=7.8 per 1,000 person-years; community incidence=75.8 per 1,000 person-years). **Conclusions:** This study provides the first age-group specific U.S. laboratory-based incidence rates for norovirus AGE in outpatient and community settings. The overall incidence rates of norovirus disease estimated in this study are similar to those reported previously among KP members in another state. These data provide a better understanding of the norovirus disease burden in the United States, including variations within different age groups, which can help inform the development, targeting, and future impacts of interventions, including vaccines.

Board 160. Outbreaks Attributed to Fish—United States, 1998-2012

K. A. Walsh[1], L. H. Gould[1], J. H. Nakao[2], E. V. Taylor[1]; [1]CDC, Atlanta, GA, USA, [2]CDC, Washington, DC, USA

Background: Foodborne diseases are estimated to cause 48 million illnesses in the United States each year. While fish is an important part of a healthy diet, it is also the most commonly implicated food category in outbreaks. **Methods:** We reviewed CDC's Foodborne Disease Outbreak Surveillance System for outbreaks of two or more cases resulting from consumption of fish during 1998–2012. Outbreaks caused by shellfish and other aquatic animals were not included. Analyses examined the number of outbreaks, illnesses, hospitalizations, year, state, etiology, fish type, and location and method of preparation. **Results:** During 1998–2012, 713 outbreaks attributed to fish were reported, resulting in 4,182 illnesses, 295 hospitalizations, and 3 deaths. The median number of illnesses per outbreak was 3 (range: 2–425). The number of fish-associated outbreaks declined from an average of 62 per year during 1998–2004 to 32 per year during 2005–2012. Hawaii (215 outbreaks; 30%) and Florida (164; 23%) reported the most outbreaks. Among 643 outbreaks (90%) with an etiology reported, scombroid toxin (355; 55%)

and ciguatoxin (209; 33%) were most common. Norovirus (65 average illnesses; range: 5–380) and *Salmonella* (53; 2–425) caused the largest outbreaks, but together represented only 2% of fish-associated outbreaks. Fish types implicated most often were tuna (35%), mahi mahi (12%), and grouper (10%). The etiology-fish pairs responsible for the most outbreaks were scombroid toxin in tuna (213 outbreaks), scombroid toxin in mahi mahi (75), and ciguatoxin in grouper (60). Of the 618 outbreaks (87%) with a single location of food preparation, 54% were attributed to fish prepared in a restaurant and 33% to fish prepared in a private home. Raw or lightly cooked fish was implicated in 53 (11%) of 486 outbreaks (68%) with a known preparation method. Tuna (34 of 173 outbreaks) and salmon (6 of 17) were reported raw most often. **Conclusions:** The number of outbreaks caused by fish declined. Most outbreaks were caused by scombroid toxin and ciguatoxin, which are not destroyed by cooking. Control measures targeted to these most common etiologies could further reduce outbreaks caused by fish.

Board 161. Changes in Overall Incidence of Foodborne Illness in the United States, by Age Group, Foodborne Diseases Active Surveillance Network (FoodNet), 1996-2013

S. M. Crim[1], M. Bazaco[2], J. Dunn[3], N. Oosmanally[4], O. L. Henao[1]; [1]CDC, Atlanta, GA, USA, [2]Food and Drug Admin., Washington, DC, USA, [3]Tennessee Dept. of Hlth., Nashville, TN, USA, [4]Georgia Dept. of Publ. Hlth., Atlanta, GA, USA

Background: The Foodborne Diseases Active Surveillance Network (FoodNet) monitors the incidence of 9 infections transmitted commonly through food in 10 US sites. To provide a concise estimate of change in the incidence of foodborne illness, FoodNet developed a measure that combines information for 6 pathogens that are predominantly foodborne. Because incidence varies by age, we conducted an analysis extending the use of this measure to examine incidence and change in incidence by age group. **Methods:** This analysis focused on 6 key bacterial pathogens (*Campylobacter*, Shiga toxin-producing *Escherichia coli* O157, *Listeria*, *Salmonella*, *Vibrio*, and *Yersinia*) for which >50% of illnesses are estimated to be transmitted through food. Incidence of each pathogen was calculated per 100,000 population; the overall incidence was calculated as the average of the pathogen-specific incidences. To estimate change in the overall incidence, we used a negative binomial regression model to adjust for the increase in FoodNet surveillance area over time, site-to-site variation in incidence of infection, and the incidence of infection for each pathogen included in the measure. Incidence in 2013 was compared with the incidence in the first 3 years of FoodNet surveillance (1996-1998) and presented as percentage change with 95% confidence intervals (CI). Age-stratified analyses used the following groupings: <5, 5-9, 10-19, 20-64, and ≥65 years. **Results:** The overall incidence of foodborne infection in 2013 was 5.2 cases per 100,000 persons. Incidence by age group ranged from 3.7 per 100,000 in persons aged 10-19 years to 15.5 per 100,000 in children aged <5 years. Compared with 1996-1998, the overall incidence of infection was 20% lower in 2013 (CI=9%-30%). During the same time period, by age group, the overall incidence was significantly lower among children aged <5 years (46%, CI=35%-56%) and children aged 5-9 years (19%, CI=3%-33%). Incidence in the older age groups was not significantly different in 2013 than in 1996-1998. **Conclusions:** The overall incidence of foodborne illness has decreased since 1996-1998, most notably among children aged <5 years. However, incidence in young children remains considerably higher than that of other age groups and focused efforts are needed to further reduce foodborne illness in this group.

Board 162. Does the Distribution of *Campylobacter* Species in the United States Differ by Geographic Region?

M. E. Patrick[1], T. Robinson[2], S. McGuire[3], A. Palmer[4], C. Nicholson[5], M. Tobin-D'Angelo[6], J. Hatch[7], S. Hurd[8], S. Hanna[9], K. Wymore[10], A. Cronquist[11], A. Geissler[1], O. Henao[1]; [1]CDC, Atlanta, GA, USA, [2]Minnesota Dept. of Hlth., St. Paul, MN, USA, [3]New York State Dept. of Hlth., Albany, NY, USA, [4]Maryland Dept. of Hlth., Baltimore, MD, USA, [5]New Mexico Emerging Infections Program, Albuquerque, NM, USA, [6]Georgia Dept. of Publ. Hlth., Atlanta, GA, USA, [7]Oregon Dept. of Hlth., Portland, OR, USA, [8]Connecticut Emerging Infections Program, New Haven, CT, USA, [9]Tennessee Dept. of Hlth., Nashville, TN, USA, [10]California Emerging Infections Program, Oakland, CA, USA, [11]Colorado Dept. of Hlth., Denver, CO, USA

Background: *Campylobacter* is the most common bacterial cause of diarrheal illness in the United States affecting an estimated 1.3 million people annually. Risk factor differences for *Campylobacter* infection vary by species. Rates of *Campylobacter* infection are highest in western states. We examine geographic associations of *ampylobacter* infections by species. **Methods:** The Foodborne Disease Active Surveillance Network (FoodNet) conducts population-based, active surveillance for culture-confirmed *ampylobacter* infections in Connecticut, Georgia, Maryland, Minnesota, New Mexico, Oregon, and Tennessee, and selected counties in California, Colorado, and New York. We analyzed cases of *Campylobacter* infection reported to FoodNet from 2010 through 2013 with species results available from CDC (all FoodNet sites) or a state public health laboratory (SPHL) (selected sites); species results obtained only from clinical labs were excluded. If species results at a SPHL and CDC differed, the CDC result was included in analysis. **Results:** A total of 26,600 *Campylobacter* cases were reported from 2010-2013. Forty-one percent had species information available; this ranged from 3% in California to 92% in Minnesota. Among 10,909 cases with species information, 9,723 (89%) were *C. jejuni*, 893 (8%) *C. coli*, 218 (2%) *C. upsaliensis*, and 75 (1%) other species. The percentage of *C. jejuni* within a state varied from 82% in Oregon to 92% in New Mexico, New York, and Tennessee. *C. coli* isolates varied from 4% in New Mexico to 16% in California. *C. upsaliensis* isolates varied from <1% in Maryland, New York, and Tennessee to 10% in Oregon. California had twice the percentage of *C. coli* cases and Oregon three times the percentage of *C. upsaliensis* cases when compared with other sites. **Conclusions:** Although we observed differences in distribution of species between states, we did not see a distinct geographic pattern overall. The wide range in availability of species data could be due to differences in isolate submission requirements between states and may have impacted our results. Additional analysis is needed to understand what role sample size, availability of species information, isolate sampling schemes, specimen source, exposure profiles, and underlying population structure play in state-specific differences.

Board 163. Phenotypic and Genotypic Characteristics of Clinical Enterotoxigenic *Escherichia coli* (ETEC) Isolates in Southern Coastal Region of China

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Background: Enterotoxigenic *Escherichia coli* (ETEC) infections are best known as an important cause of diarrhea among children in developing countries and travelers to developing areas. There was limited information about ETEC infections in China. This study was to investigate the

ETEC infections in southern coastal region of China and determine the phenotypic and genotypic characteristics of ETEC clinical isolates to provide information for developing an effective vaccine. **Methods:** ETEC were isolated from stool samples of acute diarrheal patients of all ages in Shenzhen City from 2009 to 2012. Eighteen colonization factors (CFA/I, CS1to CS8, CS12 to CS15, CS17 to CS22, and PCFO71) were detected by Multiple PCR. ETEC isolates were serotyped and antimicrobial resistance to 20 antibiotics was determined. All isolates were further genotyped by multilocus sequence typing (MLST). **Results:** A total of 121 ETEC strains were isolated and identified from 12241 stool samples. Vast majority patients infected with ETEC were belonged to the age ranged from 20 to 59 years old (n=99, 81.8%) and only five patients were children aged <5 years. One-hundred ETEC infections detected (82.6%) were distributed in warm weather months from June to September with the height in August. ST-positive ETEC strains were the most frequently detected ETEC strains (n=100, 82.6%), followed by LT-positve ETEC strains (n=16, 13.2%). One or multiple CFs were identified in almost half of the ETEC strains (n=60, 49.6%). The most frequently detected CFs was CS6 (with or without other CFs) (54/60), followed by CS21 (7/60). The most common serotype was O159:H23 (n=23), followed by O148:H28 (n=15) and O27:H7 (n=10). Resistance to nalidixic acid was 75.0% (n=91,), followed by ampicillin (n=49, 40.5%), cephalothin (n=47, 38.8%), tetracycline (n=25, 20.7%) and streptomycin (n=13, 19.0%). MDR isolates accounted for 19.0% (n=23) of all isolates studied. The antimicrobial-resistant profiles differed among different serogroups. CC218 and CC94 were the dominant clonal complexes covering 31 (25.6%) and 21 (17.4%) isolates, respectively. **Conclusions:** ETEC isolates in Shenzhen area appeared to have unique phenotypic and genotypic features. LT and ST fusion vaccine might be a good choice for vaccine development against ETEC diarrhea.

Board 164. Are All Pediatric HUS Cases the Same? A Comparison of Cases in Patients Less Than 5 Years and 5-18 Years Old, Foodborne Diseases Active Surveillance Network, 1997-2013

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Background: Hemolytic uremic syndrome (HUS) is a life-threatening syndrome characterized by hemolytic anemia, thrombocytopenia, and acute renal failure. Post-diarrheal HUS is a rare condition that most often follows gastrointestinal infection with Shiga toxin-producing *E. coli* (STEC) and is most common in children, especially those <5 years. The Foodborne Disease Active Surveillance Network (FoodNet) conducts population-based, active surveillance for physician-diagnosed pediatric HUS cases (<18 year old) and most analyses of the data in FoodNet focus on children <5, whereas the 5-18 year old case population is not well described. **Methods:** We examined FoodNet surveillance data, collected through a network of nephrologists and infectious disease specialists and by hospital discharge data review, from 1997-2013 to identify differences in demographics, clinical characteristics, and outcomes between children age <5 and 5-18 years of age. A confirmed case of post-diarrheal HUS was defined by strict criteria of age-specific hemoglobin and hematocrit levels for anemia, platelet count <150,000 /μL, elevated serum creatinine, and red cell fragmentation, all occurring within 3 weeks following a diarrheal illness. **Results:** A total of 718 cases were identified (458 [64%] were <5 and 260 [36%] were 5-18 years) and 21 cases died (17 were <5 and 4 were 5-18 years old). Sex and race were similar in both age groups (overall, 55% were female and 70% were white), however, more cases in the <5 group were Hispanic than in the 5-18 group (12% vs. 4%; p<0.01). Both groups had similar high percentages of bloody diarrhea (80%). During hospitalization, complications including pneumonia and seizure were more frequent in the <5 age group (5% vs. 2%; p=0.02, 12% vs. 5%; p<0.01), and more <5 case-patients needed dialysis (64% vs. 49%; p<0.01). **Conclusions:** Overall, our analysis showed that post-diarrheal HUS cases <5 years and those 5-18 years were similar in regards to sex, race and most clinical characteristics. However, HUS cases <5 years were more likely to be Hispanic, have complications with pneumonia and seizures, and need dialysis. Post-diarrheal HUS appears to be more severe in children <5, but additional analysis is needed to examine the observed similarities and differences further.

Board 165. Giardiasis Outbreaks in the United States, 1971-2011

E. Adam, J. Yoder, L. H. Gould, M. C. Hlavsa, J. Gargano; CDC, Atlanta, GA, USA

Background: An estimated 1.2 million cases of giardiasis occur annually in the U.S. To better understand factors implicated with ongoing *Giardia* transmission, the impact of prevention measures already undertaken, and additional areas where interventions could further reduce transmission, we reviewed reports to CDC of giardiasis outbreaks occurring during 1971-2011. **Methods:** We reviewed outbreak data and summarized the transmission modes and vehicles, case counts, and contributing factors (e.g., water system deficiencies). We compared outbreaks from two time periods, 1971-1990 and 1991-2011, considering the context of policy changes. **Results:** The 242 outbreaks, affecting ~41,000 persons, resulted from waterborne (75%), foodborne (16%), person-to-person (3%), and zoonotic (1%) transmission. An equal number of outbreaks occurred during each time period, although outbreaks were smaller in the second time period (median = 30 cases/outbreak vs. 8 cases/outbreak). Most (75%) waterborne outbreaks were associated with drinking water, followed by recreational water (18%). Treatment deficiencies were reported in 74% of drinking water outbreaks during 1971-1990, compared to 31% of those after 1990. Groundwater source and distribution system deficiencies were identified for 8% and 6%, respectively, of drinking water outbreaks during 1971-1990, compared to 36% and 22% of those after 1990. *Giardia* alone caused 73% of outbreaks associated with treated recreational water venues (e.g., pools). Among foodborne outbreaks, the most frequently implicated vehicles were produce or fruit (13%). Food was most commonly prepared in a restaurant (42%) and contaminated by an ill food handler (18%). **Conclusions:** *Giardia* outbreaks have become smaller, but continue to occur. Outbreaks over the past 4 decades have implicated a number of transmission pathways. The decreased incidence of drinking water outbreaks resulting from treatment deficiencies coincided with policy changes (e.g., 1989 Surface Water Treatment Rule). Groundwater and distribution system vulnerabilities, inadequate pool disinfection, poor food handler hygiene, and produce contamination are promising targets for future giardiasis prevention and control measures.

Board 166. The Seasonality and Climatic Drivers of Cryptosporidiosis

L. Tyndall, S. Ahmed, K. Levy; Emory Univ., Atlanta, GA, USA

Background: There is much uncertainty about the relationship between climate and diarrheal disease, due to a lack of studies that target this question, a lack of studies of the relationships between climate and individual pathogens, and true heterogeneity of effect. This study attempts to address these factors through analysis of cryptosporidiosis and its relationship with temperature and rainfall, testing for heterogeneity both within and between datasets. **Methods:** All US cryptosporidiosis cases reported monthly between 1997-2011 were obtained from the National Notifiable Disease Surveillance System (NNDSS). These data were analyzed with monthly temperature and precipitation data, using generalized linear model and generalized estimating equation regression analyses to calculate incidence rate ratios for each state, nine climate regions, and for the US as a whole. Heterogeneity of results was assessed using the I^2 statistic. A systematic review of the literature was performed, searching for studies worldwide that presented at least one full year of monthly data on cryptosporidiosis incidence. These data were extracted, matched with climate data for the same periods, and analyzed. The results were compared to the NNDSS analysis. **Results:** There is an overall positive relationship between temperature and cryptosporidiosis in the US—for every 1 °C increase in temperature, cryptosporidiosis case incidence increases by 2.51%. This is supported by the global literature review which reports a 2.96% increase in cryptosporidiosis for every 1 °C increase in temperature worldwide. There is much variability in the relationship between precipitation and cryptosporidiosis in the US, likely due to local geographic and temporal factors. There was considerable heterogeneity between climate regions, but not between states. **Conclusion:** In general there is a positive relationship between cryptosporidiosis and temperature. The relationship between cryptosporidiosis and precipitation is not as clear and is likely due to factors not considered in this study. The relationship between these climatic variables and cryptosporidiosis cases was remarkably consistent across states and between the US and global analyses. This suggests the temperature-disease relationship is robust in varying conditions.

Board 167. Geographical Variation in Listeriosis Incidence, United States, 2001-2012

A. R. Conrad[1,2], K. A. Jackson[2], B. R. Jackson[2]; [1]Atlanta Res. and Ed. Fndn., Atlanta, GA, USA, [2]Enteric Diseases Epidemiology Branch, CDC, Atlanta, GA, USA

Background: An estimated 1,600 illnesses and 260 deaths are caused by *Listeria monocytogenes* in the United States each year, nearly all through foodborne transmission. In the late 1980s, estimated listeriosis incidence was ~8 per million, declining to ≤ 4 per million by 2000. Listeriosis became nationally notifiable in 2001. To help inform control measures, we characterized the US geographical distribution of listeriosis from 2001-2012. **Methods:** US annual listeriosis incidence rates were calculated using case counts from CDC's National Notifiable Diseases Surveillance Systems (NNDSS) and annual US Census Bureau population estimates. Incidence rates were also calculated for the 4 census regions and 9 divisions and for year groups 2001-2004, 2005-2008, and 2009-2012. All rates were calculated as cases per million people. We used American Community Survey data (2006-2010) to compare birth rates per 1,000 women age 15-50 years among regions and Census data for percentage of population ≥65 years in 2010. **Results:** During 2001-2012, 9,410 listeriosis cases were reported to NNDSS. US incidence rates ranged from 2.2 in 2001 to 2.5 in 2012 (maximum 3.0 in 2005). Among regions, incidence was highest in the Northeast in all years (mean annual incidence 4.3, total cases 2,828), lowest in the South (2.0, 2,666), and intermediate in the West (2.7) and Midwest (2.2). Among divisions, mean annual incidence was highest in the Middle Atlantic (4.2) and lowest in the West North Central division (1.6). Incidence was highest for each region in the 2005-2008 time period except the West in which incidence was highest in 2009-2012 (2.8 per million), in part related to a large outbreak in 2011. The Northeast had the lowest birth rate (50) compared with other regions (≥57) and the largest proportion of population ≥65 years (14.1% vs. 11.9-13.5%). **Conclusion:** US listeriosis incidence changed little from 2001-2012. Incidence in the Northeast was more than double that in the South and was >50% higher than rates in the West and Midwest. Demographic factors (ie, age and birth rate) or regional variations in listeriosis reporting are not likely to fully account for these differences. Regional differences in food consumption or contamination are more likely explanations; further study may help identify and prevent these sources of listeriosis.

Board 168. Assessment of Food Safety Regulations for Norovirus Prevention: A State by State Analysis

A. Kambhampati, K. Shioda, D. Sharp, A. J. Hall; CDC, Atlanta, GA, USA

Background: Noroviruses are the leading cause of foodborne illness outbreaks reported in the United States. Foodborne norovirus transmission is commonly associated with contamination of food during preparation by an infected restaurant food worker, often involving bare hand contact with food or working while ill. The United States Food and Drug Administration's 2013 Food Code provides model food safety regulations to prevent transmission of foodborne illness in restaurants; however, adoption of specific provisions is left to state and local governments. **Methods:** We analyzed the food codes of all 50 states, the District of Columbia, and Puerto Rico to describe differences in the adoption of norovirus-related food safety provisions between states and the 2013 Food Code. Key areas assessed were hand washing procedures, bare-hand contact with ready-to-eat (RTE) food, management of ill workers, and certified food protection managers (CFPM). Data were abstracted from publically accessible state regulations and compiled for descriptive analysis. **Results:** Of the 52 jurisdictions assessed, all (100%) have provisions requiring hand washing and 39 (75%) prohibit bare hand contact with RTE food. There is wide variation in the adoption of criteria that specify when and for how long ill food workers should be excluded or restricted from their work. 33 states (63%) require exclusion or restriction of ill food workers for at least 24 hours after symptoms have ceased. 22 (42%) jurisdictions require at least one CFPM. **Conclusions:** Overall, most states have adopted some form of the recommended provisions to reduce foodborne norovirus transmission. However, there is considerable variation in specific regulations between states. Future analyses could examine implementation and compliance with state regulations, and potentially explore correlations between those regulations and the incidence and characteristics of reported foodborne norovirus outbreaks.

Board 169. Investigation of Trichinosis Outbreak in Ngao District, Lampang Province, August 2014

W. Toanan; Bureau of Epidemiology, Nontaburi, Thailand

Background: On 19 August 2014, Bureau of Epidemiology (BoE) was notified from Lampang Provincial Health Office (PHO) about suspected Trichinosis' food poisoning outbreak in Ngao district, Lampang province. BoE and Lampang PHO jointly conducted the investigation to confirm diagnosis and outbreak, identify source of infection and provide control measure. **Methods:** A descriptive study was conducted in the hospital

through the reviews of the ICD 10. Active case finding was performed with a case definition of at least 2 symptoms from fever, swelling of eye lids or face and muscle pain with the history of eating native pork and residence at Ban Boseeleum village, Ngao district, Lampang Province during June to August 2014. Samples were taken for laboratory testing. Environmental survey was also performed. **Results:** There were 30 Trichinosis' food poisoning cases. Regarding common source epidemic curve picture, median incubation period was 5 weeks. Eating improperly - cooked pork associated with this outbreak 83.33% (25/30). A Trichinalla spp. was found in muscle of one case and antibodies for Trichinalla spp. in serum of 9 cases. The 2 samples of pork from the village were found Trichinella spp. and antibodies for Trichinalla spp. in serum of 5 dogs, 1 cat and 1 pig respectively. **Conclusions**: This was a confirmed outbreak of Trichinosis by using laboratory confirmation from detecting Trichinalla spp. in muscle of one case. A pigs, dogs and cats were its reservoirs. Risk factor was eating improperly - cooked pork. To prevent future outbreaks should education programs emphasized on five key rules for food safety of the WHO.

Board 170. Pathogen-specific Causes of Diarrhea Among Hospitalized Children in Cairo, Egypt

A. M. Mansour[1], A. Hussein[2], A. El Gendy[1], H. El Mohammady[1], M. Moustafa[1], N. Abdel-Aziz[2], A. Yousef[2]; [1]US Naval Med. Res. Unit-3, Cairo, Egypt, [2]Cairo Univ., Pediatric Dept., Cairo, Egypt

Background: World Health Organization had set the goal to reduce mortality in children <5 years to reach 1 /1000 live births in 2025. To achieve this goal more efforts are required to enhance pathogen-specific etiology, risk factors and long term sequelae. Diarrhea is a major cause of morbidity and mortality among children and especially in developing countries. In this study, we characterize different diarrheal causing pathogens in hospitalized pediatric population due to diarrhea. **Methods:** Children 3 loose or liquid stools in a 24 hour period. Clinical data included dehydration status and other associated symptoms at presentation. Two rectal swabs and a stool specimen were collected upon child admission. Rectal swab were cultured using conventional bacteriological techniques and stool specimens were tested for antibodies against rotavirus and Cryptosporidium spp using commercial ELISA (enzyme-linked immuno-sorbent assay kits). **Results:** Of the 600 enrolled children, 80% were below one year and 14% were on exclusive breast feeding. There were more males (59%) and almost half (53%) were enrolled in the summer (May-October). Fever and vomiting were the most common clinical symptoms associated with diarrhea in 92% and 87% of the cases, respectively. One third of cases had fever >38 °C on admission and 98% of children were dehydrated (n=563, 98%). Convulsions were observed in only 8% (n=40) of diarrheal cases. Mucus was observed in stool by guardians in 73% (n=393), whereas, blood in stool was noticed in 7% (n=43) of the cases. Diarrhea and malnutrition observed in 12% (n=74) of the cases. Rotavirus was the most frequent pathogen detected (n=210, 35%), followed by Cryptosporidium spp. (n=62, 10%), and Enterotoxigenic Escherichia coli (ETEC) (n=19, 3%). Relatively low rates were detected for Campylobacter spp. (0.8%; n=5), Shigella spp. (0.6%; n=4) and Salmonella spp. (0.3%; n=2). Rotavirus-associated diarrhea was the most common cause of dehydration followed by Cryptosporidium and ETEC. **Conclusions:** These findings are in agreement with similar findings in other countries and will direct diarrhea management and the unnecessary treatment with antibiotics in pediatric diarrhea.

Board 171. Timeliness and Data Quality of the Web Based Enteric Illness Surveillance (WBEIS) in Bangladesh

Q. A. Zaki[1], F. Haque[2], M. Rahman[1], S. J. Chai[3]; [1]Inst. of Epidemiology Disease Control and Res. (IEDCR), Dhaka, Bangladesh, [2]Intl. Ctr. for Diarrhoeal Disease Res., Bangladesh (ICDDR,B), Dhaka, Bangladesh, [3]CDC, Atlanta, GA, USA

Background: The Institute of Epidemiology Disease Control and Research (IEDCR) launched Web Based Enteric Illness Surveillance (WBEIS) to detect outbreaks and observe trends of enteric illness in Bangladesh in 2009. Multiple enteric illness outbreaks have not been detected in WBEIS possibly due to incomplete data. Timely response to outbreaks also requires timely reporting of cases. We evaluated WBEIS to assess data completeness and timeliness to identify gaps to enhance outbreak detection and assessment of disease trends. **Methods:** We evaluated WBEIS using CDC's 2001 guidelines. We reviewed randomly selected inpatient records, case identification information, epidemiological data, and reporting processes from 2013 and interviewed WBEIS staff (n=24) to assess data completeness and timeliness. We identified a convenience sample of three clusters of sites with different reporting frequencies (sites submitting 0-2, 3-43, or 44-52 of 52 weekly reports) and randomly selected four subdistrict hospitals (n=12) from each cluster. **Results:** Among 572 reports submitted by 12 hospitals, 34% (195) were missing age group data, 34% (195) were missing sex data, and 0% (0) had data on address or time of onset of illness. Although all cases were referred for blood or stool examination, 0% (0) had lab confirmation of an etiologic agent. Median delay to data upload was 590 days (range 240-597), 17 days (range 0-133), and 35 days (range 0-377) days, respectively, for sites submitting 0-2, 3-43, and 44-52 of 52 required weekly reports. Two of 12 persons responsible for reporting had no training in reporting; these persons were at sites submitting 0-2 of 52 weekly reports. **Conclusion:** Key data needed for detection of outbreaks and trends, including age group, sex, place and time of onset of illness, and laboratory confirmation of etiologic agents limit the usefulness of WBEIS. Delay in reporting can delay identification of outbreaks thereby decreasing ability of investigators to assess exposures due to recall difficulties or disappearance of exposure sources. WBEIS usefulness can be enhanced by adding laboratory confirmation of etiologic agents and assessing reasons for incomplete data and delay of reporting, including lack of training.

Board 172. Foodborne Illness Outbreak at Intermediate School in North West Province, South Africa, October 2014

L. Motsuku[1,2], T. Mkhencele[1], T. Motladile[1,3], C. Lebeko[4]; [1]Natl. Inst. for Communicable Diseases, Sandringham, South Africa, [2]Univ. of Pretoria, Pretoria, South Africa, [3]North West Provincial Dept. of Hlth., Rusternburg, South Africa, [4]Provincial Dept. of Hlth., Rusternburg, South Africa

Background: *Salmonella* belongs to the family of Enterobacteria with over 2,500 subspecies that causes foodborne illnesses in humans. In South Africa, foodborne outbreaks are generally under reported. On the 28 October 2014 the local laboratory in North West Province reported receiving stool samples from the district hospital with suspected salmonella. In response, we conducted an investigation to describe and determine the aetiology and extent of the diarrhoea outbreak. **Methods:** We reviewed hospital and clinic patient records. Working case definition of salmonella was any person presenting with diarrhoea (three or more loose/ watery stools per day), nausea, vomiting and/or fever from 24 - 29 October 2014, who ate a school feeding scheme meal on 24 October 2014. Laboratory analyses were done on collected stool and food samples. We assessed the school kitchen environment and conducted informal interviews with food handlers. **Results:** There were 302 students enrolled at the school: 94% (279/302) ate samp and beans on 24 October. Sixty three percent (176/279) became ill (attack rate of 63.2 %). Male and female learners were equally affected; 92% (163/176) were < 15 years old. The case fatality rate was 0.6 % (1/176). Plotting cases by time of symptom onset identified a single peak on 25 October. *Salmonella* Heidelberg was isolated in 93% (13/14) of stools and from the samp, but not beans. Interviews with food handlers revealed inadequate food preparations and handling practices. No hazards were visually identified during the environmental assessment. **Conclusions:** Contamination of the samp likely led to the diarrhoea outbreak. It is unclear at what point the samp was contaminated with *Salmonella* Heidelberg. Review of food preparation process is recommended to identify opportunities for prevention of cross contamination.

Board 173. Burden of Diarrheal and Bacterial Foodborne Diseases in Thailand

Withdrawn at Author's Request

Board 174. US Foodborne Outbreaks of Cyclosporiasis During 2000-2014

R. L. Hall, B. L. Herwaldt; CDC, Atlanta, GA, USA

Background: Foodborne outbreaks of cyclosporiasis (*Cyclospora cayetanensis* infection) have been reported in the United States since the mid-1990s and have been linked to various types of imported fresh produce, including raspberries, basil, and mesclun lettuce. We compiled and summarized data regarding the U.S. foodborne outbreaks of cyclosporiasis that occurred during 2000-2014 and were reported to the Centers for Disease Control and Prevention. **Methods:** We included outbreaks that represented distinct temporospatial clustering of cases (e.g., associated with a social event), at least one of which was laboratory confirmed. We classified a food item as the vehicle of infection (either implicated, likely, or suspect) if a commodity or ingredient was identified in an outbreak investigation; conclusions regarding the sources of implicated vehicles were based on formal traceback investigations. **Results:** During the 15-year period of 2000-2014, 30 foodborne outbreaks and 1,554 outbreak-associated cases were reported by 16 states, New York City, and the District of Columbia. A median of 2.5 outbreaks were reported per year; however, some of the outbreaks in the same year may have been related. Most (23; 77%) of the reported outbreaks occurred in May, June, or July. A food vehicle was identified for 14 outbreaks (47%): basil (4 outbreaks), raspberries (2), raspberries and/or blackberries (2), cilantro (2), snow peas (1), sugar snap peas (1), bagged salad mix (1), and fruit salad (1). During the review period, implicated vehicles of infection came from Mexico (3 outbreaks), Guatemala (1), and Peru (1). **Conclusions:** Cyclosporiasis outbreaks have continued to be reported almost every year since the mid-1990s, primarily during spring and summer months. Some of the same types of produce have been implicated during >1 year. However, outbreak detection and response have been constrained by the lack of molecular subtyping tools with which to link individual cases to each other and to particular vehicles/sources of infection. Investments in next-generation sequencing technologies may lead to development of subtyping methods for *C. cayetanensis* and thereby facilitate detection, investigation, and prevention of cases and outbreaks of cyclosporiasis.

Board 175. Differences Among Types of Restaurant Settings Associated with Foodborne Disease Outbreaks, 2009-2013

Withdrawn at Author's Request

Board 176. Towards the Development of Potent and Selective Antiviral Therapy for Norovirus-induced Gastroenteritis

J. Rocha-Pereira, J. Van Dycke, D. Jochmans, J. Neyts; KU Leuven - Rega Inst. for Med. Res., Leuven, Belgium

Background: Human noroviruses are the leading cause of foodborne illness and are responsible for > 50% of gastroenteritis outbreaks worldwide. There are no vaccines or antiviral drugs available. Potent and safe antiviral therapy is urgently needed to reduce the burden of norovirus disease in vulnerable populations - young children, the elderly and immunocompromised - where prolonged and severe disease occurs and norovirus gastroenteritis may become chronic, linked to morbidity and mortality. Potent antivirals may also have an important place as prophylaxis i.e. to reduce transmission and to prevent infection during an outbreak. **Methods:** We reported that the viral polymerase inhibitor 2'-C-methylcytidine (2CMC) inhibits the in vitro replication of norovirus [Norwalk replicon, murine norovirus- MNV] (Rocha-Pereira et al. 2012 BBRC 427(4): 796-800). Using IFN receptors deficient- AG129 mice, we demonstrated that 2CMC efficiently protects against MNV (MNV-1.CW3) -induced diarrhea and mortality (Rocha-Pereira et al., 2013, J Virol 87:11798-805). We here established a MNV-transmission model and assessed the ability of an antiviral molecule to prevent/ reduce transmission of MNV. Furthermore, we used the MNV.CR6 strain, which persistently infects AG129 mice, to establish a mouse model of chronic norovirus infection for the study of the antiviral efficacy of small molecule inhibitors against chronic norovirus-induced gastroenteritis. **Results:** We here established a MNV transmission model in which we demonstrate that (i) MNV is efficiently transmitted from infected animals to non-infected (sentinel) mice; (ii) treatment of infected mice with 2CMC reduced viral shedding and markedly reduced transmission to uninfected sentinels and (iii) prophylactic treatment of sentinels with 2CMC resulted in a sterilizing protection against infection. While MNV.CR6-infected AG129 show prolonged MNV shedding in stool, a 2-week treatment with 2CMC reduces MNV titres to undetectable levels. **Conclusions:** We have assembled a unique toolbox of in vitro and small animal models to study norovirus infection which will be used to launch a

drug discovery campaign for noroviruses. Supported by EU FP7 project SILVER (260644) /KULeuven IOF-HB14-00425/ WHRI #343.

Board 177. The Burden and Impact of Acute Gastroenteritis and Foodborne Diseases in the Caribbean

L. -. Indar[1], B. Olowokure[1], E. Perez[2]; [1]Caribbean Publ. Hlth. Agency, Port of Spain, Trinidad and Tobago, [2]Pan American Hlth. Organization, Washington, DC

Background: The burden of acute gastroenteritis (AGE) and the proportion of AGE that is foodborne is unknown in the Caribbean. To better understand the epidemiology of AGE and foodborne disease (FBD) and measure their true burden and impact, the Caribbean Epidemiology Center (CAREC), now part of the Caribbean Public Health Agency (CARPHA), in collaboration with the Pan American Health Organization, and the Caribbean Eco Health Program executed a Caribbean Burden of Illness (BOI) study from 2008-2013 in nine countries. We provide a descriptive analysis of these studies. **Methods:** BOI studies were conducted in Barbados, Belize, Bermuda, Dominica, Guyana, Grenada, Jamaica, St Lucia and Trinidad and Tobago from 2008-2013. In each country, reprospective, cross-sectional population surveys, were conducted during the low and high AGE seasons, and laboratory surveillance of AGE specimens was conducted for a year. The economic burden of AGE was based on medical care costs and loss of productive days. **Results:** Underreporting of syndromic AGE in the nine countries ranged from 64%-83% and for laboratory-confirmed FBD pathogens from 74%-99%. Monthly prevalence of AGE ranged from 4.03%-12.7% and the yearly incidence from 0.52 to 1.4 episodes/year. Children aged 1-4 years had the highest prevalence of AGE (13%-25%). Prevalence of AGE also varied by season, and district/parish level in countries. Between 15.4% -36% of cases of AGE sought medical care and 12.5-28% of these were requested to submit a stool specimen. The proportion of AGE that tested positive for a FBD pathogen ranged from 8.5%- 40.9%. Loss of productive days due to AGE ranged from 1-20 days. Norovirus had the highest estimated burden, followed by *Salmonella, Campylobacter* and *Giardia* infections. Annual economic costs of syndromic AGE ranged from $US2.2M- 40.4M. Underreporting, infrequent stool collection, inadequate laboratory capacity and underdiagnoses were the major surveillance gaps identified. **Conclusions:** This is the first time such a study has been carried out in the Caribbean, and provides meaningful information to guide resource allocation and prevention measures. There is an urgent need to improve the surveillance of AGE and FBD and implement appropriate and targeted food safety measures in the countries.

Board 178. Foodborne Diseases in the Caribbean, 2005-2014: Changing Epidemiology and Implications for Prevention and Control

L. Indar, L. Francis, S. Quesnel, E. Bisssessarsingh, B. Olowokure; Caribbean Publ. Hlth. Agency, Port of Spain, Trinidad and Tobago

Background: Foodborne disease (FBD) is an increasing public health concern in the Caribbean, as reflected by the increasing number of cases and outbreaks of gastroenteritis and FBD reported to the Caribbean Epidemiology Centre (CAREC) (1990-2013) and the Caribbean Public Health Agency (CARPHA) from 2013 onwards. CARPHA (which includes CAREC) is the Caribbean's health monitoring and disease prevention agency. We describe the epidemiological trends of FBD and *Salmonella* infections in the Caribbean from 2005-2014. **Methods:** Regional surveillance data for 21 English speaking Caribbean countries from 2005-2014 was derived from laboratory-confirmed *Salmonella, Shigella, Campylobacter, Vibrio,* pathogenic *Escherichia coli and* Norovirus FBD infections, clinically-diagnosed *Ciguatera* poisoning and *Salmonella* subtypes reported on monthly communicable diseases forms. Additional *Salmonella* and Norovirus subtyping data were derived from CARPHA's laboratory. **Results:** During 2005-2014, the number of reported human FBD pathogens in the Caribbean increased by 26%. Non- typhoidal *Salmonella* was the most common infection (47%), followed by *Ciguatera* poisoning (24%) Typhi (9.8%), *Shigella* (8%), *Campylobacter* (6%) and *Norovirus* (3.9%). There was an increase in non-typhoidal *Salmonella* (51%), *Norovirus* (26%) and C*ampylobacter* (25%) from 2005 to 2014 and decline in Typhi (-99%), *Shigella* (-54%) and *Ciguatera* (-18%) during the same time period. *Salmonella* and *Shigella* were reported from more than half of the countries. *Campylobacter* and *Ciguatera* were reported from 3-6 countries and Norovirus from 5-7 countries. A wider range of pathogens were reported from 2010 onwards. *Salmonella* serotyping data indicated that whilst 146 serotypes were identified, Enteritidis (29%) and *Typhi*murium (21%) were the two most prevalent serotypes isolated from 2005-2014, followed by Mississippi (4.9%). Enteritidis was the most commonly isolated in Trinidad and Tobago, Jamaica and Suriname. Typhimurium was dominant in Barbados and Mississippi n Bermuda. **Conclusions:** The epidemiology of FBD in the Caribbean has changed from 2005-2014 and implies the need for country and pathogen-specific prevention measures. Measures to reduce *Salmonella, Campylobacter, Norovirus* would significantly reduce FBD infections in the region.

Effective and Sustainable Surveillance Platforms

Tuesday, August 25, 12:30 PM - 1:45 PM
Grand Hall

Board 179. Tuberculosis Case Finding Using Population Based Disease Surveillance Platforms in Kenya

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Background: Tuberculosis (TB) case finding is an important part of TB control as it can reduce transmission of *Mycobacterium tuberculosis* (MTB) through prompt detection and treatment of infectious TB cases. **Methods:** The Kenya Medical Research Institute collaborating with the US Centers for Disease Control and Prevention has conducted population based infectious disease surveillance (PBIDS) in two sites in Kenya - one urban and the other rural. We examined the yield of intensified TB case finding at community level and at PBIDS clinics, as an adjunct to passive case finding. From April 2012 -April 2014, PBIDS participants ≥15 years were screened at home or at the clinics for TB symptoms - defined as any cough, fever, night sweats or weight loss in the past two weeks. At home, those symptomatic were consented for collection of sputum. At the clinic, symptomatic patients with HIV were invited to produce sputum. Those without HIV but with TB symptoms lasting seven days including the day of the visit had x-rays done and were asked for sputum if the-rays were abnormal. Sputum samples were tested for presence of MTB using the MTB/RIF PCR assay. TB detection rates were calculated per 100,000 persons screened. **Results:** Of 11,536 participants aged ≥15 years screened in person at home at both sites 2,752 (23.9%) had TB symptoms of whom 2,152 (78.2%) produced sputum specimens. MTB was detected in 32 (1.5%) of the specimens resulting in a detection rate of 277/100,000 persons. At the clinics, a total of 11,762 person were screened, 7,500 (63.8%) had TB symptoms of whom 1,289 (17.2%) produced sputum samples. MTB was detected in 69 (5.4%) of the samples resulting in an overall detection rate of 587/100,000 among persons screened. The TB detection rate was significantly greater for clinic compared to home-based screening (rate ratio [RR] 2.12, 95% CI 1.39 - 3.21). Significantly more TB was detected in persons with HIV than those without at both home (HIV-infected - 1319/100,000, HIV-uninfected 164/100,000, RR - 8.02, 95% CI 3.25 - 22.37), and clinic (HIV-infected 3931/100,000, HIV-uninfected 379/100,000, RR 10.34, 95% CI 6.18 - 18.44). **Conclusion:** Facility based intensified case finding identified more TB cases, including those with HIV, than home screening and should be further evaluated to determine the potential programmatic impact.

Board 180. Surveillance for Avian Influenza Viruses in Live Bird Markets, Bangkok, Thailand, 2013

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Background: Live bird markets (LBM) have been implicated in the transmission of low pathogenic avian influenza (LPAI) viruses, most recently with influenza A (H7N9), which has caused severe disease in humans in China. Because LPAI viruses, such as H7N9, cause asymptomatic infections in poultry, active surveillance is required to detect infection and prevent transmission to humans. Transmission of H7N9 in nearby China via LBM has prompted active surveillance for avian influenza in Bangkok LBM to detect any LPAI influenza viruses in this area. **Methods:** In November 2013, the Bangkok provincial One Health team, consisting of local human and animal health agencies, organized avian influenza surveillance activities in all nine districts of Bangkok with LBM. Oropharyngeal swabs and sera were taken from poultry, feces were collected whenever possible and water samples were taken from every shop. Samples were tested for influenza A viruses, at the National Institute of Animal Health, using real-time reverse transcription polymerase chain reaction. All samples were also inoculated in eggs and resulting virus identification confirmed by H5N1- and H7N9-specific antigens. Serum samples were tested by hemagglutination inhibition using similar antigens. In addition to collecting samples, the team distributed disinfectants and personal protective equipment while providing health checks and seasonal influenza vaccine to live bird vendors. All participating shops received a certificate of recognition from the Bangkok One Health team to promote cooperation and raise public awareness of the surveillance activity. **Results:** In 75 out of 87 shops where live birds were sold, the team collected oropharyngeal swabs (n=834), fresh feces (n=410), and sera (n=375) from 400 chickens, 20 ducks, 20 geese and 394 pet birds. Additionally, drinking water (n=208) and cleaning water (n=26) were collected. No sample was found positive for influenza A virus. **Conclusion:** These data provide evidence that avian influenza viruses, including LPAI viruses such as H7N9, were not circulating during the study period in Bangkok live bird markets. Future surveillance activities are planned to conduct longitudinal monitoring of live bird markets and this effort may serve as a model for other urban areas of Thailand and for the region.

Board 181. Annual Deaths from Selected Waterborne Pathogens in the United States

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Background: Advances in water treatment and sanitation have reduced the burden of classical enteric diseases transmitted through ingestion of fecally-contaminated water; pathogens associated with biofilms are now an emerging concern. Biofilm pathogens colonize water systems, fountains, spas and cooling towers, and can cause illness after inhalation of aerosolized water, or via skin or wound contact. We aimed to estimate the annual number of deaths in the United States from 14 diseases potentially transmitted by water and to understand the relative contributions of classical enteric and emerging biofilm-associated pathogens. **Methods:** We incorporated data from U.S. death certificates (ICD-10 codes), the Nationwide Inpatient Sample (nationally weighted sample utilizing ICD-9-CM codes), and disease-specific surveillance systems for the years 2003--2009 to estimate the number of annual deaths with diagnoses potentially linked to ingestion (campylobacteriosis, cryptosporidiosis, *Escherichia coli* infections, hemolytic uremic syndrome, giardiasis, hepatitis A, salmonellosis, shigellosis) and those linked to inhalation and contact (Legionnaire's disease [(caused by *Legionella*]), non-tuberculous *Mycobacterium* [(NTM]), *Pseudomonas*, vibriosis, free-living ameba, otitis externa). **Results:** We identified an average of 2516 documented deaths annually involving these diagnoses. The three diagnoses with the greatest number of documented deaths were *Pseudomonas* pneumonia or septicemia (1544), NTM infections (551), and Legionnaire's disease (109). Of illnesses potentially linked to ingestion of contaminated water, the greatest numbers of deaths were attributable to hepatitis A (103), hemolytic uremic syndrome (64), and vibriosis (49). **Conclusion:** Three biofilm pathogens, *Pseudomonas*, NTM, and *Legionella*, were associated with 88% of the documented deaths from 14 potentially waterborne diseases. Although surveillance data consistently show that transmission of waterborne diarrheal diseases is ongoing, these illnesses are not often fatal in the United States. These findings demonstrate that the burden of

mortality from waterborne pathogens in the United States has shifted away from classical fecal-oral transmission, as new transmission modes have emerged.

Board 182. Reassessing the Global Capacity for Timely Detection and Reporting of Emerging Infectious Diseases

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Background: Five years ago, a publication by Chan et al. confirmed that timeliness of disease detection and reporting had improved since the introduction of digital surveillance methods. Since that report, there have been continued innovations in public health infrastructure and digital surveillance. This study evaluates whether timeliness of outbreak detection and reporting has continued to improve in recent years. **Methods:** Following the methods of Chan et al., we collected data from all global outbreaks reported by the WHO in the past five years and appended them to the original dataset from 1996 - 2009. Outcomes of interest were time (in days) from outbreak start to detection and to public communication. We evaluated trends over time both graphically, using loess curves and boxplots, and statistically, using Cox proportional hazards models. **Results:** Our results to date only include outbreaks through the end of 2013. Since 1996, timeliness of outbreak detection has improved by an average of 6% per year [hazard ratio (HR) 1.060; 95% CI (1.037 - 1.084)]. Timeliness of communication has improved by an average of 2.5% per year [HR 1.025; 95% CI (1.004 - 1.046)]. A smoothed curve shows that the speed of outbreak detection stopped increasing and began to plateau around 2008, while the speed of public communication stopped increasing in 2006 and has been slowing down. Loess curves for each region suggest that timeliness of outbreak detection has continued to improve for Africa, the Americas, Europe, and South East Asia, while the Western Pacific region has plateaued and the Eastern Mediterranean has seen increasing delays in detection. For timeliness of public communication, only the Americas and Europe continued to improve, while the Western Pacific region has plateaued and timeliness has slowed down in all other regions. **Conclusions:** Timeliness of disease detection and public communication showed little improvement over the past four years. It is unclear if this is a true plateau, if early success left little room for improvement, or if the trend is attributable to unadjusted factors such as heterogeneity between regions or diseases. If time to communication is indeed increasing, then the international community must take steps to reverse this trend.

Board 183. Validation of an Estimating Procedure as an Alternative Method for Lyme Disease Surveillance

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Background: Many disease surveillance programs are currently challenged by marked increases in Lyme disease (LD) reports, including those of the Massachusetts Department of Public Health and the Minnesota Department of Health. The purpose of this study was to retrospectively analyze LD reports from 2005 through 2012 to determine whether key epidemiologic characteristics were statistically indistinguishable when an estimation method was utilized. **Methods:** Estimates of LD cases were produced by taking 20% and 50% random samples of laboratory-only reports, multiplying by 5 or 2 respectively, and adding the number of provider-reported confirmed cases. Estimated LD case counts were compared to observed, confirmed cases each year. In addition, the proportions of cases that were male, were ≤ 12 years of age, had erythema migrans (EM), had any late manifestation of LD, had a specific late manifestation of LD (arthritis, cranial neuritis, or carditis), or lived in a specific region were compared to determine if estimated proportions were representative of observed proportions. **Results:** Estimated case counts of LD were consistently similar to observed, confirmed LD cases and accurately conveyed temporal trends. Most of the key demographic and disease manifestation variables were not significantly different ($p \leq 0.05$), although estimates for the 20% random sample demonstrated greater deviation than the 50% random sample. **Conclusions:** Applying this estimation procedure in endemic states could conserve limited resources by reducing follow-up effort while maintaining the ability to track disease estimates and trends.

Board 184. Enhanced Surveillance for Novel H7 Avian Influenza Virus Among Poultry in Dhaka City Live Poultry Markets, 2013-14

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Background: A novel avian-origin influenza A(H7N9) virus has caused severe illness and death among humans in China. Many cases (47%) had a history of poultry exposure from live poultry market (LPM). Detection of A(H7N9) in specimens of poultry and the environment from LPMs in China further implicate LPMs as a source of H7N9 infection. Surveillance of H7N9 in animals is challenged by the fact that H7N9 is of low pathogenicity in avian hosts and therefore infection is asymptomatic. LPMs are common in Bangladesh and there is a highest density of LPMs in Dhaka City. Considering the threat posed by this novel H7N9, we decided to enhance our ongoing avian influenza surveillance in Dhaka LPMs. **Methods:** Cloacal swabs and pooled fecal specimens were collected from chicken, duck, quail and pigeon in 9 LPMs in Dhaka City twice a month for 8 months (September 2013-April 2014). All samples were tested, using real-time reverse transcription polymerase chain reaction assay, to detect influenza A virus RNA and subtyped for novel H7, H5 and H9. We collected cloacal swabs from 375 chickens, 301 ducks, 211 quails and 258 pigeons, as well as 234 pooled fecal samples. **Results:** Out of a total of 1145 cloacal samples, 126 (11%) tested positive for influenza A viral RNA. Of the 234 fecal pool samples, 50 (21%) were positive for influenza A viral RNA. None of the cloacal and pooled fecal specimens were positive for H7. Among the influenza A virus positive cloacal samples, 48 (38%) were positive for H5, 30 (24%) for H9 and the rest of positive samples were not able to be subtyped in our laboratory. Among the influenza A virus positive fecal pool samples, 21 (42%) had detectable RNA for H5 and 15 (30%) for H9. The prevalence for influenza A virus for cloacal samples was higher in ducks (24%) than other species (9% in chickens and 10% in quails) ($p<0.01$). The H9 subtype was most commonly detected in quails (7%). **Conclusions:** Our surveillance did not detect circulation of H7 avian influenza virus in poultry from Dhaka City LPMs. However, as previously described in our surveillance system, avian influenza A viruses, including the H5 and H9 subtypes, circulate in chickens, ducks and quails. H7N9 continues to circulate in China and may spread regionally. LPM based surveillance should be strengthened for early detection of novel H7 avian influenza virus and preparedness planning.

Board 185. The Influenza Electronic Surveillance System in Kazakhstan

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Introduction: Provision of timely information for operational decision-making will always remain one of the major tasks for an influenza surveillance system. **Materials and Methods:** In order to further improve the sentinel surveillance system for influenza, and ensure timely and uninterrupted collection of data, filling of databases, and automated reports generation without any additional time outlays, in 2011 Kazakhstan introduced an electronic influenza surveillance system which enables online data entering. Interface of the system represents a specialized protected-access web-portal (http://ses.dec.kz). Starting from the epidemic season of 2012-2013, the system was added an automatic data entry module which scans and digitizes paper forms with records of all ILI cases in sentinel sites. Starting from the epidemic season of 2014-2015, the electronic system includes a section on routine surveillance for acute respiratory virus infection and influenza. **Discussion and Results:** Fully functional online, the system enables epidemiological situation analysis and etiology monitoring of ARVI and influenza, automatic generation of tabulated reports using the inputs from administrative reports for any time period, including the results of weekly laboratory PCR and virological tests by age groups of patients, as well as clinical and epidemiological data. The interface enabling data entry online demonstrated its high usability, while the system itself proved to be very efficient in aggregating weekly, monthly and cumulative reporting data. **Conclusions:** Generation of reports online enabled their expedient distribution at all levels, organization and implementation of anti-epidemic measures, and effective use of resources available to healthcare. The software enabled significant time savings with respect to submission and distribution of reports, simplified the work of the staff concerned, and enabled timely correction of errors.

Board 186. Laboratory-based Sentinel Surveillance for Bacterial Etiologies of Acute Infectious Diarrheal Disease in Southern Coastal Region of China, 2007-2013

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Background: To determine the main bacterial etiology of acute infectious diarrheal disease, monitor infection trends and detect outbreaks caused by these organisms in the southern coastal region of China. **Methods:** A laboratory-based sentinel surveillance of acute infectious diarrheal disease network was established in July 2007 in Shenzhen city, Guangdong province, China. Twelve sentinel hospitals distributed in seven districts were recruited till 2011. Five bacterial species, including *Salmonella* spp., *Shigella* spp., *Vibrio cholerae*, *Vibrio parahaemolyticus*, and diarrheagenic *Escherichia coli,* were detected. Isolates obtained were serotyped. Pulsed-field gel electrophoresis (PFGE) typing was performed to detect the clusters and epidemiological investigations were launched. **Results:** A total of 30641 fecal specimens were collected from outpatients with acute diarrhea from July 2007 to December 2013. Bacterial pathogens were recovered from 9.9% stool specimens. The three main pathogenic species recovered were *V. parahaemolyticus* (n=1588, 5.8%), *Salmonella* spp. (n=950, 3.1%) and diarrhoeagenic *E. coli* (DEC) (n=377, 1.1%) and each demonstrated seasonal prevalence. The *V. parahaemolyticus* infections decreased from 2009 and Salmonella infections increased from 2012 with the isolation rate up to 5.2% in 2013. The O3:K6 serotype was predominant (n= 1062, 66.9%) in *V. parahaemolyticus* isolates, followed by the O4:K8 (n= 170, 10.7%) and O3:K29 (n= 51, 3.2%) serotypes. The most commonly isolated serotype of *Salmonella* was *S. Typhimurium* (n=315, 33.2%) and *S. Enteritidis* (n=236, 24.8%). *Shigella flexneri* accounted for 69.2% (74/107) of *Shigella* spp. isolates and DEC isolates demonstrate diverse serotypes. More than 100 PFGE clusters were identified during the surveillance years. A total of 9 investigations were initiated based on lab data from 2010 to 2013 and two point-source outbreaks were epidemiologically confirmed, including one O3:K6 *V. parahaemolyticus* outbreak and one *S. London* outbreak. **Conclusions:** The laboratory-based surveillance network provides the framework to respond rapidly and collaboratively to emerging foodborne disease or acute diarrheal disease and the gathered information has the potential to significantly impact public health policy development in Shenzhen.

Board 187. Hospitalization Surveillance for Severe Acute Respiratory Infection in Vietnam, 2011-2013

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Background: To early detect viral pathogens that cause of Severe Acute Respiratory Infection, that may causes of epidemic spread, the SARI sentinel surveillance was established in Vietnam in 2011. That is a component of National Influenza Surveillance in Vietnam and contains selected hospitals located in biggest cities of four regions in Vietnam: Hanoi (North); Khanhhoa (Central); Daclak (Highland) and Hochiminh city (South). **Methods:** Respiratory specimens (throat swabs/ tracheal aspirates) were collected according to the WHO Guideline. Twelve different viral respiratory pathogens (Influenza A, B; Para influenza 1,2,3; RSV; HMPV; Adeno; Picorna; SARS-CoV and Rhino) were determined by conventional RT-PCR or real-time RT-PCR using WHO and CDC, Atlanta, US procedures. **Results:** During 2011- 2013, total 2379 respiratory samples were collected and tested in NIHE, Hanoi, Vietnam. The result showed a proportion of influenza infection is 12,7% (301 samples), among them 93 samples were determined as influenza A/H3N2(rate 31%); and same number (93 samples) were influenza A/H1N1pdm09 (31%) and 115 samples were influenza B (38%) revealed. Other respiratory pathogens were detected on 448 samples (18,8%) and Picorna infection was predominant with 50,3% , then Adeno (18,6%); hMPV (11,1%), Parainfluenza 3(7,4%), parainfluenza 2 (5,7%), RSV (4.7%)··· We did not find any A/H5N1; A /H7N9 or SARS-CoV. **Conclusions:** Hospitalization surveillance for SARI can provide scientifically valid information, including animal influenza viruses with human pandemic potential and technical guide for national preventive policy and share epidemiological, virological data and materials to WHO-reference laboratories and GISRS. To sustain and improve the NISS system is needed since appearance of new pathogens (MERS-CoV, influenza A/H7N9) have emerged.

Board 188. Active Surveillance for Oseltamivir Resistance Among Influenza Viruses, Northern Vietnam, 2009-2013

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Background: Antiviral resistance has been reported in seasonal influenza A viruses and avian influenza A/H5N1 viruses in Vietnam, raising concerns about the efficacy of treatment. **Methods:** We analyzed isolates

from influenza-positive samples collected from influenza-like illness patients at sentinel clinics of NISS in the north of Vietnam and isolates from patients with confirmed A/H5N1 infections during 2009-2013. Pyrosequencing was used to detect mutations: H275Y (for A/H1N1 and A/H5N1), E119V (for A/H3N2) and I117V(for A/H5N1). The neuraminidase inhibition (NAI) assay was used to determine the IC_{50} values for all influenza A and B isolates. **Results:** All 19 seasonal A/H1N1 samples collected in 2009 showed H275Ymutation on the NA gen, and the IC_{50} values observed from six isolates (6/19) were 1000-fold higher than baseline. A total of 215 samples and 27 A/H1N1pdm09 isolates were tested; we determined H275Y on three (0.7%) samples and referred with IC_{50} values ranging from 118.59 to 127.91 nM (i.e. >200-fold higher than baseline). Other subtypes A/H3N2 and A/H5N1 were determined to be sensitive to oseltamivir by both pyrosequencing and NAI assays. Influenza B (67 isolates) was determined to be sensitive to oseltamivir as IC_{50} values were within the susceptibility range. **Discussion:** Mutations associated with oseltamivir-resistance were identified in seasonal influenza A/H1N1 and A/H1N1pdm09 viruses from northern Vietnam. The circulation of influenza A/H1N1pdm09 and H5N1 viruses is continuing. Seasonal influenza vaccines and human H5N1 vaccines are not currently available in Vietnam, underscoring the need for effective treatment. To control the efficacy of oseltamivir for treatment, active surveillance for oseltamivir resistance among influenza viruses circulating in Vietnam should be expanded.

Board 189. Estimated Numbers of Community Cases of Non-typhoidal *Salmonella* Infections in Guangdong Province, China

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Background: China has very limited information on epidemiological burden of specific foodborne pathogens, and the establishments of surveillance systems on foodborne diseases are still at its initial stage. This study estimated the number of nontyphoidal *Salmonella* infections in Guangdong in 2012, by using the burden of illness (BOI) pyramid model, and also make a comparison between active and passive surveillance strategies on foodborne diseases. **Methods:** A laboratory-based surveillance is conducted among patients with diarrhea in 27 sentinel hospitals in Guangdong Province, China. Stools from diarrhea cases were cultured for several enteric pathogens, including nontyphoidal *Salmonella*. A population-based survey among residents of surveillance sites were conducted, and data from the National Notifiable Disease Reporting System (NNDRS) were also collected, to estimate the percentage of cases reported at each step of surveillance system. The reported cases in the NNDRS was then divided by the percentages to yield the actual number of cases. Multipliers of both active surveillance and passive systems were calculated for the surveillance strategies comparison. **Results:** With high ratio of cases losing at each steps of surveillance, for every case of nontyphoidal *Salmonella* infection under passive surveillance, there were an estimate 294.1 cases annually in the Guangdong population, yielding a total of 291539 (95%*CI*: 251485-342474) nontyphoidal *Salmonella* infections, and an associated incidence of 279.5 (95%CI: 241.1-328.3) cases per 100,000 persons. While under active surveillance, with underestimates adjusted, there were 20.4 estimated cases for every nontyphoidal *Salmonella* infection case confirmed by the surveillance system. **Conclusions:** The estimate of the annual nontyphoidal salmonellosis highlighted that the nontyphoidal salmonellosis presents a serious burden to public health in Guangdong Province. By using the BOI pyramid model and sentinel active surveillance system, the active surveillance present remarkable advantages in making more accurate estimate of epidemiological burden imposed by pathogen specific foodborne diseases than passive surveillance.

Board 190. Timeliness of Oman Communicable Diseases Surveillance System

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Background: Public health surveillance is the ongoing and systematic collection, analysis, interpretation, and dissemination of data regarding a health-related event for use in public health action to reduce morbidity and mortality and to improve health. Data disseminated by a public health surveillance system can be used for immediate public health action, program planning and evaluation, and formulating research hypotheses. To ensure that problems of public health importance are being monitored efficiently and effectively surveillance systems are evaluated. The evaluation of public health surveillance systems should involve an assessment of system attributes, including timeliness. The timeliness of a public health surveillance system should be evaluated in terms of availability of information for control of a health-related event, including immediate control efforts, prevention of continued exposure, or program planning. Timeliness reflects the speed (time interval) between steps in a surveillance system. This is an indirect evaluation of the timeliness of the communicable diseases surveillance system at the governorate level in Oman during the first quarter of 2014. **Method:** Communicable diseases notifications from the health institutes are faxed to the surveillance system at the governorate level. Where the information are then entered into electronic format using EpiData 3.1 software. The electronic REC files then should be sent, by email, weekly (on Monday of the next week) by the epidemiologist to the national level. In this assessment the date on which the REC files sent to the national level was noted and evaluated as being on time or not. Then the "not on time" are further scaled into a three point of Likert scale, as < 3 days late, >3 days late and not sent. **Result and Conclusion:** Overall, there was a big difference between the governorates in term of timeliness of sending the weekly communicable diseases REC files. Although both S. Batinah and Alwusta governorates had the highest proportions in sending the information on time. But none of the governorate sent the information on time for the entire 13 weeks (Figure 1). Figure2 shows the Likert scale. The use of electronic data collection from reporting sources (web-based), as well as the data interchange by the surveillance system, could promote timeliness.

Board 191. The Potential Impact of Changing Diagnostics on Surveillance for Invasive Bacterial Infections: Emerging Infections Program's Active Bacterial Core Surveillance (2014)

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Infections Program, Hartford, CT, USA, [9]Maryland Emergining Infections Program, Baltimore, MD, USA

Background: Active Bacterial Core surveillance (ABCs) is active, laboratory and population-based surveillance for invasive group A *Streptococcus* (GAS), group B *Streptococcus* (GBS), *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Neisseria meningitidis* and methicillin-resistant *Staphylococcus aureus* (MRSA) at 10 sites in the United States. Cases are defined by isolation of one of these organisms from a normally sterile site. The use of culture-independent diagnostic tests (CIDTs), including nucleic acid tests (NATs), has the potential to fundamentally change the way surveillance systems measure disease burden. We conducted a survey to determine current use of NATs in labs that serve the ABCs catchment area. **Methods:** A web-based or telephone survey of all labs that serve a subset of the ABCs surveillance population (catchment of ~30 million persons) was conducted in the fall of 2014. The survey asked whether facilities offered NATs that can identify ABCs pathogens from positive blood cultures or that can directly detect them from sterile sites (e.g. whole blood, cerebrospinal fluid). **Results:** We received responses from 234 (89.3%) of 262 eligible labs representing 9 of 10 ABCs sites. Eighty-one percent were hospital labs, 10% were commercial or private reference labs and 4% were public health labs. Twenty-seven labs (12%) had the capability to use NATs to identify pathogens from positive blood cultures. Of those with this capability, 16 (60%) still obtain cultures for all ABCs pathogens and 7 (26%) only obtain cultures if *S. aureus* is identified. Thirty-six (15%) labs had the capability to use NATs to directly detect at least one ABCs pathogen from a sterile site. The most common pathogens that could be detected this way were MRSA (6% of all labs), *N. meningitidis* (2%) and *S. pneumoniae* (2%). **Conclusions:** ABCs has relied on a specific case definition based on culture to determine disease burden trends. Only 6% of labs reported being able to directly detect at least one ABCs pathogen without concomitant culture, so isolation appears to remain the main method of microbiologic identification. Surveillance systems, including ABCs, must monitor changes in the use of diagnostic tests in order to continue to make a meaningful impact on public health policies and priorities.

Board 192. The NCBI Pathogen Pipeline: Supporting Surveillance of Bacterial Foodborne Pathogens with a Whole Genome Sequencing Analysis Pipeline to Deliver Real Time Results

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Background: The identification of common sources of contamination from food products that cause disease and sickness in people is critical for quickly resolving outbreaks. For bacterial pathogens the highest resolution is obtained when using the whole genome sequence to cluster isolates that come from a common source. A number of agencies in the US, including FDA-CFSAN, CDC, USDA-FSIS, and state and public health laboratories have started national genome sequencing projects to improve surveillance methods: 1) all of the food and clinical *Listeria* isolates collected within the US since Sept 2013, 2) retrospective and prospective food and environmental *Salmonella* isolates, 3) *Salmonella* Enteritidis clinical samples from select states, 4) the 100K pathogen diversity project. NCBI has collaborated with these agencies to provide database and analytical support for whole genome sequencing for surveillance. **Methods:** Once sequencing is completed in federal and state public health labs the raw sequence reads are submitted to the NCBI Sequence Read Archive, and the sample metadata to the Biosample database using a template to describe foodborne pathogens. The data are integrated globally from all public submissions by the NCBI pipeline to produce in real time: 1) assemblies generated from the raw reads, 2) a distance tree based on comparison of kmers extracted from the assemblies in GenBank and those submitted from the public health agencies to obtain rough clusters, 3) tight clusters based on SNPs for closely related isolates. **Results:** As of Sept 5, 2014, 8810 samples have been sequenced and the raw reads submitted to NCBI including 1) 1775 *Listeria*, 2) 6694 *Salmonella*, 3) and 341 *E. coli*. The NCBI analysis pipeline results were reported back to the public health agencies. A real time demonstration showed results were obtained in under 6 hours once the sequences were deposited. **Discussion:** Whole genome sequencing has been used to quickly establish the similarity of isolates from clinical patients and a contaminated food products, distinguishing isolates that were part of the outbreak from those that were not. The elimination of false positives and negatives to speed up epidemiological investigations is greatly enhanced by using genome sequences where the comparison results have the resolution of millions of base pairs.

Board 193. Hospital-based Severe Acute Respiratory Infection (SARI) Surveillance System in Indonesia, 2013-2014

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Background: Indonesia established a hospital-based severe acute respiratory infection (SARI) surveillance system in 6 hospitals geographically dispersed around Indonesia to monitor influenza disease and virological trends. The aim of this study was to assess the proportion of influenza among SARI cases and to describe influenza vaccination history of SARI cases. **Method:** Inpatients meeting the World Health Organization's SARI case definition (an acute respiratory infection with history of fever or fever ≥ 38oC, cough, onset of symptoms within 10 days, and hospitalization) were enrolled and interviewed by hospital SARI teams. Nasal and throat swabs were collected and tested for influenza virus by rRT-PCR. Data were analyzed descriptively to calculate proportion of influenza-positive SARI cases and assess frequency of vaccination history. **Results:** In May 2013 to August 2014, from 92,295 inpatients, 1,046 (1%) were identified as SARI cases. Mostly SARI cases were aged 1-4 years (39%) and <1 year (28%). Of 978 specimens tested, 133 (14%) were influenza-positive with subtype A/H3N2 (43%), A/H1N1pdm09 (19%), and type B (38%). Of the 133 influenza-positive cases, 14% were active smokers, 12% had asthma, and 8% had Chronic Obstructive Pulmonary Disease (COPD). One patient, a 54 year-old female with influenza B virus infection, died. Only 4 out of 1,046 SARI cases (0.4%) had influenza vaccination history. None of the influenza positive cases reported prior vaccination. **Conclusion:** This system provided information on the clinical presentation of SARI cases in Indonesia. No influenza type A/H5N1 cases were detected from this system despite parts of Indonesia being endemic for the virus in birds. Influenza vaccination was not utilized widely. Overall, the findings from this SARI surveillance system, provide epidemiological and virological data to target groups for disease prevention policy.

Board 194. Population-based Rates of Diarrheal Disease Associated with Norovirus, Sapovirus, and Astrovirus in Kenya

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Background: Diarrheal diseases remain a major cause of mortality in Africa and South Asia. While the burden of rotavirus (RV) is well described, population-based rates of disease caused by norovirus (NoV), sapovirus (SaV), and astrovirus (HAstV) are lacking, particularly in developing countries. With the expected decline of RV rates after vaccine implementation, monitoring of other diarrheal pathogens will be important to assess changes in their relative burden. **Methods:** Data on diarrheal cases were collected through a population-based surveillance platform including collection during healthcare encounters and household visits. We analyzed data from June 2007 to October 2008 in Lwak, a rural site in western Kenya, and from October 2006 to February 2009 in Kibera, an urban slum. Stool samples from patients of all ages who presented to study clinics with diarrhea were collected and tested for NoV, SaV, and HAstV by RT-PCR. Incidence estimates were adjusted by three factors: 1) proportion of patients who sought medical care among all diarrheal cases identified in household surveillance, 2) proportion of patients seeking care that visited the designated study clinics, and 3) proportion of patients from which stool specimens were collected. **Results:** Of 359 stool specimens collected and tested from Lwak and 746 from Kibera, 94 (26%) and 214 (29%) tested positive for NoV, 15 (4%) and 49 (7%) for SaV, and 28 (8%) and 31 (4%) for HAstV, respectively. Healthcare seeking rates among cases were lower in Lwak (28%) versus Kibera (47%), but the majority in both sites (53-80%) sought care at the study clinics. The adjusted incidence per 1,000 person-years was the highest for NoV (151 in Lwak, 86 in Kibera), followed by SaV (24 in Lwak, 20 in Kibera) and HAstV (45 in Lwak, 12 in Kibera). In both sites, children <2 years of age had the greatest adjusted incidence for all three viruses. **Conclusions:** This is the first study to estimate the community incidence of NoV, SaV, and HAstV across the age spectrum in Kenya, suggesting a substantial disease burden imposed by these viruses, although a link with disease cannot be confirmed given lack of samples from non-diarrheal controls. The high incidence of NoV-associated diarrhea, particularly in young children, highlights the consideration that targeted interventions should be considered in Kenya.

Board 195. Coccidioidomycosis: A Possibly Underreported Cause of Death—Arizona, 2008-2013

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Background: Coccidioidomycosis is a respiratory disease caused by inhalation of *Coccidioides* species spores from soil. In Arizona, despite increased incidence of reported coccidioidomycosis during 1990-2012 (from 5.2 to 198.8/100,000 persons), the age-adjusted mortality rate was unchanged at ~10.6 deaths/1,000,000 persons. We compared coccidioidomycosis-attributable deaths (CADs) derived from death certificates with hospital discharge data to validate mortality surveillance. **Methods:** Arizona death certificate CADs were defined as any coccidioidomycosis-related *International Classification of Disease* (10th rev.) (ICD-10) codes/text that included "coccidioidomycosis" or "valley fever" listed in causes or conditions contributing to death. Hospital discharge data CADs were defined as deceased at the hospital with a coccidioidomycosis ICD-9 diagnostic code; if no matching death certificate CAD, a death certificate and laboratory-confirmed reported coccidioidomycosis were required. We estimated total CADs for 2008-2013 among Arizona residents by capture-recapture analysis. Hospital discharge data CADs with a matching death certificate were compared with those without a death certificate match. **Results:** During 2008-2013, a total of 530 reported death certificate CADs (incidence: 13.6 deaths/1,000,000 persons) were reported compared with 580 hospital discharge data CADs (incidence 14.9 deaths/1,000,000 persons). Of these 580 hospital discharge data CADs, 251 (43%) were identified in death certificates. Capture-recapture estimated CADs at 1223 (incidence 31.4 deaths/1,000,000). Among the 329 hospital discharge data CADs without matching death certificate, median age was 64 (range: 4-92) years; 205 (65%) were male; 215 (65%) were white non-Hispanic; 29 (9%) were black non-Hispanic, and 21 (6%) were American Indian; 50 (15%) were Hispanic; 152 (46%) were immunocompromised; and 64 (19%) had disseminated coccidioidomycosis. There were no significant differences compared with hospital discharge data CADs with a matching death certificate. **Conclusions:** CADs are underreported two-fold on Arizona death certificates, demonstrating a need for education of death certifiers to document coccidioidomycosis mortality.

Board 196. Annual Burden of Acute Infectious Diseases in Ambulatory Care Settings—United States, 2006-2010

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Background: Disease burden estimates are important for planning and tracking the effectiveness of public health interventions. Infectious diseases (IDs) potentially transmitted by water result in >2500 deaths and >40,000 hospitalizations annually in the United States. However, the majority of infections are probably treated in ambulatory care settings, where precise diagnoses and modes of transmission are usually not captured. We aimed to estimate the annual acute ID burden in outpatient offices (including physician offices and hospital outpatient departments) and emergency departments (EDs). **Methods:** We analyzed National Ambulatory Medical Care Survey and National Hospital Ambulatory Medical Care Survey visit data from 2006-2010. We used weighted analyses to generate nationally representative estimates of the annual frequency of visits to outpatient offices and EDs for seven acute ID categories: acute gastrointestinal, acute upper respiratory tract, acute lower respiratory tract, dermatologic, opthalmologic, otitis media, and otitis externa. **Results:** IDs were diagnosed in 168 million ambulatory visits, or 14% of all visits. The ID visit rate was 564 visits per 1000 persons. Most (84%) of ID visits occurred in outpatient offices, and 16% occurred in EDs. In outpatient offices, upper respiratory tract infections were the most common reason for ID visits (54 million/year), followed by dermatologic infections (25 million/year) and lower respiratory tract infections (21 million/year). In EDs, upper respiratory tract infections were the most common reason for ID visits (7 million/year), followed by gastrointestinal infections (6 million/year) and lower respiratory tract infections (6 million/year). Gastrointestinal infections had the largest proportion (29%) diagnosed in EDs. **Conclusions**: About one in seven visits to ambulatory care settings resulted in an ID diagnosis. Although the proportion of ambulatory ID visits resulting from waterborne transmission is unknown, many IDs are preventable through water, sanitation, and hygiene interventions. When combined with attribution data, these estimates can be used to direct research and inform providers and policymakers of the impact of potentially preventable infectious diseases in these settings.

Board 197. Global Health Benefits from Investments in Robust Surveillance Systems

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Background: Surveillance is the cornerstone for prevention and control of emerging public health threats. The 2005 International Health Regulations (IHR) obligated all national governments to meet core surveillance requirements. By June 2012, only 40 of the 194 jurisdictions (20%) had complied with IHR. Despite the potential to galvanize support for global health investments in surveillance, outbreaks that have spread to multiple countries, such as the current Ebola virus disease (EVD) epidemic, are inadequately described. **Methods:** We analyzed web-based data on EVD collected during 2000-2014 to assess the number of countries and regions involved, human illnesses, deaths, and whether the outbreak was declared a public health emergency of international concern (PHEIC). To assess the affordability of robust surveillance, for countries involved in EVD outbreaks, we obtained national gross domestic income (GDI) in 2013 US$ from World Bank indictors. **Results:** Nine countries in four regions reported EVD outbreaks during the study period. As of October 17, 2014, there have been 10260 EVD infections and 5046 deaths. Although the majority of cases (87.5%) occurred in 2014, 9.8% of the cases occurred in Uganda during 2001-2012. Prior to 2014, EVD outbreaks occurred in four countries in two regions, Africa and Asia. The 2014 outbreak, which was classified as a PHEIC, has spread to Spain in Europe and to the United States in North America, involving two additional regions. All countries involved in EVD outbreaks prior to 2014 had total GDI of $414.1 billion while the two that were only involved in the 2014 outbreak, Spain and the US, had combined GDI > $18.36 trillion. **Conclusions:** The current EVD outbreak underscores the urgent need for collaborative efforts to ensure reliable surveillance systems in all countries. During the past decade, Ebola virus outbreaks occurred in multiple countries across two regions and most recently in two additional countries in separate regions. While the current outbreak is the largest ever, previous outbreaks had caused >1000 human illnesses, predominantly in countries with limited resources. A fraction of national incomes invested in surveillance systems would meet IHR requirements as well as strengthen efforts to detect and quickly prevent the spread of pathogens such as Ebola.

Board 198. Ability of the National Influenza Surveillance, Bangladesh (NISB) to Inform Influenza Response in Bangladesh

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Background: The Institute of Epidemiology, Disease Control and Research (IEDCR) established the National Influenza Surveillance Bangladesh (NISB) in May 2010 to understand the burden of influenza and to monitor strains of influenza virus in the community. These parameters are important to mitigate the impact of influenza on public health. Data completeness and timeliness are important to measure whether the system can support identification of circulating strains and provide linked epidemiological data to initiate responses to outbreaks. We conducted a study to evaluate the timeliness and data completeness of NISB. **Methods:** We used CDC's 2001 guidelines to evaluate surveillance systems to assess data quality and timeliness of NISB. Three case entry forms submitted to NISB from each of seven surveillance sites were randomly selected from each month from June 2013-December 2013. We also reviewed the NISB registrar book which records all samples submitted to IEDCR's central lab. **Results:** The average time from sample collection to receipt at the central lab was from 24 to 36 hours for the 126 case entry forms reviewed. This is below the NISB's Lab Protocol reference time of 72 hours or less. Laboratory testing, data analysis, and reporting were complete for every month. An updated report was found for each month on the IEDCR website. Samples were collected twice a month from all sites on scheduled days. For data quality, date of interview, specimen collection, and unique identifier were reported in 100% (126/126) of forms, patient's demographic data in 67% (84/126), patient's symptoms in 83% (105/126), and history of treatment and exposure in 0% (0/126) of cases. No forms were completely filled out and there was no mechanism for error checking. **Conclusions:** NISB is a system that provides timely sample delivery and reporting but the data is often incomplete. Timeliness supports prompt response to influenza events but missing exposure data and demographic characteristics hinders responders from using the system to improve the health of the community. Data collection completeness can be enhanced by assigning a person in every surveillance site who implements regular data quality checks of the case report forms to ensure the quality of NISB data.

Board 199. Enhancing Surveillance of Emerging Infectious Diseases Using Mobile Data Collection and Open Data Kit (ODK) Technology: A Cross-sectional Study of Febrile Patients in Kilombero, Tanzania

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Background: Traditional paper-based data collection systems for disease surveillance pose many challenges related to cost, timeliness and quality of data. Recent developments of mobile devices and open source softwares have allowed for innovative methods of efficient data collection and data sharing from remote areas. **Methods:** In the context of surveillance for acute febrile illness in a rural setting in Tanzania, we assessed feasibility, timeliness, data quality and user acceptability of android Samsung tablets, using an Open Data Kit (ODK) application for remote data collection. Case report forms and epidemiological surveys were programmed into ODK with skip patterns and validation checks to enhance quality control. Electronic data were submitted over the internet to a secure password-protected formhub web server using the phones 3G internet. We concomitantly utilized paper-based method which was manually entered into a separate database for comparison. We later merged these two databases and conducted double-entry data comparisons so as to identify entry discrepancies. **Results:** From June 11th- July 12th, 2014, 205 febrile patients were enrolled and all patient data was entered both electronically and manually. The electronic patient data was automatically uploaded to the server and this enabled us to continuously monitor and fix issues with the data collection process as the study continued. It was so laborious to revise the paper questionnaires based on the feedback from the training than it was for the electronic system. The paper-based system was more expensive (USD ≈1724) than the electronic (USD ≈1000) system which eliminated paper printing, mailing and data entry costs. All three study clinicians expressed high user acceptability on the use of the tablets, citing programmed validation checks and automated skip

patterns which reduced the average time required to complete the study surveys, while minimizing human error in data entry. **Conclusions:** Mobile-based data collection with open source technologies is feasible in resource-constrained settings. The real-time submission of data reduced cost, facilitated timely availability of accurate information for decision-making and improved the efficiency of data collection.

Board 200. Understanding Lyme Disease Surveillance: Burden, Alternative Approaches, and Degree of Misclassification

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Background: Maryland ranks in the top 14 states for reported Lyme disease (LD) cases. In 2009, 4,768 LD reports were received and entered into the surveillance database by the 24 local health departments (LHDs). More LD reports were received, although with limited resources, LHDs cannot investigate all reports. Thus, many are not classified nor entered into the surveillance database. Use of ICD9-CM billing codes have been suggested as a possible alternative to traditional surveillance methods. We aimed to assess: (1) the burden of LD surveillance on LHDs, (2) the utility of ICD9-CM billing codes to identify LD cases for surveillance, and (3) the degree of case misclassification. **Methods:** During 2009-2012, we surveyed LHDs to determine how many LD reports were not investigated among all received. To evaluate the use of ICD9-CM codes, we requested codes from providers for a 10% sample of the 2009 LD reports and determined the proportion having the LD code, 088.81, by case classification (Confirmed, Probable, Suspect, and Not A Case) . We reviewed medical records of sampled reports to calculate a multiplier for Suspect and Not A Case reports that could be reclassified as Confirmed or Probable according to the national surveillance case definition for LD. **Results:** For each of the 4 years under study, LHDs did not investigate an average of 3,845 (range 2,462-5,722) LD reports, resulting in an average of 7,952 (range 5,764 -10,490) LD reports received annually. The LD code, 088.81, was reported for 39% of Confirmed; 27% of Probable; 22% of Suspect; and 27% of Not A Case reports. Following record review and reclassification of Suspect and Not A Case reports, we determined that 36% (CI=22%, 51%) of Suspect Cases and 6% (CI=2%, 14%) of Not A Case reports should be classified as Confirmed or Probable cases. **Conclusions:** With thousands of LD reports received annually, LD surveillance is a burden on the public health system, especially in the face of competing public health priorities. Using the LD billing code does not appear to be a viable alternative to identify LD cases for surveillance purposes. Based on the percent of our Suspect and Not A Cases being reclassified, we estimate that our 2009 data would yield an additional 270 Confirmed and Probable LD cases.

Board 201. Flu News Europe—A Joint Collaboration of Influenza Surveillance in the European Region

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Background: Data from a regional influenza surveillance network of 50 countries in the World Health Organization (WHO) European Region, coordinated by the WHO Regional Office for Europe and the European Centre for Disease Prevention and Control (ECDC), are collected and published online in Flu News Europe. Building on the legacy of the WHO EuroFlu Bulletin and ECDC Weekly Influenza Surveillance Overview, this network launched in week 40/2014 and aims to provide a comprehensive view of influenza activity in the European Region. **Methods:** Influenza data are reported weekly to The European Surveillance System (TESSy) database during the influenza season (week 40 to week 20 in the following year). Some countries also report during the interseasonal period. A survey of current case definitions and surveillance methods used in the 50 countries was performed in March 2014 to better understand and interpret data across Europe. **Results:** Influenza surveillance in the network is based on nationally organized physician networks covering ≥ 1- 5% of the country's population. Influenza-like illness (ILI) data is reported by 43 countries, acute respiratory infections (ARI) by 23, and both by 18. Primary care surveillance based on a sentinel system is reported by the majority of countries (80% for ILI and 70% for ARI), while others report data from all health facilities (universal surveillance). Severe disease data is reported from 19 countries: 13 countries, mainly in the eastern part of Europe, conduct sentinel surveillance for hospitalized cases with severe acute respiratory infection (SARI), while 6 report laboratory-confirmed intensive care unit cases. Populations under surveillance and data formats differ among these countries. Semi-quantitative indicators of national intensity, geographic spread and trend of influenza activity are also reported. The majority of countries use the WHO or European Union (EU) case definitions (73% for ILI and 64% ARI) and 51% of the countries performing SARI surveillance use the WHO case definition. **Conclusion:** Flu News Europe provides comprehensive influenza surveillance data from a network of 50 countries covering a population of 900 million people. This unique surveillance platform allows for better understanding and interpretation of influenza activity in the European Region.

Board 202. Suite for Automated Global Electronic Bio-Surveillance (SAGES) Update: Re-engineering Software to Improve Ease of Installation, Use, and Sustainability

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Background: SAGES is a suite of open source software tools that enables electronic disease surveillance in resource-limited settings. The SAGES architecture uses mobile and web-based methods to collect surveillance data from SMS, Wi-Fi, and Internet connected devices. The past five years have seen significant advancements in open-source software, technological approaches to data collection and analysis, and our understanding of the issues involved with deployment of SAGES systems. All of these factors called for a re-engineering effort to improve our SAGES tools, and address emergent technical issues in electronic disease surveillance. At the same time, while our initial engagement strategy of customized installations was successful, it required significant external technical support during installation and hampered independent configuration of SAGES tools. **Methods:** We followed a structured spiral systems engineering process that encompasses critical needs assessment, capability assessment, concept exploration, solution validation, solution implementation, and deployment. We conducted analyses of alternative current software technologies that would meet the original objectives of

the SAGES suite, while keeping in mind the trade-offs between designing customized systems versus designing generic '80% solution' systems that are closer to functioning 'out of the box'. **Results:** Our re-engineering effort has resulted in SAGES tools which are easier to install, configure, and use. Users now have significantly improved web and mobile interfaces, with greater flexibility when querying the data and generating analysis products. The result is an improved 'out of the box' capability while still allowing advanced developers to enhance or customize SAGES systems. **Conclusion:** The SAGES project is intended to enhance electronic disease surveillance capacity in resource-limited settings around the world. We have re-engineered our SAGES electronic disease surveillance tools with an eye toward ease of installation and use, with an ultimate goal of creating a self-sustaining SAGES users community. We believe the SAGES tools facilitate local and regional electronic disease surveillance, regional public health collaborations, and increased WHO IHR 2005 compliance.

Board 203. Multiagency and Multidisciplinary Collaboration for Improved Integrated Real-time Whole Genome Sequence Surveillance of Foodborne Pathogens in the United States

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Background: Accurately and quickly identifying sources of foodborne outbreaks is critical for their control and prevention. Whole genome sequencing (WGS) offers enhanced specificity in identifying strains of foodborne pathogens isolated from ill people, foods, and food manufacturing/processing environments. Comparing whole genome (WG) sequences of isolates with accompanying epidemiological evidence in real time helps identify sources of outbreaks and timely public health and regulatory action. Collaboration among laboratory and food scientists, bioinformaticians, and epidemiologists at federal, state, and local levels is essential for the integration, interpretation and use of WGS information. HHS/FDA, HHS/NCBI, HHS/CDC, and USDA/FSIS have assigned high priority to developing an integrated, laboratory-based, real-time, food safety surveillance platform. **Methods:** A pilot integrated, WGS real time surveillance system for *Listeria monocytogenes (Lm)* was launched in 2013. The system is built upon CDC-led PulseNet (the national subtyping network for foodborne disease surveillance), the FDA-supported Genome-Trakr network, and the unique large-scale bioinformatics and analytical infrastructure of NCBI. WG sequences of *Lm* and minimal metadata from all clinical, contaminated food, and environmental isolates are uploaded real time into an NCBI database. The sequences, metadata, and NCBI analyses of their relatedness are immediately available to the four agencies. Most data also are publicly accessible except for confidential information. **Results:** Public health officials at federal, state, and local levels are using information from comparisons of *Lm* genomic sequences from clinical, food, and environmental isolates in this integrated database, combined with epidemiologic information systematically collected on all cases and food trace-back information, to successfully identify sources of outbreaks. **Conclusions:** This groundbreaking, multi-agency, integrated surveillance platform is successfully providing critical information for investigating, responding to, and preventing foodborne *Lm* and *Salmonella spp.* outbreaks. Discussions are underway in considering foodborne pathogens beyond *Lm* for real time surveillance.

Board 204. Surveillance: Nontuberculous Mycobacteria Isolations from Residents of Three Counties, North Carolina, 2006-2010

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Background: Nontuberculous mycobacteria (NTM) are emerging infections among the elderly and immunocompromised but the epidemiology is poorly characterized. Reports of NTM isolation from clinical specimens is a readily available, if imperfect surrogate for disease prevalence. **Methods:** We collected reports from clinical laboratories of initial NTM isolation among residents of 3 counties with isolation dates during 2006 - 2010. Demographic data included age, gender, and race. Isolates were characterized by date of isolation, species or complex and site of sample collection. We calculated prevalence per 100,000 persons with 2010 US Census base population data. **Results:** We identified 1033 unique individuals with NTM isolation during 2006 - 2010. Of these, 51% were male, 46% were ≥60 years of age. Of the 800 with reported race, 66% were white, 23% black and 10% 'other'. Overall isolation prevalence was 15.9 per 100,000. Prevalence was highest (54.8) in those ≥60 years, and lowest (3.3) among those <20 years. Prevalence among those ≥60 years was highest among whites, 49.3 and 'other' race, 45.8. Of 945 isolates of known anatomic origin, 750 (79%) were isolated from respiratory specimens (prevalence 11.5), 5.6% were from sterile sites (0.81), 1.6% from dermal specimens (0.23), and 0.7% from catheters (0.11). Prevalence of sterile site isolation was highest: among those 20 - 39 (0.31) and 40 - 59 years (0.35); among those of black race (0.40, vs. 0.28 for whites and 0.06 for 'other' race). *M. avium* complex was most frequently identified, comprising 51% of pulmonary and 73% of sterile site isolates. Other species predominated at: dermal sites where *M. abscessus* comprised 47% of isolates; and catheter sites where *M. immunogenum* comprised 57% of isolates. **Conclusions:** This is the first population-based surveillance of NTM isolate reports in the southeastern United States. NTM isolation was highly prevalent from respiratory sites, particularly in older whites, reflecting prior understanding of the epidemiology of NTM pulmonary disease. Sterile site isolation was not rare and likely reflects a combination of disseminated *M. avium* complex in persons with advanced HIV and a mixture of disseminated NTM infections among persons with other forms of immune compromise. This abstract does not necessarily reflect EPA policy.

Board 205. Two Year Findings from an Acute Febrile Illness Enhanced Surveillance Study in Puerto Rico

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Background: Dengue has been endemic in Puerto Rico for four decades, but little is known about other acute febrile illnesses (AFI) on the differential diagnosis of dengue. To better understand the burden of dengue and other AFI, a Sentinel Enhanced Dengue Surveillance System (SEDSS) was implemented at one tertiary care and one secondary care hospitals in southern Puerto Rico. **Methods:** Patients with fever or history of fever for <7 days were enrolled and followed through their illness. Blood, urine, nasopharyngeal, and oropharyngeal specimens were collected at enrollment. Specimens were tested by RT-PCR and immunodiagnostic methods as appropriate for dengue viruses (DENV) 1-4); Influenza virus A (Flu A) and B (Flu B); ten other respiratory viruses (ORV) including adenovirus, respiratory syncytial virus, metapneumovirus and parainfluenza viruses 1 & 3; enteroviruses; *Leptospira* spp., and *Burkholderia pseudomallei*. **Results:** Of 23,627 patients presenting with AFI during May 7, 2012 through May 6, 2014, 5,325 (23%) were enrolled. Of these, 31% were hospitalized, 50% were female, and median age was 12 years (range: 0-103 years). An etiologic agent of AFI was identified in half (50%, 2,742), including DENV (35%), Flu A or B (30%), ORV (26%), enteroviruses (2%), *Leptospira* spp. (<0.1%), and *B. pseudomallei* (<0.1%). In addition, 80 co-infections were confirmed by PCR, nearly half (44%) included DENV. Most (95%) of the 717 DENV PCR positive cases were DENV-1. Dengue patients were slightly older than other enrolled patients (median age: 15 versus 9 years), but similar in age to influenza patients (median age: 16 years). Dengue patients were more likely to be admitted than other enrolled patients (OR = 2.36, 95% CI: 2.04-2.72) and influenza patients (OR = 3.37, 95% CI: 2.72-4.18). **Conclusions:** Half of all AFI cases had a pathogen detected and most cases were caused by either a DENV, a viral respiratory pathogen (Flu A, Flu B or ORV), or an enterovirus. Leptospirosis and melioidosis cases were sporadic and focal; study of these diseases may require study sites in high risk areas of the island. Reasons for why dengue cases were more likely to be hospitalized will be studied further. We expect to use SEDSS as a platform to conduct clinical and laboratory research and provide a setting for evaluating current management practices.

Board 206. Serological and Vector Surveillance Studies to Reported Rift Valley Fever Free Status in South Korea

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Background: Rift Valley Fever Virus (RVFV) is a member of the genus *Phlebovirus* in family *Bunyaviridae*. RVFV is a mosquito-borne viral disease affecting both livestock and humans. RVFV was first identified in Kenya in 1931 and reported endemic in Africa but has recently spread to Arabian Peninsula. There is great concern that the disease will spread to worldwide such as Europe, Asia and Americas. Possibility of RVFV introduction was increasing as climate change and globalization of trade in animals and animal products. Although RVFV has not been reported in South Korea and the neighboring countries so far, transmissible mosquito vectors are present. For this reason, serological and vector surveillance was conducted to confirm disease free status in South Korea. **Methods:** All sera and mosquitoes samples were collected in 2013. Animal was random selected in goats and cattle from the local Veterinary Service. Blood samples were collected and sera stored at -20°C until use. Sera samples were tested for anti RVFV antibodies using commercial kit. The mosquitoes were collected from 6 areas surrounding airport and harbor. The mosquitoes were identified and pooled into groups up to 30 specimens. Total RNA were extracted and tested by real time RT-PCR. **Results:** A total of 875 animal sera were collected and tested. Among the sample, 76.8% were cattle (n=672) and the remaining 23.2% were goats (n=203). All animal samples were negative for antibodies against RVFV. A total 661 mosquito pools were used for real time RT-PCR assay. All mosquito pooled samples were negative. **Conclusions:** RVF is reportable disease in OIE and designated first class official diseases of domestic animals in South Korea. There has been no report of presence of RVFV in South Korea. However, while increasing the risk of introduction of RVFV, serological and vector surveillance is important to monitor and decrease the potential risk in RVFV free countries. This result suggests that the disease is not present in South Korea and furthermore confirms the RVFV free status of this country. This surveillance is to be carried out continuously and the need to establish early warning system to prevent the introduction of RVFV.

Board 207. Evaluation of the National Case-based Measles Surveillance in South Africa, January 2009 to December 2013

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Introduction: Measles is a vaccine preventable disease but remains the leading cause of death among children under five years. In South Africa the case-based measles surveillance was initiated in 1998 in line with the recommendation from World Health Organization (WHO) to monitor progress towards measles elimination. Blood specimens are collected from suspected measles cases at all health facilities at district and provincial level. This study described the epidemiology of measles in South Africa from 2009-2013 and evaluated seven specific performance indicators for measles surveillance recommended by WHO. **Methods:** A retrospective descriptive analysis was conducted on secondary measles surveillance data routinely collected from measles suspected cases in all age groups from 2009-2013.The blood samples were tested at the measles serology laboratory at the NICD. The percentage for each of the indicators was calculated and compared with the WHO minimum standard values for measles surveillance. **Results:** In 2009-2011, there were 18,000 confirmed measles cases reported, which included cases identified during the measles outbreak from June 2009 to July 2010 in all nine provinces. The number of cases decreasedto335between 2011-2013. From 2009-2013 the age group most affected were those >14years, while the least affected were those between the ages of 2-4 years. Out of the seven performance indicators evaluated, five met WHO specified targets, including all districts reporting at least one measles case per year (WHO target ≥ 80% of the districts)and blood specimens collected in more than 80%of the suspected measles cases (WHO target of ≥ 80%).Two laboratory indicators did not meet the WHO targets; between 2009 and 2013, 32%, 28%, 46%, 49% and 52% of blood specimens respectively reached the laboratory within three days of being sent (WHO target ≥ 80%) and between 2009 to 2013,14%,15%,65%, 68% and 66% of blood samples respectively were tested within seven days (WHO target≥ 80%). **Conclusion:** The case-based measles surveillance met most of WHO-specified performance indicators. Addressing timeliness of specimen delivery to the laboratory, timeliness of laboratory testing and subsequent feedback of the results to the health facility will ensure proper management of cases and rapid response to outbreaks.

Board 208. Estimating the Burden of Foodborne Illness for *Campylobacter*, *Salmonella* and *Vibrio parahaemolyticus* in Japan from Laboratory Confirmed Numbers of Infections and Data from Telephone Surveys

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Background: Numbers of food poisoning and cases are reported mandatory in Japan. However, these do not exactly reflect the real burden of foodborne illnesses due to the passive surveillance nature. We estimated the burden of foodborne illnesses associated with *Campylobacter*, *Salmonella* and *Vibrio parahaemolyticus* in Japan, from laboratory confirmed numbers of infections. **Methods:** Data on laboratory-confirmed infections of three pathogens were collected from clinical laboratories from January 2006 to December 2012. The physician consultation rate and the stool submission rate were estimated from telephone population surveys for whole of Japan, conducted in summer and winter to correct for seasonal differences. Each estimate was introduced into the Monte-Carlo simulation model as a probability distribution. **Results:** Response rate was 15.2% (2,039/13,396) and the acute gastroenteritis illness rate was 4.4%, of which 18.9% sought medical care in the latest telephone survey. The physician consultation rate and stool sampling rate were estimated from the two telephone surveys as 28.2% and 5.8%. The estimated mean numbers per year of foodborne illnesses for *Campylobacter*, *Salmonella* and *V. parahaemolyticus* in whole of Japan were 4.7-11.3 million, 1.0-2.3 million, and 95-366 thousand during 2006-2012. The numbers of reported foodborne illnesses per year in Japan for the same period for *Campylobacter*, *Salmonella* and *V. parahaemolyticus*, were 1,800-3,100, 670-3,600 and 90-1,300. Considering the population of Japan, the estimated burden of foodborne illness for *Campylobacter*, *Salmonella* and *V. parahaemolyticus* for whole of Japan were 3.7-8.9 thousand, 0.78-1.8 thousand, and 74-288 per one hundred thousand population, during 2006-2012, respectively. **Conclusions:** Data from the telephone surveys gave us the latest information on patient behavior and physician practice. Our estimates revealed a significant difference between the burden of foodborne illnesses and reported foodborne disease cases associated with the three pathogens. Need for continuing active surveillance system to complement the present passive surveillance is strongly suggested, in order to identify and prioritize food safety issues more precisely and to monitor the effectiveness of risk management options.

Board 209. Biosurveillance Ecosystem—A Sustainable, User-friendly System That Meets the Needs of Global Biosurveillance Stakeholders, Analysts, and Decision Makers Alike

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Background: The BSVE is a virtual, customizable, collaborative system that ingests a wide variety of data sources: open source data; social media, point-of-need diagnostic data, national and international surveillance system data. Analytic applications "apps" within the BSVE use the aggregated data streams to provide near-real-time modeling, analyses, and visualized results. The BSVE supports the biosurveillance analysts' and decision-makers' needs by providing automated, intelligently suggested data, tools, and analyses. The BSVE also provides modern collaboration and reporting features. **Methods:** The BSVE is a cloud-based system on the Amazon (AWS) cloud using open source software and systems allowing easier integration, increased transparency for broader user base and customizability, and reduced costs due to licensing. The BSVE ingests and utilizes large data streams such as open source social media feeds, RSS feeds, disease ontologies, de-identified diagnostic results, historic outbreak data, zoonotic data, and non-health data as well as machine learning and natural language processing algorithms to intelligently identify aberrations in disease signals. **Results:** The analytic apps include a variety of applications to perform signal detection, "intelligent" searching, epidemiological curve modeling and analysis, heat mapping, social media data visualization, among others. The broad app approach allows the workbench to be customizable for operational or strategic level analysts as well as decision makers. New applications will be developed and made available to the BSVE community through a Software Development Kit (SDK) and the app store. Additionally, collaboration abilities such as chat, "circles of trust", in-system report sharing, image sharing, dataset and analysis sharing, and export capabilities from app analyses provide for user-friendly data sharing between experts, analysts, and decision makers. **Conclusions:** The BSVE will provide for a unique system that can facilitate rapid and better situational awareness across a wide variety of users, disciplines, and geographic locations. The focus on user-feedback loops and collaboration aims to augment other systems' use of structured data with analysis of unstructured and aggregated data.

Board 210. Influenza Sentinel Surveillance in Ukraine and Characteristics of Isolates During the 2014-2015 Season

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Background: Since 2008 the influenza sentinel surveillance system was existed in Ukraine in the frame of Cooperative agreement with CDC (USA). The clinical and epidemiological information were collected from 18 adult and pediatric clinics in four cities which locate in different geographical regions of the country (Kyiv, Dnepropetrovsk, Odessa and Khmelnitsky). The epidemiological and virological information collect during the whole year. **Materials and Methods:** Both epidemiological and virological data were collected on the weekly basis. The specimens (throat swabs) were tested for influenza by real-time polymerase chain reaction (RT-PCR) and viruses were isolated in MDCK and MDCK-SIAT cell culture from PCR-positive samples. **Results:** 838 samples from patients with ILI and SARI were collected during 2014-2015 influenza season. The numbers of positive samples in PCR were 176 (21%). But the proportion of laboratory confirmed influenza among SARI and ILI cases reached 50 % during the peak of the 2014-2015 season. The season 2014-2015 was caused mostly by virus B/Yamagata linage (90%). And other 10% were viruses A(H3N2) subtype. The National Influenza Center (NIC) and the sentinel laboratories in the 4 regions have isolated 129 influenza viruses on cell culture. 119 of this isolates were identified by the NIC laboratory as B influenza virus and 10 as A(H3N2) subtype influenza virus. All B isolates were related to B/Massachusetts/2/2012-like strain and all A(H3N2) isolates were related to A/Switzerland/9715293/2013-like strain.The most part of current A(H3N2) viruses no agglutinated of chicken red blood cells (RBC). We used RBC of guinea pig. The high match between SARI hospitalizations and percent of influenza positive samples demonstrates adequate of sentinel SARI surveillance in the country. **Conclusions:** The dominant influenza virus was distinguished in Ukraine and in most European and North American countries in 2014-2015 influenza season.

Board 211. Influenza in District Hospital Patients in Bangladesh: Results from National Influenza Surveillance

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Background: Data on seasonality, highly affected populations, and circulating strains of influenza virus are important to implement interventions to decrease influenza burden. Previous influenza surveillance data in Bangladesh originated from tertiary care level hospitals which tend to serve referred and severely ill patients. Our aim was to understand seasonality, highly affected populations, and circulating strains of influenza virus in patients with generally less severe and less serious illness than referral hospitals by examining outpatients attending district level hospitals. **Methods:** We analyzed data from May 2010-August 2014 from available sites of the National Influenza Surveillance (NISB). NISB captures demographic information and nasal and throat swab test results from the first 10 selected outpatients with influenza-like illness (ILI) from each of the participating sentinel district hospitals each month. ILI is defined as history of or measured fever (≥100^{0}F) and cough onset within the last 10 days. We analyzed circulating strains, patient demographic characteristics, and percent of laboratory-confirmed influenza cases from ILI patients. **Results:** We enrolled a total of 4901 ILI patients from 14 sites during 2010-2012, 7 sites during 2013, and 9 sites during 2014. Five hundred eighty-one (12%) patients were influenza positive by real-time reverse transcriptase polymerase chain reaction. Of these, 349 (60.1%) were influenza B positive, 230 (39.6%) were influenza A positive, and 2 (0.3%) were both influenza A and B positive. Among influenza A positive samples, the dominant subtype was H3 (167, 73%). Median age of patients was 10 years (interquartile range, 2-26 years) and the highest proportion of influenza positive patients was in the ≤5 year age group (216/581, 37.2%). Every year, except for 2013, there was a clear seasonality with ≥80% influenza cases identified from May to September, which is the monsoon (wet and humid) season. **Conclusions:** Influenza interventions among outpatients with generally less severe and less serious illness than patients of tertiary care hospitals should account for the May to September peak in influenza cases. Prevention strategies in this patient population should target both type A and type B influenza and focus on children ≤5 years of age.

Board 212. Development and Piloting of *Enterobius vermicularis* Surveillance System in Sri Lanka

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Background: *Enterobius vermicularis* is the causative agent of enterobiasis, which is considered to be one of the commonest human parasitic infections in the world. A considerable number of people in Sri Lanka live in poor living conditions (e.g.-slums) mostly in congested urban areas and also in the plantation sector. In Sri Lanka limited information about enterobiasis was reported due to small number of studies have been conducted to explore the distribution and risk factors for enterobiasis. Therefore, this study was designed as a preliminary study to determine the prevalence of *Enterobius vermicularis* infections, associated risk factors and the impact on nutritional status. **Method:** Children aged between 1-12 years in a poor urban and plantation area community in Sri Lanka were enrolled from September 2013 - June 2014. Socio - demographic factors and behavioral habits of children were recorded. Hemoglobin and albumin concentrations were determined in blood samples and *Enterobius* infection was investigated using cellotape perianal swab method. Anthropometric measurements were taken to calculate height- for-age (HAZ), weight-for-age (WAZ) and weight-for-height (WHZ) to determine stunting, underweight and thinness respectively. **Results:** 204 children (mean age 6.2±3.4) participated in the study and the prevalence of *Enterobius* infections was 31.9% (65/204) from cellotape perianal swab method. But only 3.9% children 8/204 had *Enterobius* eggs in stool samples. Hand washing before a meal ($p<0.001$) and after defecation ($p = 0.029$), de-worming period ($p<0.001$), and parents' education level ($p=0.001$) significantly associated with *Enterobius vermicularis* infections. 19.6% were stunt, 34.3% were underweight and 23.5% were thin. In addition, 14.5% of children had a low serum albumin level and 22.9% had anaemia. However, there was no significant association between nutritional status and *Enterobius vermicularis* infections. **Conclusions:** The identified factors will be used in the establishment of the *Enterobius vermicularis* surveillance system among children in Sri Lanka.

Board 213. Surveillance for Severe Disseminated Disease Among Reported Coccidioidomycosis Cases, Arizona, 2009-2013

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Introduction: Disseminated disease is a rare and potentially debilitating form of coccidioidomycosis. Previous studies have suggested that less than 1% of coccidioidal infections result in dissemination. Coccidioidomycosis is reportable to the Arizona Department of Health Services (ADHS). However, reports largely consist of laboratory results and lack clinical characteristics. We investigated whether routinely collected surveillance and hospital discharge data could be used to identify severe disseminated disease among reported coccidioidomycosis cases. **Methods:** Coccidioidomycosis cases reported to ADHS from 2009 to 2013 were matched to hospital discharge records from all non-federal facilities in Arizona. Hospital discharge records with admission dates between 2009 and 2013 and discharge diagnosis ICD9 codes for disseminated coccidioidomycosis [primary extrapulmonary (114.1), coccidioidal meningitis (114.2), other forms of progressive disease (114.3)] were used to define hospitalizations associated with disseminated disease. Descriptive and inferential statistics were calculated using SAS 9.3. **Results:** 1.5% (n=874) of coccidioidomycosis cases reported between 2009 and 2013 (n=57,374) were hospitalized for disseminated coccidioidomycosis. The percentage of annually reported cases that were eventually hospitalized ranged from 1.2% (n=157) for cases reported in 2012 to 2.1% (n=157) for cases reported in 2009. 86% (n=755) of all cases were admitted within a year of being reported. 58% (n=507) were admitted before being reported. 95% of cases admitted prior to report were reported within 91 days of admission. Cases with a diagnosis code for extrapulmonary disease were 2.1 (95% CI: 1.16, 3.76) times more likely to be admitted before being reported. For cases admitted after report, mean time to admission was 306 days (IQR: 40 - 484 days). Mean time to admission did not differ significantly by diagnosis code. **Conclusion:** Hospitalization due to disseminated coccidioidomycosis is rare among reported cases. Matching of surveillance and hospital discharge data can identify cases hospitalized due to disseminated disease. Further studies are needed to validate this surveillance methodology.

Novel Surveillance Systems

Tuesday, August 25, 12:30 PM - 1:45 PM

Grand Hall

Board 214. Variation by Age Group in Exposures Associated with *Salmonella* Serotype Enteritidis Infection—Foodborne Diseases Active Surveillance Network, United States, 2014

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Background: The Foodborne Diseases Active Surveillance Network (FoodNet) conducts active population-based surveillance for culture-confirmed salmonellosis in 10 US sites. *Salmonella* serotype Enteritidis (SE) accounts for 20% of salmonellosis cases reported to FoodNet; 9% occur in children aged 1-4 years. We analyzed exposure data to better understand sources of SE infection among different age groups. **Methods:** We used a case-case comparison approach to examine differences in exposures between SE cases and other *Salmonella* cases. We calculated odds ratios (aOR), adjusted for site and season during which illness occurred. We excluded outbreak- and international travel-associated infections. **Results:** In 2014, FoodNet identified 4,681 sporadic *Salmonella* cases aged ≥1 year of age; 3,161 (68%) had exposure data reported. Among these, 433 (14%) were 1-4 years, 496 (16%) were 5-17 years, 1,676 (53%) were 18-64 years, and 556 (18%) were ≥65 years old. Exposures significantly associated with SE infection varied by age. In the 1-4 year age group, SE case-patients were more likely to have consumed chicken than other *Salmonella* cases (aOR=2.8; p<0.01; 92% SE cases vs. 79% other *Salmonella* cases). In the 5-17 year age group, SE cases were more likely to have consumed chicken away from home (aOR=1.9; p<0.04; 38% vs. 42%) and sprouts (aOR=9.4; p<0.01; 5% vs. 2%) than other *Salmonella* cases. In the 18-64 year age group, SE cases were more likely to have consumed ground chicken (aOR=1.9; p=0.04; 5% vs. 6%), chicken away from home (aOR=1.5; p<0.01; 47% vs. 39%), and spinach (aOR=1.5; p<0.01; 29% vs. 22%). Among those aged ≥65 years, SE cases were more likely to have consumed unpasteurized juice than other *Salmonella* cases (aOR=5.0; p<0.01; 8% vs. 2%). The effect of adjusting odds ratios for site and season was especially apparent for the two increased risk exposures that were reported by a smaller proportion of SE cases than other *Salmonella* cases. **Conclusions:** Exposures associated with SE infection varied by age group and were influenced by site and season. Poultry consumption was associated with SE infection in all except the ≥65 years age group; the type of poultry exposure varied by age group. Information regarding risk factors among different age groups could help in designing age-specific evidence-based control measures.

Board 215. Early Indicators of Dengue Based on Date Post Onset of Fever Among Children and Adults in Puerto Rico

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Background: Early identification of dengue patients and timely initiation of correct treatment can reduce complications and mortality; however, early clinical diagnosis can be challenging as dengue has a non-specific presentation similar to other acute febrile illnesses (AFI). **Methods:** To identify early clinical predictors of laboratory-positive dengue (LPD) by date post onset of illness (DPO) of presentation, we analyzed data from the Sentinel Enhanced Dengue Surveillance System (SEDSS). Outpatients with fever or history of fever for <7 days were enrolled. Blood, urine, oropharyngeal, and nasopharyngeal specimens were collected. Specimens were tested by RT-PCR and immunodiagnostic methods for evidence of infection with dengue viruses 1-4, *Leptospira* spp., *Burkholderia pseudomallei*, five enteroviruses, Influenza A and B viruses, and 10 other respiratory viruses. We compared clinical laboratory findings, signs and symptoms from LPD and laboratory-negative dengue (LND) case-patients. Laboratory-indeterminate cases, co-infections and children aged <1 year were excluded. **Results:** Of 1,580 patients enrolled during May 7, 2012 to May 6, 2013, 617 (39%) were LPD cases, and 963 (61%) were LND cases. Half (46%) of LPD cases and 29% of LND cases were admitted to the hospital. Of the LND cases, 683 (71%) had evidence of infection with another virus or bacteria, no pathogen was identified in 280 (29%). The majority (405, 66%) of LPD cases were infected with DENV-1. Leukopenia, thrombocytopenia, rash and facial erythema were independently associated with LPD (p <0.001). Sore throat, nasal congestion and cough were less frequent in LPD case-patients. Clinical predictors of LPD varied by patient age and DPO. Predictors of LPD in patients presenting 0-3 DPO were leukopenia, rash and joint pain in children aged <9 years; leukopenia and thrombocytopenia in children aged 10-19 years; and leukopenia, rash, joint pain, nausea, and thrombocytopenia in adults aged ≥20 years. Predictors of LPD in patients presenting 4-7 DPO were leucopenia and thrombocytopenia in children <9 years old and adults, rash and leucopenia were predictors in children 10-19 years. **Conclusions:** Findings can be used to assist in early identification of dengue, as well as direct anticipatory guidance and timely initiation of correct clinical management.

Board 216. Enhanced Surveillance for Severe Group A Streptococcal Infections in Three Active Bacterial Core Surveillance Sites, 2010

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Background: Necrotizing fasciitis (NF) and streptococcal toxic shock syndrome (STSS) are severe manifestations of invasive group A *Streptococcus* (iGAS) infection, contributing to high case fatality ratios and considerable morbidity and sequelae post-infection. Incidence of these syndromes is thought to be under-estimated in the United States. We sought to identify severe iGAS cases not previously identified by routine

surveillance methods and calculate the percentage increase in measured severe disease burden. **Methods:** We reviewed iGAS cases reported by three sites, (Connecticut, New Mexico, and New York; 2010 population 7.6M), participating in Active Bacterial Core Surveillance (ABCs), an active, population- and laboratory-based surveillance network. Routine surveillance practices utilized review of medical records and discharge summaries to identify NF and STSS cases. Enhanced surveillance captured clinical diagnostic criteria for STSS and soft tissue necrosis via retrospective chart review. We defined severe iGAS as iGAS cases with NF, STSS, septic shock or resulting in death. **Results:** Of the 335 iGAS cases reported via routine surveillance, 61 (18.2%) had one or more severe syndromes indicated in the discharge summary; 23 (6.8%) had NF, 12 (3.5%) had STSS and 44 (13.1%) had septic shock. Sixteen cases died without a reported diagnosis of NF, STSS or septic shock. Enhanced surveillance for severe iGAS cases identified 99 cases with one or more severe manifestation; 34 (10.1%) had NF, 62 (18.5%) had STSS, 57 (17.0%) had septic shock, and 9 cases died without reported NF, STSS or septic shock. Severe iGAS cases identified via enhanced surveillance included all those reported by routine surveillance. Percent increases of severe diagnoses detected via enhanced surveillance were 48% for NF, 417% for STSS and 30% for septic shock. Surgery, debridement, amputation or rehabilitation was reported for 23.5%, 19.2%, 8.1% and 20.2% of severe iGAS cases, respectively. **Conclusions:** Enhanced iGAS surveillance allows for a more complete understanding of severe iGAS disease burden. Improvements in disease recognition and surveillance are warranted for revised incidence estimations of these severe syndromes and accompanying post-infection sequelae.

Board 217. Rabies Response: A Novel Approach to Animal Bite Surveillance in Georgia

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Background: Rabies is endemic in Georgia wildlife; each year 350-450 animals are confirmed with rabies. Timely and complete reporting of animal bites is critical in preventing human and domestic animal rabies. Although animal bites are reportable in Georgia, prior to 2012 there was no central mechanism to capture reports from numerous agencies. In 2011 the Georgia Department of Public Health (DPH) developed the Animal Bite Module (ABM), an expansion of the web-based State Electronic Notifiable Disease Surveillance System (SendSS). The ABM is a single portal for capturing animal bite data, including bite investigation and laboratory results. Training for the ABM was completed in mid-2012 and went live statewide in January 2013. **Methods:** Animal bite data pre-ABM was compared with data collected in the ABM during an equivalent period of time (14 months) to evaluate improvements in bite incident capture and documentation of follow up. A post-ABM implementation survey was administered to 471 users to assess system attributes and user satisfaction. **Results:** Between 1/2009 - 3/2010 (pre-ABM), 3601electronic bite reports were entered in the non-ABM SendSS database. From 1/2013 - 3/2014, 11216 bite incidents were captured in the ABM. Of the 142 (30.0%) survey responders, 134 (93.1%) indicated agency use of the ABM to report all animal bites. 103 (78.0%) reported the ABM as the same or better than previous reporting tools. Users also provided feedback on ways to improve the system. 52 (36.1%) of users were dissatisfied with closing an incident, survey comments indicated that better search options and auto-population functions were needed. **Conclusions:** The number of bites reported after ABM implementation increased 3.1 times compared to a similar period pre-ABM suggesting the ABM provides a centralized user-friendly system for collecting animal bite data. Data captured in the ABM are more complete as it includes laboratory results and animal disposition information, both critical for rabies post-exposure prophylaxis risk assessment. Survey results led to improvements in the system e.g., a search function for microchip information and auto-population for addresses. The ABM is a novel system which has improved animal bite surveillance in Georgia and increased opportunities for rabies prevention and control interventions.

Board 218. Medical Examiner Investigated Norovirus Deaths, Minnesota, 2006-2014

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Background: Since 1996, deaths investigated by medical examiners (MEs) that are unexplained and appear to be associated with an infectious cause are reportable to Minnesota Department of Health (MDH) Unexplained Critical Illness and Death Project (UNEX). Priority is given to cases <50 years of age with no significant underlying conditions; however, any reported ME case with infectious disease hallmarks may be investigated. Norovirus is the leading cause of acute gastroenteritis in the US. While rare, norovirus deaths do occur. We investigated cases reported to MDH to identify deaths potentially caused by norovirus. **Methods:** We reviewed cases investigated from 2006 to 2014. Autopsy and death scene investigations were used to target testing for an etiologic agent. Fecal samples were collected at autopsy from deaths that were suspected to be associated with a gastrointestinal syndrome. Norovirus was detected at MDH Public Health Laboratory utilizing reverse transcription polymerase chain reaction (RT-PCR). **Results:** We identified 37 UNEX cases with an associated gastrointestinal syndrome, 21 (57%) had specimens available for testing. Norovirus genogroup II was identified in colon contents of 4 (19%) cases including a 4-month-old sudden unexplained infant death whose mother had a 48-hour history of vomiting and diarrhea prior to the infant's death; a 1-year-old child with multiple congenital abnormalities included hypertrophic cardiomyopathy; a 47-year-old female with a history of panhypopituitarism; and a 69-year-old male with no underlying health conditions. Three cases had a history of vomiting and diarrhea yet only the child received medical treatment prior to death. The infant case had no known symptoms prior to death. **Conclusions:** UNEX surveillance in collaboration with MEs has enabled identification of potential infectious causes of death. We identified norovirus in approximately 20% of cases with available specimens and an associated gastrointestinal syndrome. Our findings support that individuals with underlying conditions are at higher risk for severe outcomes despite our surveillance focus on cases without co-morbidities. It is important for individuals with underlying conditions to seek healthcare for acute gastroenteritis to prevent potential complications from existing conditions.

Board 219. Linking HIV Diagnostic Testing Algorithm Electronic Laboratory Reports by Local Codes in the New York State Surveillance System

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Background: Accurate processing of diagnostic lab reports transmitted to health departments via electronic laboratory reporting (ELR) assists in identifying new HIV diagnoses. The three-step HIV diagnostic testing

algorithm (DTA) recommended by the Centers for Disease Control and Prevention and Association of Public Health Laboratories poses new challenges. As DTA components can be ordered and reported separately and potentially performed by different labs, linking results from a single specimen can be difficult. This analysis describes an ELR needs assessment and a strategy to link DTA components within the New York State (NYS) Department of Health (DOH) HIV surveillance system. **Methods:** To determine the potential volume of reports, a survey was administered to 266 labs applying for NYS Clinical Lab Permit renewal. For labs currently reporting, ELR procedures, test panels, and reported Logical Observation Identifiers Names and Codes (LOINC) obtained by lab communication and analysis of surveillance reports were aggregated. HIV surveillance data received October to December 2013 were used to assess the efficacy of LOINC versus lab test panel or result test code (local codes [LC]) to accurately link DTA components. LC identify specific tests or series ordered and results of those tests; LOINC classifies test method performed and is used by NYSDOH to link DTA steps. DTA step 2 results (N=121) from one high-volume lab were used for a focused analysis. **Results:** Of labs surveyed (N=266), 206 used or expected to use the DTA. The DTA was used by 31 of 86 labs currently reporting to NYSDOH; 30 populated LC and 29 reported LC specific to DTA components. LC reflected the clinician order and identified 100% (N=121) of reported step 2 only or step 2 and 3 DTA results. Conversely, based on LOINC, the results appeared to be lab reporting gaps. **Conclusions:** Our findings indicate the need to recruit labs performing DTA components for NYS residents and/or providers. Although 100% populated, LOINC alone did not identify the series of tests performed on a specimen. However when populated, LC accurately identified and linked DTA steps to a single specimen, enabling accurate assessment of the completeness of reporting. Health departments should incorporate LC into ELR surveillance procedures and quality assurance methods with high confidence.

Board 220. Claims Data Evaluation for Lyme Disease Surveillance—Tennessee, 2011-2013

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Background: Lyme disease (LD) is the most frequently reported tickborne disease in the United States, with >36,000 cases reported during 2013. Although Tennessee reported only 25 LD cases during that time, a recent study of claims data estimated >200 cases may have occurred. We analyzed claims data to investigate their utility for supplementing LD surveillance. **Methods:** We examined LD cases reported to the Tennessee Department of Health (TDH) during January 2011-June 2013 that met the Council for State and Territorial Epidemiologists (CSTE) case definition and compared them with cases identified during the same period by Blue Cross Blue Shield (BCBS), a managed care organization covering ~50% of Tennesseans. We evaluated BCBS cases, defined as a Tennessee resident beneficiary with ≥3 primary or secondary *International Classification of Diseases, Ninth Revision* (ICD-9) codes for LD (088.81) recorded in their claims. Medical records of BCBS cases were randomly sampled to abstract and classify cases per CSTE case definition. **Results:** During the study period, 74 LD cases were reported to TDH, and 391 BCBS cases were identified. Five cases matched in both datasets. Of BCBS cases, 123 (31%) were sampled; 4 (3%) met the CSTE case definition for LD. Of the remaining 119 cases, 22 (18%) were subsequently ruled out by laboratory testing, 53 (45%) had a history of Lyme disease before the study period, 27 (23%) lacked sufficient evidence for case classification, and 17 (14%) lacked an available medical record. **Conclusions:** Our claims data review identified additional LD cases, but a more efficient means of differentiating cases from noncases is needed before using this method to supplement TDH surveillance. Because the majority of cases identified using claims data did not meet the CSTE case definition, underreporting in Tennessee might be lower than previously estimated.

Board 221. Lyme Disease Surveillance Using Sampling Estimation: Evaluation of an Alternative Methodology in New York State

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Background: In the 14-year period from 1993 to 2006, New York State (NYS) accounted for over one-quarter (27.1%) of all confirmed Lyme disease (LD) cases in the United States. During that time period, a nine-county area in southeast NYS reported 90.6% of the LD cases in the state. Based on concern voiced by local health department (LHD) staff in this area regarding the burden of traditional LD surveillance, the NYS Department of Health (DOH) sought to develop an alternative to traditional surveillance that would reduce the investigative workload while maintaining the ability to track LD trends. Thus, a surveillance system was developed and implemented in 2007 to estimate county-level LD cases based on a twenty-percent random sample of positive laboratory reports. **Methods:** A random number generator was used to generate and assign an investigative indicator to 20% of all laboratory reports reported to the NYSDOH. The records assigned the investigative indicator were forwarded to LHDs for investigation. Estimates were calculated by multiplying the number of confirmed and probable cases resulting from LHD investigation of laboratory reports by five and adding cases with no associated laboratory report (primarily physician-reported erythema migrans cases). The estimates were compared to the number of cases using the traditional surveillance methodology in nine instances over the seven-year period that sampling estimation has been conducted. The representativeness of demographic and symptom variables were also examined. **Results:** Four counties with high LD investigative burden agreed to conduct sampling estimation in 2007. The number of counties (outside of New York City) using the sampling methodology grew to 19 (33.3%) by 2013. Significant differences between actual and estimated case counts were found in three of the nine evaluations conducted. Few (5.1%) significant differences were found when comparing proportions of demographic and symptom variables for the sampling estimation versus traditional surveillance. **Conclusions:** Overall, sampling estimation was efficient and accurate in estimating LD cases at the county level and reduced investigative burden. Use of case estimates for LD should be considered as a useful surveillance alternative by health decision makers in states with endemic LD.

Board 222. Developing a Surveillance Definition for Binational Tuberculosis Cases

R. Yelk Woodruff, M. Mark, R. Miramontes; CDC, Atlanta, GA, USA

Background: Treatment of tuberculosis patients that cross international borders requires significant collaborative efforts among TB programs. Currently the U.S. lacks a uniformly applied surveillance definition for binational TB cases, resulting in an inability to describe the burden on TB program resources. **Methods:** Characteristics associated with binational TB cases were identified via chart review in collaboration with state and local TB programs. Data were collected from 9 pilot sites in 5 states (AZ, CA, CO, NM, and TX) during January 1-June 30, 2014 and transferred to the Centers for Disease Control and Prevention for compilation and

analysis. **Results:** A total of 87 cases reported had at least one binational characteristic. The most common characteristics were: crossed the border while infectious (80.5%), contact investigation done in another country (other than the country where TB was diagnosed; 55.2%), and contacts identified in another country (48.3%). Less than six percent had a source or epidemiologically linked case identified in another country. **Conclusions:** Few reported cases had epidemiologically linked or source cases identified in another country, indicating difficulty obtaining this information from patient records. Promising components of a binational TB case surveillance definition include characteristics that were generally available, such as whether a patient crossed the border while infectious. Although our pilot project focused on the U.S.-Mexico border region, our findings are relevant to other areas of the country. Using surveillance data to educate policy makers and partners in TB control can help ensure that resources are made available to treat these high-burden cases.

Board 223. Epidemiology of Carbapenem-resistant *Acinetobacter baumannii* Identified Through the Emerging Infections Program, 2012-2013

S. N. Bulens[1], A. Y. Guh[1], Y. Mu[1], W. Bamberg[2], S. J. Janelle[2], J. T. Jacob[3,4], J. Reno[3,5], L. Wilson[6], E. Vaeth[6], R. Lynfield[7], K. Shaw[7], G. Dumyati[8], C. Concannon[8], Z. Beldavs[9], P. Cassidy[9], A. Kallen[1]; [1]CDC, Atlanta, GA, USA, [2]Colorado Dept. of Publ. Hlth. and Environment, Denver, CO, USA, [3]Georgia Emerging Infections Program, Atlanta, GA, USA, [4]Emory Univ. Sch. of Med., Atlanta, GA, USA, [5]Atlanta VA Med. Ctr.; Atlanta Res. and Ed. Fndn., Decatur, GA, USA, [6]Maryland Dept. of Hlth.and Mental Hygiene, Baltimore, MD, USA, [7]Minnesota Dept. of Hlth., St. Paul, MN, USA, [8]New York Rochester Emerging Infections Program at the Univ. of Rochester Med. Ctr., Rochester, NY, USA, [9]Oregon Hlth. Authority, Portland, OR, USA

Background: Multi-drug resistant (MDR) *Acinetobacter baumannii* is a known healthcare acquired pathogen. Reports of MDR *A. baumannii* are increasing in the U.S. We established a multi-state surveillance program to describe the epidemiology of carbapenem-resistant *A. baumannii* (CRAB). **Methods:** During January 2012-December 2013, 6 Emerging Infections sites (CO, GA, MD, MN, NY, OR) participated in active laboratory- and population-based surveillance for CRAB, defined as *A. baumannii* isolates nonsusceptible to ≥ 1 carbapenem (excluding ertapenem). A case was defined by isolation of CRAB from a sterile site or urine in a resident of the surveillance catchment area. Case medical records were reviewed to collect healthcare risk factors (HCRF), including hospitalization, dialysis, long-term care residence, surgery in the prior year, or presence of an indwelling device. Crude population based incidence rates were calculated based on 2012 and 2013 census data. The Standardized Infection Ratio (SIR), adjusting for age, race and sex, and 95% confidence intervals (CIs) were calculated to compare rates of disease among sites. **Results:** In total, 302 cases were reported from 270 patients. Most CRAB (74%) was isolated from urine; 22% was isolated from blood. CRAB incidence rates (per 100,000 population) ranged from 0.12 in OR to 4.12 in MD (0.43, CO; 2.5, GA; 0.35, MN; 0.53, NY). Higher than expected CRAB SIRs were observed for GA (1.85, CI: 1.07- 3.19) and MD (2.73, CI: 1.07-3.19), but lower than expected SIRs were observed for OR (0.12, CI: 0.07-0.22), MN (0.35, CI: 0.2-0.61), CO (0.43, CI: 0.28-0.84), and NY (0.53, CI: 0.28-0.84). Of 282 cases with data available, 279 (99%) had documented HCRF: 205 (73%) required hospitalization, 85 (41%) were admitted to an ICU within 7 days of culture, 48 (17%) died. Among 64 cases with positive blood cultures, 66% were admitted to the ICU and 52% died. **Conclusions:** The crude incidence of CRAB varied across sites with 4 having lower adjusted rates of disease than expected, illustrating geographic heterogeneity in CRAB distribution. Almost all CRAB were detected in patients with preceding healthcare exposures, underscoring the importance of interventions to reduce healthcare-associated transmission. Continued data collection is needed to monitor the incidence of CRAB in these populations.

Board 224. Fatal Cases of *Listeria monocytogenes* Infection Among Pregnancies and Children in Phuket, November 2013

Withdrawn at Author's Request

Board 225. *Coccidioides immitis*: Developing a One Health Approach for Surveillance of a Newly Emerging Fungal Pathogen in Washington State

H. Oltean[1], R. Wohrle[1], P. VanderKelen[1], M. Goldoft[2], T. Chiller[3], A. Litvintseva[3], O. McCotter[3], W. Clifford[1]; [1]Washington State Dept of Hlth., Olympia, WA, USA, [2]Washington State Dept of Hlth., Shoreline, WA, USA, [3]CDC, Atlanta, GA, USA

Background: *Coccidioides immitis* is an emerging fungal pathogen for the Pacific Northwest region. Three human cases have been reported and identified as locally acquired in the South-central region of Washington. Environmental sampling from the site of exposure in two cases resulted in detection of *C. immitis* DNA and recovery of viable *C. immitis* isolates from soil. Whole genome sequencing of the recovered isolates confirmed genetic identity between isolates from soils and one of the case-patients indicating local acquisition. A review of veterinary data indicates animal cases back to mid-1990. **Methods:** We brought together experts in environmental health, veterinarians, and public health to develop a surveillance strategy for this emerging infection. We combined multiple surveillance sources, including soil sampling, rodent trapping and testing, veterinary serosurveys, veterinary and human case investigations, air sampling, and spatial analysis, to enhance surveillance for this emerging pathogen. **Results:** We established a surveillance strategy for coccidioidomycosis. Enhanced surveillance has identified human cases without reported travel to previously defined endemic regions for this infection. Environmental sample testing is strategically targeted near likely soil exposure locations. Positive environmental samples are assisting the understanding of the ecological niches and boundaries of this pathogen. Much of the geography in the south-central region of Washington State is similar to the location where *C. immitis* was identified. **Conclusion:** Utilizing human, animal, and environmental approaches we have established surveillance for coccidioidomycosis in a one health model. The surveillance is important to understand this emerging pathogen in this region, and to provide education for local health care providers and veterinarians.

Board 226. Optimal Surveillance Network Design: A Value of Information Model

M. Convertino; Univ. of Minnesota, Minneapolis, MN, USA

Background: Infectious diseases are the second leading cause of death worldwide. Of the estimated 57 million deaths that occur throughout the world each year, about 15 million, that more than 25% of all deaths, are directly caused by infectious diseases. Food is a crucial component in such picture. Traceability of food is extremely important for food safety and defense. 1.5 million deaths are estimated every year worldwide due to diarrheal foodborne diseases alone. Thus, the ability to early detect outbreak sources via a highly efficient surveillance system is hugely important for health and economic outcomes of populations. **Methods:**

A model analogous to wave pattern recognition models is proposed to detect ''zero-patient" areas based on outbreak spread. Model effectiveness is shown with real data from the Cholera epidemic in Cameroon, foodborne Salmonella epidemic in USA, and the H5N1 avian influenza pandemic. The model is coupled to an optimal selection algorithm of surveillance networks based on their value of Information (VoI) of reporting nodes that are sub-networks of mobility networks in which people, food, and species move. We consider the surveillance network as the response variable to be determined in order to maximize the accuracy in detection of outbreak sources. **Results:** The optimal surveillance network has the highest VoI and lowest detection error. A 40\% minimum increased accuracy in detecting outbreak sources is estimated by maximizing the VoI versus the random surveillance model independently of outbreak epidemiology. Such accuracy is achieved with an average 25\% reduction of required surveillance nodes. **Conclusions:** We emphasize that accuracy in systems diagnosis increases when system syndromic signs are the most informative. Only in this way surveillance network can reveal linkages of outbreak patterns and network processes. The developed model is extremely useful for the design of optimal surveillance networks that can drastically reduce the burden of infectious diseases. Such model is a cyber-technology that governments and industries can use in real-time in order to avoid dramatic and costly outcomes. Further applications are for chronic diseases and for other detection problem.

Board 227. Integrating Area Profile and Environmental Surveillance in Monitoring the Risk of Arboviral Disease Transmission in Harris County

M. E. Vigilant; Harris County Publ. Hlth. and Environmental Services, Houston, TX, USA

Background: The climatic conditions in Harris County, Texas, is conducive for the propagation of mosquito populations the have been implicated in the transmission of arboviral diseases**. Method:** Harris County has been demarcated into two hundred and sixty-eight areas. Surveys were conducted in each area gathering geographic, environmental and demographic data to determine which areas has the greatest potential for mosquito-borne disease transmission. Mosquito trapping events were conducted utilizing modified Center for Disease Control (CDC) miniature light traps in storm sewers, modified CDC Reiter Gravid Traps and BG Sentinel Traps on private and public properties. Traps were strategically positioned based on geographic proximity and ease of access within the County. After 18 hours, these traps were retrieved, mosquito species collected were sorted, identified, pooled based on the order of importance for disease transmission, and sent to the laboratory for viral testing. **Results:** Each year, from 2011 to 2014, approximately 10,000 trapping events were conducted yielding on average more than 900,000 female mosquitoes. More than 55,000 pools were submitted for viral testing during that period resulting in 2538 positive isolates for West Nile Virus and four positive isolates for St Luis Encephalitis. **Conclusion:** Based on species emergence, adaptability, environmental conditions and both mosquito and human populations, the potential threat of emerging mosquito borne disease such as Dengue Fever, Chikungunia, and Malaria remains a major concern to the citizens of Harris County.

Board 228. Enhanced Testing of Norovirus-negative Gastroenteritis Outbreaks

N. Gregoricus, L. Barclay, J. Lewis, J. Vinje; CDC, Atlanta, GA, USA

Background: The burden of viral gastroenteritis outbreaks in the United States is largely attributed to norovirus; however no etiologic agent is identified in up to 16% of norovirus negative outbreaks. The lack of etiological agents in these unexplained outbreaks warrants a systemic exploration of viruses involved to better understanding underlining disease mechanisms. **Methods:** To investigate the etiologic agents in norovirus negative outbreaks reported in 9 states were submitted to 3 CaliciNet Outbreak Support Centers (California, Minnesota, and Oregon) and fecal specimens (at least 2 per outbreak) were tested for sapovirus, astrovirus, and rotavirus by realtime RT-PCR. Positive specimens were typed by sequencing of conventional RT-PCR products. **Results:** From 2012-2014, specimens from 80 norovirus-negative outbreaks were analyzed of which 18 (22.5%) outbreaks tested positive for sapovirus, 2(2.5%) for astrovirus, 1 (1.2%) for rotavirus, and 1 (1.2%) outbreak had a mixed infection of sapovirus and rotavirus. Eleven (61%) of the sapovirus outbreaks could be genotyped; 3 as GI.1, 1 as a GI.2, and 5 as GIV. Of the 2 outbreaks positive for astrovirus 1 was typed as type 4 and one as type 1. The 2 rotavirus outbreaks could be typed as G12P[8]. **Conclusions:** Of the 80 norovirus negative outbreaks, 26.2% could be attributed to a known gastroenteritis virus, of which, sapovirus had the highest positivity rate (22.5%). Future testing will include deep sequence analysis which allows identification of established gastroenteritis viruses that were missed by current realtime RT-PCR assays or novel viruses.

Board 229. Using Multiple Data Sources to Monitor Influenza Epidemics

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Background: Seasonal and non-seasonal influenza outbreaks are unpredictable and cause 3,000 to 50,000 deaths a year in the United States of America. Non-traditional methods that leverage data sources such as: Google searches, crowd-sourced disease surveillance data, clinician's databases, medical records management companies; to independently track influenza activity have recently been suggested as alternatives to get timely estimates of influenza activity ahead of the Centers for Disease Control influenza reports. Different methods and data sources have strengths and weaknesses when taken independently. Here we present a methodology that combines the strengths of four data sources and produces a single influenza predictor capable of delivering improved influenza predictions. **Methods:** A machine learning ensemble approach is implemented to extract the most meaningful information from multiple non-traditional real-time influenza surveillance systems and produce a single influenza predictor. **Results:** The influenza predictor obtained with our methodology displays superior accuracy and robustness (as measured by the root mean square error and the maximum absolute error), during the 2012-2013 and 2013-2014 flu seasons, than any of the real-time predictors separately. Moreover, our methodology delivers improved predictions up to four weeks ahead of the most recent influenza CDC reports, effectively providing forecasts of influenza activity up to two weeks ahead of current week. As expected, the accuracy of our predictions decreases as the number of weeks ahead of CDC reports increase. **Conclusions:** We show that efficiently combining multiple independent influenza predictors is a superior approach than just using the best predictor to monitor influenza activity over the US during two flu seasons.

Board 230. Participatory Surveillance: The Influenza Experience

R. Chunara[1,2], A. W. Crawley[3], O. Wojcik[2], K. Baltrusaitis[2,4], J. Olsen[3], J. S. Brownstein[1,2], M. Smolinski[3]; [1]Harvard Med. Sch., Boston, MA, USA, [2]Boston Children's Hosp., Boston, MA, USA, [3]Skoll Global Threats Fndn., San Francisco, CA, USA, [4]Boston Univ., Boston, MA, USA

Background: Information about the activity of influenza-like-illness (ILI) in the United States (U.S.) is limited and traditional surveillance systems take time to aggregate data. **Methods:** Flu Near You (FNY) is a participatory surveillance system that was developed to capture influenza-related symptoms reported by participants on a weekly basis providing estimates of influenza-like-illness incidence. Individuals contribute an email address, gender, age and zip code. On the website (flunearyou.org) or through mobile phone app they are requested to fill in a short survey asking if they had any of 10 symptoms: fever, cough, sore throat, shortness of breath, chills/night sweats, fatigue, nausea or vomiting, diarrhea, body aches and headache. Users can also enroll their household members and report weekly for them. Spatio-temporal trends of the symptom reports were compared to measures of ILI-incidence from the Centers for Disease Control and Prevention (CDC) ILINet. In subsequent work, we examined how other subsets of the symptom reports compared to repots from HealthMap, FOOD database, NoroCORE, CalciNet and NoroStat, by developing exclusion and inclusion criteria in regards to two contemporaneous disease outbreaks in the U.S.; norovirus and enterovirus EV-D68. **Results:** 54,747 FNY individuals had at least two reports between October 1, 2012 and May 19 2014; ILI from those reports correlated with ILINet ($\rho = 0.906$). ILI reports peaked the week of December 23rd for both FNY and CDC at 3.4% and 4.6%, respectively (2013-2014 season). In examining non-flu syndromes, we found increases in our defined "norovirus case" reports contemporaneous with norovirus prevalence and in common enterovirus symptoms (breathlessness, cough, body aches) at times of reported enterovirus outbreaks in U.S. populations in 2014. **Conclusions:** Participatory surveillance can be useful for infectious diseases; with further specificity desirable for distinguishing different infectious disease outbreaks.

Board 231. *Coccidioides immitis*: Developing a One Health Approach for Surveillance of a Newly Emerging Fungal Pathogen in Washington State

O. McCotter[1], R. Worhle[2], P. VanderKelen[2], M. Goldoft[3], T. Chiller[1], A. Litvintseva[1], H. Oltean[3], W. Clifford[2]; [1]CDC, Atlanta, GA, USA, [2]Washington State Dept. of Hlth., Tacoma, WA, USA, [3]Washington State Dept. of Hlth., Shoreline, WA, USA

Background: *Coccidioides immitis* is an emerging fungal pathogen for the Pacific Northwest region. Three human cases have been reported and identified as locally acquired in the South-central region of Washington. Environmental sampling from the site of exposure in two cases resulted in detection of *C. immitis* DNA and recovery of viable *C. immitis* isolates from soil. Whole genome sequencing of the recovered isolates confirmed genetic identity between isolates from soils and one of the case-patients indicating local acquisition. A review of veterinary data indicates animal cases back to mid-1990. **Methods:** We brought together experts in environmental health, veterinarians, and public health to develop a surveillance strategy for this emerging infection. We combined multiple surveillance sources, including soil sampling, rodent trapping and testing, veterinary serosurveys, veterinary and human case investigations, air sampling, and spatial analysis, to enhance surveillance for this emerging pathogen. Much of the geography in the south-central region of Washington State is similar to the location where *C. immitis* was identified. **Results:** We established a surveillance strategy for coccidioidomycosis. Enhanced surveillance has identified human cases without reported travel to previously defined endemic regions for this infection. Environmental sample testing is strategically targeted near likely soil exposure locations. Positive environmental samples are assisting the understanding of the ecological niches and boundaries of this pathogen. **Conclusions:** Utilizing human, animal, and environmental approaches we have established surveillance for coccidioidomycosis in a one health model. The surveillance is important to understand this emerging pathogen in this region, and to provide education for local health care providers and veterinarians.

Board 232. Genetic Heterogeneity of *Listeria monocytogenes* in Northern Italy

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Background: Invasive listeriosis is a rare foodborne disease. Septicaemia and meningoencephalitis with high letality are the most common clinical presentations in vulnerable population. The etiologic agent, *Listeria monocytogenes*, displays a high genetic heterogeneity. Thus, implementation of strain discrimination techniques is of major importance for prompt outbreak detection and improvement of surveillance. The aim of this study was to detect emerging strains and monitor their prevalence in the Lombardy region, Northern Italy. **Methods:** In Lombardy, the mandatory notification system has been integrated since 2005 with a laboratory-based surveillance network based on voluntary referral of clinical isolates to a Regional Reference Laboratory. All human *L. monocytogenes* isolates collected during the period 2005-2013 (n=245) were serotyped and subtyped by Multi-locus Sequence Typing (MLST). Sequence Types (STs) were assigned in accordance to the *Listeria* MLST database (Pasteur Institute, France). **Results:** The predominant serotypes were 1/2a (59.6%), 4b (26.1%) and 1/2b (10.6%). Forty-nine STs were identified, of which 36 had been previously reported in the same area. The 6 most common STs were ST38 (16.7%), ST1 (11.8%), ST8 (9.4%), ST155 (6.5%), ST2 (5.7%) and ST3 (4.9%), accounting for 55% of the strains. The high prevalence of ST38 and ST155 led us to hypothesize the likely occurrence of two outbreaks which had gone undetected by local health authorities during the period 2009-2011. In particular, identification of ST155 isolates began in 2008 (n=1), peaked in 2011 (n=10) and continued in 2013 (n=5) with 3 pregnancy-related cases closely linked in space and time. For these cases, an epidemiological investigation had been implemented which failed to identify their source. Only in one case (ST8), the implicated food (brique cheese) was recognized. Finally, ST1, ST2 and ST3 showed a persistent trend being widely disseminated across time and space. **Conclusions:** This study identified the prominent STs circulating in our regional area and contributed to our understanding of the genetic heterogeneity of *L. monocytogenes* isolates. Monitoring STs will provide essential information for preventing listeriosis and supporting epidemiological investigations in this field, which are often challenging.

Board 233. Real Time Surveillance of Influenza Using Wireless Reporting of RIDT Results

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Background: Delays in reporting are inherent in influenza surveillance. Consequently, public health response to outbreaks is offset by 2-to-3 weeks. The feasibility of a statewide array of rapid influenza detection test (RIDT) analyzers using wireless connectivity to report in real time was assessed over a two-year period. **Methods:** We evaluated the feasibility of a real-time primary care influenza surveillance network, including site recruitment, engagement, training, and implementation of analyzers. Secondary objectives included assessment of performance over two seasonal outbreaks of influenza as compared to existing influenza surveillance programs. We used the Quidel Sofia Influenza A+B FIA--a RIDT with wireless connectivity. Analyzers were deployed in all public health regions of Wisconsin, starting in October 2013. Twenty primary care practices located in urban, suburban and rural locations participated. We compared the total number of influenza A and B detections per week to the prevalence of influenza-like illness visits at primary care sites in Wisconsin (ILI-Net) and detections from existing PCR and RIDT networks. **Results:** IRB exemption and university clearances were obtained by late August 2013. The full complement of practices was recruited by 11/20/2013. Installations of Sofia analyzers were completed by 12/18/2013. Data accumulated as soon as sites were activated and reporting from 16 sites (80%) was fully operationalized by 12/31/2013. Data were aggregated and analyzed on a daily and weekly basis public health region, and for the Wisconsin composite. The system identified the onsets of the 2013-2014 and 2014-2015 seasonal influenza outbreak extremely early. High correlations existed between the weekly real-time influenza detections and ILI-Net ILI visits (r=0.769; P<0.001), PCR detections, (r=0.896; P<0.001), and RIDT detections (r=0.914; P<0.001). **Conclusions:** Effortless, real time reporting of RIDT results was achievable over a very short time frame in practices using RIDT coupled with immediate wireless transmission of results. Such reporting eliminated the need for clinicians or laboratorians to take time to aggregate and transmit information. This approach is a reasonable model for public health surveillance for any pathogen identifiable by clinic-based technology.

Board 234. Crowdsource Reporting of Infectious Diseases

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Background: Crowdsourcing of patient text data related to infectious diseases such as viral respiratory diseases and water borne diseases is a viable option for reporting of cases in the event of a natural disaster such as floods, hurricanes and other man-made disasters. The challenge during a natural or man-made disaster is access to the Internet is limited and traditional websites for logging infectious reports may be down. The data gathered from this process will be kept confidential and used as planning data and tracking cases for healthcare provider resources in a community during a disaster event. **Methods:** A personal cloud server is a solution to host a data collection system that will crowd source infectious disease data for a community such as gender, age of patient, patient history and medications, etc. Community citizens, public employees, healthcare providers can input data to the wireless personal cloud infrastructure via a smartphone or a laptop. These personal cloud servers can be co-located in storm-protected buildings with a back-up power source and be connected to a wireless wide area network (WAN). Even in the absence of general Internet connectivity, a user just has to be in the range proximity of the wireless WAN and be able to upload their text data to the personal cloud server. After regular Internet connectivity is restored to the community, an administrator can download the text data from the personal cloud server to a larger database for cartographic and statistical analysis. **Results:** The outcome of this project is to identify the user and technical requirements and human interface and security challenges for connecting several connecting personal cloud servers to a larger cloud-based database and creating a strategy for implementing, testing and evaluating this process in a real-world natural or man-made disaster. **Conclusion:** Local healthcare administrators will find this system a viable alternative to reporting of infectious diseases during a natural or man-made event. The continuous reporting of infectious diseases at ground zero level is important for planning, monitoring and tracking of these cases. This novel approach allows for the uninterrupted collection of infectious disease text data and for later analysis.

Early Warning Systems

Tuesday, August 25, 12:30 PM - 1:45 PM

Grand Hall

Board 235. A Girl Infected with *Salmonella* Typhimurium Due to Pet Turtle Contact in Guangdong, China

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Background: An estimated 94% of *Salmonella* infections are food-borne, many studies have shown that direct contact with infected animals is a risk factor for salmonellosis. In the recent two years, *Salmonella* outbreaks associated with pets were increased in USA. However, there isn't any report about human *Salmonella* infections associated with pets contact in China. Lack of surveillance system integration animals, food, and human data in China now could partly explain the reason. **Methods:** A two-year-old Chinese girl lived in Foshan city, Guangdong province sought treatment at Nanhai People's hospital in May 2012 with fever and bloody diarrhea for three days. Because stool cultures of the girl were repeatedly positive for *Salmonella* Typhimurium, the healthcare worker of the hospital noticed the local CDC and the case was interviewed and investigated at the first time. **Results:** Epidemiologic and environmental investigations indicated exposure to the pet turtle in the girl's home was the cause of her infection. The turtle was purchased as a pet from the market one week before the girl get sick, and the shell length was about 8cm. The girl played with the little pet everyday and sucked her fingers very often. No more specific exposures of food, water, traveling history were found. The anus swab of the girl's mother and body swab of the pet turtle were taken. The body swab of the turtle was positive for *Salmonella* Typhimurium and the Xba1 and Bln1 PFGE patterns were both 100% similar to that of the girl. Antimicrobial susceptibility pattern of the *Salmonella* Typhimurium isolated from the pet and the girl were the same, which were resistant to ampicillin, cefotaxime, cefepime and gentamicin. After two weeks treatment in the hospital, the girl covered. The pet and the aquarium were removed and no illness news got from the girl any more. **Conclusions:** Although the present report is the first time of pet turtle associated *Salmonella* infection in China, many cases and even many outbreaks

were hidden under the iceberg due to the weak surveillance system for animals, food, and human. It is time for the Chinese government to pay more attention to the enteric infectious diseases associated with animals in public settings and in higher risk population.

Board 236. A Review of Dengue Deaths in 2013 in Vientiane Capital and Champasack Province of Lao PDR

B. Sengkeopraseuth; Med. Univ. of Lao PDR, Vientiane, Lao People's Democratic Republic

Background: Dengue is endemic in Lao People's Democratic Republic. Dengue cases have exceeded the epidemic threshold since January 2013. The epidemic curve shows a peak at Epi-Week 28 with a downward trend in later weeks. The number of reported cases and deaths was double from the big outbreaks in 2010. This study aims to identify the causes of high case fatality dengue fever during the 2013 outbeak in Vientiane capital and Champasak province in order to make recommendations for further case management improvement. **Methods:** This is a retrospective study of dengue deaths from 7 hospitals in two provinces during the dengue epidemic in 2013. Data was collected by chart reviews of adult and paediatric patients using a standardised form. The dengue case management forms were reviewed. An Epidata software and Microsoft excel are used for data analysis. **Results:** A total of 44,171 cases and 95 deaths were reported (case fatality rate-CFR 0.21%) as of Epi-Week 52. The majority mortality [61/95 (64.2%)] of deaths were reported from Champasack (n=35) following Vientiane Capital (n=26); and most of the deaths was under 15 years of age. Median and mode between symptom onset and first presentation to hospital was 4 days. Patients visited physicians too late when they developed high fever. Patients had infusions at home before going to the hospital (34%). Regarding the health care services, most of the death cases were admitted to hospital late (with fever on day 4) with severe bleeding (59%), fluid overloading due to prior IVF therapy (41%) and eventually becoming fluid overloaded and dying from respiratory failure rather than shock. Late or incorrect diagnosis for dengue with warning signs is common among the deaths cases and lack of constant monitoring of vital signs (due to the shortfall of doctors and nurses). **Conclusion:** This is the largest dengue epidemic year in Lao PDR since dengue was made a notifiable disease, with ah high number of fatal cases. Therefore, ongoing training to health care providers should be implemented to improve diagnosis and case management outcomes. Further community-based survey on the health-seeking behavior of patient may indicate whether traditional practitioners or other practices remain as risk factors.

Board 237. National Dengue Surveillance in the Lao PDR, 2006-2012: Epidemiological and Laboratory Findings

B. Khamphaphongphane; Natl. Ctr. for Lab. and Epidemiology, Vientiane, Lao People's Democratic Republic

Background: Dengue is the most rapidly spreading mosquito borne viral disease in the world. The disease is caused by infection with one of four related viral subtype (DEN 1-4). The vector-borne disease is primarily transmitted by Aedes aegypti mosquitoes. It was estimated that there are 390 million persons infected by dengue per year. Dengue has been a public health problem in the Lao People's Democratic Republic and the magnitude of the disease burden and Epidemiological trends remain poorly understood. **Methods:** We did the descriptive analysis on Epidemiology and Laboratory data reported within the indicator-based National Surveillance System for Notifiable Selected Diseases that consists of passive weekly reports of clinically suspected cases, on admission, from all health care facilities across the countries. Specimens are transfer to NCLE on wet ice by bus or air for further laboratory diagnosis. **Results:** During 2006 to 2012, the annual dengue notification rate ranged between 62 and 367 cases per 100 000 population. The case fatality rate was 0.2% for all year except for 2008 when it was significantly higher at 0.5% ($P < 0.01$). The largest number of cases occurred among 10 to 20 year old (34%) with significantly more male (12 000 cases) than female (9119 cases, $P < 0.01$). Case report was highest from May/June to October/November with peak in late August or September. There was a lower proportion of laboratory confirmed dengue in 40 year old age group (33.9%, $P < 0.01$) compare to young age groups (43.4-51.6%). The number of provinces with notification rate ≥ 200 per 100 000 increased from one in 2006-2008 to five in 2009 and to 10 in 2010 (the first year that all provinces in the country reported dengue cases). All four serotypes were detected. **Conclusions:** There are many challenges to effective Dengue surveillance and response in Lao PDR. The dengue case reported indicate a gradually expansion of geographic areas. Effort need to be focus on using available data to prompt more effective outbreak response to guide the design and implementation of intervention strategy

Board 238. NoroSTAT: Enhanced Norovirus Outbreak Surveillance Network

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Background: The Norovirus Sentinel Testing and Tracking (NoroSTAT) network, launched August 2012, is a network of five state health departments and CDC working to establish and maintain standards for norovirus outbreak reporting to national surveillance systems. These standards aim to improve timeliness, completeness, and consistency of norovirus outbreak reporting and provide near real-time assessment of norovirus activity in the US. **Methods:** Participating health departments report specific epidemiologic and laboratory data on suspected or confirmed norovirus outbreaks to CDC within seven business days of notification. We summarized data from the first two years of NoroSTAT, August 1, 2012 through July 31, 2014. We evaluated the performance of NoroSTAT by comparing timeliness and completeness of reports from participating sites after and in the three years before the creation of the network. **Results:** During the first two years of NoroSTAT, 1391 norovirus outbreaks were reported. The most common primary mode of transmission was direct person-to-person contact, reported in 1022 (73%) outbreaks, followed by foodborne (n=190, 14%). The most common exposure setting was long-term care facilities (n=836, 60%). Other common settings included restaurants (n= 152, 11%) and schools (n=109, 8%). Median reporting lag decreased from 18 days in the three years before NoroSTAT to 2 days during NoroSTAT. A total of 1388 (99.8%) outbreak reports contained all required data elements, but only 945 (71%) of the 1322 outbreaks in the three years preceding NoroSTAT contain these data. Of the 751 (54%) outbreaks for which genotype was reported, the most frequent were GII.4 Sydney (n=428, 57%) and GII.6 (n=48, 6%). The median time required for testing and genotype reporting decreased from 22 days to 3 days. **Conclusions:** These data reaffirm that most norovirus outbreaks occur in long-term care facilities and are spread through direct person-to-person transmission.

Norovirus outbreak reporting through NoroSTAT has improved both the completeness and timeliness of reports. This information can be used to quickly evaluate current norovirus outbreak activity, make comparisons to previous years, and assess strain-specific characteristics of norovirus outbreaks, including the impact of new strains on outbreak frequency and severity.

Board 239. Evaluation of Enhanced Surveillance Strategies for World Pride Celebration in Toronto, Canada

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Background: In June 2014, Toronto, Canada hosted World Pride (WP), an international event that celebrates lesbian, gay, bisexual, and transgender communities through parades, festivals, and cultural events. WP involved a large number of international travelers and 2 million expected participants, increasing the likelihood of public health threats related to mass gatherings. Given the number of visitors and the increased attention to invasive meningococcal disease (IMD) among MSM weeks before the event, Toronto Public Health (TPH) developed and implemented an enhanced surveillance plan. The focus was on communicable diseases assessed to have a high probability of occurrence and/or high potential impact. This summarizes the evaluation of the enhanced surveillance plan for communicable disease threats during WP. **Methods:** The evaluation questions captured both outcomes and process: 1) How effective was the surveillance plan in early outbreak identification, and 2) Was the plan easy to implement and acceptable? The questions examined relevant attributes of a surveillance system as outlined in the CDC *Guidelines for Evaluating a Public Health Surveillance System*. A mix of qualitative and quantitative methods was used. **Results/Outcomes:** Potential events of interest were detected during the surveillance period, including 2 IMD cases, 3 reports of food poisoning linked to restaurants in the core area for WP events, and a cluster of shigellosis among MSM. None of these cases or clusters could be directly linked to WP or of any measureable consequence to WP participants. As such, sensitivity and positive predictive value could not be assessed. **Process:** Users of the system deemed it useful, simple and flexible. The system however did not meet expectations for stability, as the emergency department syndromic data system experienced power issues and was down for the main WP weekend. **Conclusions:** The enhanced plan for this mass gathering in Toronto demonstrated current surveillance tools are useful and easy to adapt for special events. Areas to be strengthened included contingency planning for power outages or other obstacles to accessing key data sources. The information gained through this evaluation will be used to strengthen preparedness for the Pan/ParaPan American Games, to be hosted by Toronto in the summer of 2015.

Board 240. Hantavirus Fever Without Pulmonary Syndrome in Panama

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Background: In Panama, hantavirus pulmonary syndrome (HPS) is caused by Choclo virus, a species phylogenetically related to Andes and Maporal viruses. Up to 60% of the population has been positive for specific serum antibody in community-based surveys, but mortality is very uncommon. **Methods:** In four western Panama clinics, we tested individuals presenting with a severe febrile prodrome for acute hantavirus (HV) infection by immunoglobulin M enzyme-linked immunosorbent assay and reverse transcription polymerase chain reaction as well as clinically similar infections, such as dengue and leptospirosis. **Results:** From 2006 to 2009, at least 21%of 117 patients diagnosed with HV infection had HV Fever (HF) with no evidence of pulmonary edema (no respiratory distress or radiographic lung infiltrates), and 44%of patients had very mild HPS (radiographic pulmonary edema but no respiratory insufficiency). **Conclusions:** Hantavirus infection caused by Choclo virus in Panama presents often as HF, which contrasts with HV in the Americas but is consistent with the high seroprevalence in endemic regions.

Board 241. An Evaluation of the Pacific Outbreak Early Warning Detection System—The Pacific Syndromic Surveillance System

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Background: The Pacific Syndromic Surveillance System (PSSS), launched in 2010, provides a simple mechanism by which 121 sentinel surveillance sites in 21 limited-resource Pacific island countries and areas (PICs) undertake routine indicator based surveillance for the detection of infectious disease outbreaks. Four years on, this evaluation aims to assess whether the PSSS is meeting its objectives; measure progress since a formative evaluation conducted in 2011; and provide recommendations to enhance the PSSS's performance in the future. **Method:** Data were collected between July and December 2014. Eighteen key informant interviews were conducted with users of the system. Resulting data were thematically analysed. Historic quantitative system data were collected and analysed to assess timeliness and completeness of reporting. It was not possible to analyse sensitivity of the PSSS as a gold standard was not available. **Results:** The evaluation found that the PSSS has enhanced PICs' ability to undertake early warning surveillance and, in doing so, has contributed to efforts to comply with surveillance-related obligations under the International Health Regulation (2005). The system is performing well in terms of its simplicity, acceptability and usefulness for public health decision makers. Despite this, issues with timeliness and completeness of reporting, data quality and system stability remain challenging. **Conclusion:** The evaluation found that in four years the PSSS has made a significant contribution to improving public health security in the Pacific. Further, the system has supported PICs' to develop and maintain infectious disease surveillance, a core public health capacity required to implement the IHR effectively. This evaluation's findings highlight the utility of simple syndrome-based early warning surveillance methods to detect disease outbreaks in settings with limited capacity and limited access to confirmatory diagnostic services, as is the case in the Pacific. As the PSSS evolves, a balance between simplicity (and hence implementability, flexibility and adaptability) and technological advances to improve timeliness and data quality performance will need to be found to ensure long-term sustainability.

Board 242. Use of Surveillance Data to Estimate Seasonal Influenza Thresholds in Canada

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Background: In Canada, *FluWatch* is the national surveillance system that monitors the spread of influenza and influenza-like illness (ILI). A primary objective of *FluWatch* is to detect influenza activity across Canada as early as possible. Influenza thresholds have been developed and used by many countries to indicate influenza activity levels that would signal the start or end of a season, as well as to detect periods of increased or severe activity. Canada has not yet established validated thresholds for use in its surveillance system. The World Health Organization (WHO) has developed a novel method to establish seasonal and alert thresholds for influenza. The objective of this study was to use the WHO's method to calculate thresholds for select surveillance indicators and determine the feasibility of use in Canada. **Methods:** Data from three indicators were used in this study: national ILI consultation rates per 1,000 patient visits, percent positive influenza laboratory specimens, and number of hospitalizations due to influenza. Data were analyzed from influenza seasons 1994-1995 to 2013-2014 from September through August. The 2008-2009 and 2009-2010 seasons were excluded due to the H1N1 pandemic. Using the WHO methodology, alert and seasonal thresholds were determined for each indicator. **Results:** The seasonal thresholds for each indicator were determined to be 20.3 ILI consultations per 1,000 patient visits, 3.1% positive influenza detections and 27.6 hospitalizations due to influenza. Seasonal thresholds of each indicator defined the start and end of influenza season in different weeks and the duration of the influenza season also varied. The weekly alert thresholds calculated using the upper 95th percentile ranged from 7.7 to 80.6 consultations per 1,000 patient visits for the ILI, 0.1% to 3.0% positive for laboratory detections and 0 to 716 hospitalizations. **Conclusions:** This study demonstrated that the WHO seasonal influenza threshold protocol may be used to calculate seasonal and alerts thresholds within a Canadian context. Further analysis with internal and external data is required to validate the results and determine the applicability of these thresholds. Refinements to this method may be needed to provide an accurate picture for seasonal influenza in Canada.

Board 243. Ebola Response in the District of Columbia: Early Warning Surveillance in the United States Capital

A. K. Hennenfent, K. Li, K. Dassie, M. Grant, K. Zamore, J. Davies-Cole; District of Columbia Dept. of Hlth., Washington, DC, USA

Background: The Centers for Disease Control and Prevention (CDC) announced in October 2014 the start of enhanced monitoring for travelers arriving in the USA from countries undergoing widespread transmission of Ebola virus disease (EVD). With this enhanced effort, six District of Columbia (DC) Department of Health (DOH) epidemiologists were tasked with rapidly establishing contact with all domestic and international travelers arriving in DC. The following describes their approach in implementing an infectious disease early warning surveillance system. **Methods:** Returning DC residents (or visitors) were actively monitored with the goal of completing the initial risk assessment phone interview within 24 hours of receiving arrival notifications from the CDC or another jurisdiction. To help achieve this goal, a contact and monitoring protocol was created establishing standardized timelines and methods for first contact and failed contact, which remained consistent for all team members once in place, including on weekends and holidays. **Results:** From 10/17/2014 through 3/15/2015, over 92% (286/309) of PUM who completed all or a portion of their monitoring period under DC DOH supervision were successfully contacted. The highest successful contact rate was achieved in March 2015 (31/31, 100%), with the lowest in December 2014 (73/86, 84.9%). Average time from the initial arrival notification to first contact attempt was approximately 15.3 hours with 57.9% (179/309) of PUM interviewed within 24 hours of notification. DOH was consulted on 22 persons seeking medical care at a DC healthcare facility. Collaboration between the treating hospital, DC DOH, and CDC determined EVD testing was necessary for six of these individuals with none ultimately testing positive. **Conclusion:** The small size of the DC Ebola response team created a situation where six epidemiologists closely collaborated in implementing an early warning surveillance system, developing contact and monitoring protocols, as well as interviewing PUM. This allowed for a timely completion of interviews and an overall high successful contact rate that improved over time as protocols evolved from gained experience. This unified small team approach to surveillance and individual case management can serve as a model for future outbreak scenarios within the District and other urban settings.

Board 244. Sporadic Norovirus Surveillance and Outbreak Trends, Tennessee, 2012-2014

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Background: In Tennessee (TN), sporadic cases of norovirus are not reportable; however, norovirus outbreaks are reportable and are monitored through the Norovirus Sentinel Testing and Tracking Network (NoroSTAT). Sporadic norovirus incidence data from a CDC-sponsored New Vaccine Surveillance Network (NVSN) in Davidson County, TN and NoroSTAT data were used to compare the temporal trends of sporadic norovirus incidence and reported outbreaks. **Methods:** Sporadic norovirus cases were identified through acute gastroenteritis (AGE) surveillance among children ≥15 days and ≤17 years enrolled from Vanderbilt Emergency Department and outpatient clinics during 2012-2014. AGE cases positive for norovirus and the total number of outbreaks from selected middle TN counties documented in NoroSTAT were compared by year. All norovirus positive specimens were sequenced. Sporadic and outbreak genogroups were compared. A moving average of 4 weeks was implemented to identify peaks in trends. **Results:** Of the 2330 children with AGE enrolled in the NVSN surveillance system, 346 (15%) were positive for norovirus during August 2012-July 2014. During the same time period, 33 confirmed norovirus outbreaks occurred within middle TN counties, with 52% occurring in long-term care facilities. No outbreaks of Genogroup I were reported during Year 1 (August 2012-July 2013), but 15 outbreaks were characterized as Genogroup II. In Year 2 (August 2013-July 2014), 5 outbreaks were characterized as Genogroup I and 13 outbreaks were Genogroup II. During both years, sporadic cases increased precipitously prior to the reported outbreaks. The number of weeks from the peak of sporadic norovirus cases identified in NVSN surveillance to the peak in outbreaks reported was 10 weeks for Genogroup II during Year 1. In Year 2, the interval was 12 weeks for Genogroup II and 13 weeks for Genogroup I. **Conclusions:** Increases in pediatric norovirus infections appear to precede outbreaks in the community, which provides key insights into community transmission dynamics and potential opportunities for prevention. Surveillance for sporadic norovirus can provide an early signal for increasing norovirus outbreaks. Early indications of norovirus activity can allow for timely warnings to intensify infection control measures among vulnerable populations.

Board 245. Rabies Surveillance Evaluation in an Area Without Human Cases in Brazil

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Background: Rabies has been kept under control in São Paulo State, Brazil with no human, only three canine and seven feline cases in 2003-2013 (all AgV-3). **Methods:** Accordingly, a rabies surveillance system in this area was evaluated following the CDC (Centers of Diseases Control, Atlanta, USA) methodology. **Results:** The system was based on investigation of pet bites in human beings, aggressor pet monitoring and brain testing of suspected animals, which was dependent of post-mortem diagnosis in dogs and cats (low simplicity). Despite new technologies on data processing and diagnosis were introduced, the system has been poorly adapted to disease dynamics overtime, with no increment on animal case registration (low flexibility). Although local services have highly demonstrated system perception (high acceptability), private clinics have shown low participation and awareness (low acceptability). Total geographic area without data of surveillance actions increased 30% from 2003 to 2013 (low representativeness). No standardize database between cities and laboratories and no data archiving of animals under surveillance were found (low data quality). The system was unable to define the real population under surveillance, even when receiving dogs with suspicious symptoms (potentially suspect cases); in overall, 39.2% of local services and 72.8% of private clinics have not suspect rabies in these cases (low sensitivity). In 2012, the positive predictive value was 0.03% for dogs (2/5,566) and 0.06% for cats (1/1,797). The average time elapsed between clinical signs and laboratorial result in 2012/2013 was 25 days for suspicious dogs and cats (low opportunity). Evaluation of local services facility to accomplish actions showed that only 25% had available pet housing and 16% had temporary disposal of carcasses (low stability). **Conclusions:** Under these indicators, the current rabies surveillance system of São Paulo has shown incapacity for early disease detection once based in dog and cat population.

Improving Preparedness for Infectious Disease Emergencies

Tuesday, August 25, 12:30 PM - 1:45 PM

Grand Hall

Board 246. Utility of Established Severe Acute Respiratory Illness Surveillance in the Early Identification of EV-D68 in Minnesota

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Background: In August 2014, clusters of severe respiratory illness among children were reported in the Midwest as associated with enterovirus D68 (EV-D68). While EV's normally circulate in summer and fall, uncertainties about the spectrum of disease associated with EV-D68 and its prevalence in relation to other viruses remain. The Minnesota Department of Health (MDH), in collaboration with CDC, established sentinel surveillance for severe acute respiratory illness (SARI) at 3 hospitals (including a children's hospital) in the Minneapolis-St. Paul metro area between April and September 2013. **Methods:** Through SARI surveillance, medical charts of hospitalized patients with acute respiratory symptoms were reviewed and specimens tested by PCR for 16 viral and 4 bacterial pathogens (including rhinovirus). A pan-EV PCR was added September 1, 2014. Specimens PCR-positive for EV were cultured or had EV-D68 RT-PCR testing; EV isolates were subtyped by sequencing. **Results:** The first Minnesota EV-D68 case was identified on September 17, 2014 from an infant admitted September 5, 2014. Of 363 SARI specimens tested by MDH from September 1 through October 31, 2014, 100 (28%) were positive for EV by PCR or culture, including 52 also reactive with the rhinovirus assay. Among 16 EV culture-positive specimens, EV-D68 was detected in 4 patients (25%), coxsackievirus A21 in 3 patients (19%), and rhinovirus in 3 patients (19%); coxsackievirus B3, coxsackievirus B5, echovirus 18, echovirus 25, and parechovirus type 1 were detected in one patient each. A viral agent was not isolated in 2 (13%) patients. Sixty-two (62%) specimens were positive for EV-D68 by PCR. Co-detections of EV and other viral pathogens were identified in 11 patients including adenovirus (7), RSV (4), HMV (1), and influenza (1). **Conclusion:** The establishment of a sentinel surveillance system for SARI played a critical role in the early identification of EV-D68 in MN. A broadly defined surveillance system of patients hospitalized with severe respiratory illness, along with multi-pathogen molecular testing can be used to identify specific pathogens of interest. The longitudinal nature of SARI surveillance will further allow MDH to compare trends in respiratory illness over time and contextualize circulation of EV-D68, and other emerging respiratory pathogens.

Board 247. Risk Assessment and Mitigation Strategies Associated with Testing Persons Under Investigation for Ebola Virus Disease

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Background: Reference laboratories within the Laboratory Response Network (LRN) recently have been approved by the LRN to test clinical specimens derived from persons under investigation to detect Ebola Zaire virus using a U.S. DoD rRT-PCR assay that received FDA Emergency Use Authorization. To ensure the safety of laboratory staff and the community, the North Carolina State Laboratory of Public Health (NCSLPH, an Advanced Reference Laboratory within the LRN) conducted a risk assessment to characterize risks related to receiving specimens and conducting Ebola-specific diagnostic testing. Furthermore, the NCSLPH developed risk mitigation strategies to reduce identified risks prior to the final implementation of the Ebola assay. **Methods:** The comprehensive assessment involved identifying hazards, prioritizing risks, and listing facility specific safeguards and work practices to mitigate risks. Pre-analytical, analytical, and post-analytical processes associated with suspect Ebola virus Disease (EVD) specimens were evaluated along with staff competencies and existing hazard and administrative controls. Examples of controls include personal protective equipment, engineering controls, decontamination and waste management, and facility policies and procedures that aim to mitigate risk. The APHL template for Public Health Laboratory Risk Assessment provided a framework for this analysis. **Results:** NCSLPH staff identified varying degrees of risks throughout all stages of the testing process and formulated strategies to mitigate risk using existing control measures. These risks spanned from breakage of specimen containers upon initial delivery and aerosolization of specimens during testing, to external contamination of waste containers post-testing. Mitigation strategies included requiring specimens to be packaged and shipped as Category A hazardous materials, wearing multiple layers of fluid-resistant PPE, and following procedures to properly inactivate and destroy infectious materials prior to disposal. **Conclusion:** Conducting the evaluation highlighted the need for laboratories to conduct facility-specific

risk assessments if they consider undertaking testing associated with specimens collected from a PUI for EVD. This process allowed for the development of a comprehensive toolkit for clinical diagnostic and public health laboratories to increase laboratory preparedness for EID testing.

Board 248. Surveillance of ILI/SARI in Republic of Djibouti for Pandemic Influenza Preparedness

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Background: The aim of this task is to assess the feasibility to establish a sentinel site for ILI and SARI surveillance including the influenza sample collection, shipment and transfer of samples for laboratory testing to a reference influenza laboratory in the WHO Eastern Mediterranean Region. **Methods:** The two sentinel sites proposed by the MoH namely Peltier hospital, a university hospital and Doctor Chakib hospital, a respiratory diseases hospital, were assessed using a WHO prescribed checklist for selection of sentinel sites for influenza surveillance. **Results:** The sentinel site selected was the Peltier hospital and the National Public Health Institute of Djibouti was identified as laboratory to ensure the virological diagnosis of influenza. In addition, an activity plan to use funds available under Pandemic Influenza Preparedness (PIP) for 2014-2015, was developed and agreed with the MoH and other stockholders involved in influenza surveillance. **Conclusion:** For successful implementation of ILI and SARI surveillance and to ensure its sustainability, it is necessary to use and build upon the existing MoH surveillance system. The implementation must be accompanied by training of medical personnel, laboratory workers and Epi-surveillance officers. **Keywords:** Sentinel site; Influenza surveillance; Influenza preparedness.

Board 249. A North/South Collaboration Between Two National Public Health Institutes: A Model for Global Health Protection

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Background: Rapid international spread of emerging infections has increased interest in strategic collaborations, as they may be the best way to protect populations. Strategic collaborations can build capacity in less resourced settings. As specialised institutions that provide a stable locus of expertise, continuity of experience, scientific knowledge, and appropriate human, technical, and financial resources, national public health institutes (NPHIs) are well prepared to tackle public health challenges. **Methods:** We describe how a collaboration between the national public health institutes of England and South Africa built a mutually beneficial professional relationship to help implement the WHO International Health Regulations, build capacity for health protection, and promote the exchange of information, advice, and expertise. We illustrate how this can be achieved in a mutually beneficial way. **Results:** Over a period of two and half years (2011 to 2013), a senior consultant epidemiologist from PHE worked in NICD and 35 staff participated in short-term exchanges of two weeks to 3 months duration between both institutes. As epidemiologists were an uncommon resource in South Africa, NICD, the senior epidemiologist led not only to significant public health outputs but also facilitated the exchange of expertise and information between the UK and South Africa. On the other hand PHE staff working in South Africa were exposed to infectious disease outbreaks that are now rare occurrences in the UK, preparing them for similar challenges in the future. **Discussion:** In an inter-connected world, relationships with strategic partners may provide the best protection for the health of the public as they build capacity in less resourced settings. This collaboration between two national public health institutes led not only to important public health outputs for both countries, but also facilitated the exchange of public health expertise and information. This partnership may constitute a model for future public health collaboration and support implementation of International Health Regulations. Collaboration among NPHIs globally can increase our collective wisdom about using medical and public health services to contribute to understanding preventable causes of ill health.

Board 250. Rapidly Detecting and Containing Ebola Virus Disease When Introduced Into a Previously Unaffected Country, 2014

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Background: The Ebola Virus Disease (EVD) epidemic is the largest in history and the first in West Africa. Widespread transmission in Guinea, Liberia, and Sierra Leone places unaffected countries at risk for EVD. The International Task Force for EVD response at the Centers for Disease Control and Prevention (CDC) created a unit, the Unaffected Countries Team (UCT), to provide technical assistance to rapidly detect and contain EVD introduction. **Methods:** UCT's strategic approach is to rapidly detect, contain, and eliminate EVD upon introduction to a previously unaffected country. This strategy focuses on rapid detection of EVD cases through strengthening of country-specific early warning systems, alerting mechanisms, and ensuring timely access to an appropriate laboratory. Rapid containment and elimination includes a preparedness assessment followed by a workshop to correct identified deficiencies, field-level training in incident management and contact tracing, and case isolation. Establishment of CDC Ready Response Teams for immediate deployment to newly affected countries provides an opportunity for early intervention across a wide geographic area. Implementation of the strategy is a multi-national and multi-agency effort. **Results:** Thirteen priority countries were selected based upon proximity and air traffic to the countries with widespread transmission. Five of these are "high priority:" Guinea Bissau, Cote d'Ivoire, Senegal, Mali, and Ghana. Six of 13 countries (46%) have in-country capacity for specimen testing for EVD. In-country preparedness assessments revealed deficiencies in early warning systems, contact tracing, and availability of an incident management system. Country workshops focus on containment goals and contact tracing guidelines, with the execution of a real-time simulation exercise to test newly developed incident management infrastructure and operational plans. **Conclusions:** Unaffected countries must be prepared for introduction of an EVD case. The CDC UCT is working with the World Health Organization (WHO) and other international and regional partners to strengthen the ability of at-risk nations to quickly and efficiently detect and contain an introduction of EVD within their borders.

Board 251. Training and Capacity Building Initiatives in Support of the Global Health Security Agenda, 2012-2014

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Background: The Global Health Security Agenda, launched on 13 February 2014, called upon US government agencies to work together towards a vision of "a world safe and secure from global health threats posed by infectious diseases" by engaging with partner nations to strengthen their capacity for preventing avoidable epidemics, detecting infectious disease threats early, and responding rapidly and effectively. The Global Emerging Infections Surveillance and Response System Division of the Armed Forces Health Surveillance Center (AFHSC-GEIS) supports programs that strengthen global networks for real-time biosurveillance capabilities, train an effective biosurveillance workforce, and strengthen laboratory systems. **Methods:** Qualitative analysis was performed on quarterly and annual reports from AFHSC-GEIS partners engaged in capacity building initiatives. Through keyword and thematic analysis, these reports were analyzed for goals, objectives, and outcomes aligning with those of the GHSA. **Results:** In fiscal years 2012-14, AFHSC-GEIS supported a global health capacity building portfolio that included 67 projects in 34 countries. Specifically, AFHSC-GEIS partners executed health system improvements in six main areas: 1) electronic disease and biosurveillance systems (29 projects in 15 countries); 2) workforce development in WHO-approved epidemiology and outbreak response methods (23 projects in 20 countries); 3) tropical medicine training for host-country civilian and military personnel (11 projects in 10 countries); 4) training in, and capacity for, entomological surveillance and control methods (10 projects in 7 countries); 5) accredited laboratory practices and quality assurance efforts (34 projects in 21 countries); and, 6) health care facility and laboratory diagnostic capacity development (18 projects in 16 countries). **Conclusions:** While addressing global health security goals involves many challenges, there has been a progressive evolution of health security capacities within the Department of Defense partner network.

Board 252. Surveillance of Prion Diseases in São Paulo State—A Pioneer Experience in Brazil

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Background: Creutzfeldt-Jakob Disease (CJD), an ancient prion disease, acquired importance in 1996 with the first cases of the new variant of CJD (vCJD) in the UK associated with the consumption of meat cattle with Bovine Spongiform Encephalitis. We summarize the surveillance system of prion diseases coordinated by the Center for Epidemiologic Surveillance of the State of São Paulo and the results during the period 2000-2013. **Methods:** Description of the system, analysis of database and epidemiological research records and presentation of the epidemiological characteristics of cases according to the WHO classification criteria. **Results:** Of the 228 suspects reported, 179 (78.5%) were diagnosed as CJD: 84 (46.9%) as sporadic CJD, eight (4.5%) as familial CJD and 87 (48.6%) without genetic tests. No cases were identified as vCJD. Among the 179 cases, 15.1% were classified as Definite CJD, 61.5% as Probable, 11.7% as Possible and 11.7% in investigation. The average annual incidence rate was 0.34 cases/1,000,000 inhabitants; 48.6% were male; median age 64 years (range=20-86 years) and median duration until death 4 months (range=1-23 months). Genetic polymorphism was performed in 62 patients from 2010 to 2013, analyzed by direct sequencing of the PRNP gene: 58.1% showed methionine homozygosity at codon 129 (M129M), 24.2% heterozygosity methionine-valine (M129V) and 17.7% valine homozygosity (V129V), the latter described as less frequent but it gives the sporadic form clinical and laboratory characteristics of the vDCJ, when associated with prion protein type 1. Neuropathological study was performed after brain necropsy or brain biopsy *in vivo* or *post mortem* in 22 cases confirming the diagnosis in 20 (90.9%) of them. **Conclusions:** Although no patients with vCJD were registered, the system is capable to identify all prion diseases. However, some aspects require new discussion to improve the system: 1) Change the definition of suspected cases to be notified with more accuracy; 2) Reorganize and better prepare the autopsy services to increase brain necropsy on the cases; 3) Evaluate the cost-effectiveness of this surveillance considering the clinical complexity, the long incubation period and evolution, the tests carried out, the numerous biosafety and psychosocial issues involving patients relatives.

Board 253. Association of Public Health Laboratories: Partnering in the 2014 Ebola Outbreak Response

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Background: The Association of Public Health Laboratories (APHL) is the national nonprofit representing governmental laboratories that monitor and detect public health threats. These laboratories are at the forefront of protecting the nation's health with activities ranging from testing for biological threat agents, identifying outbreaks of infectious diseases, screening newborns for genetic and metabolic conditions to detecting chemical contaminants in people and the environment. However, the 2014 Ebola outbreak that began in West Africa presented new challenges for public health laboratories. To respond to these challenges, APHL strengthened its partnerships between multiple organizations, including the Centers for Disease Control and Prevention (CDC), the American Society of Microbiology (ASM) and the African Society for Laboratory Medicine (ASLM), to provide timely guidance and technical support to public health laboratories for domestic and international response efforts during the 2014 Ebola outbreak. **Methods**: APHL collaborated with CDC to prepare state and local public health laboratories to conduct Ebola testing and respond to questions from clinical laboratories. Additionally, APHL quickly developed and issued a template to assist the over twenty state and local public health laboratories selected to receive the Department of Defense real-time reverse transcription polymerase chain reaction (rRT-PCR) test to conduct a risk assessment of their facilities. APHL coordinated communications to the selected and other state and local public health laboratories and engaged the ASM in the development of guidelines for clinical laboratories. APHL worked with CDC and other partners, notably ASLM, to share situational updates and develop communication vehicles, including a webpage and the African Public Health Laboratories Network Listserv. **Results:** Public health laboratories are better prepared to respond to public health emergencies, specifically Ebola. **Conclusion:** APHL and its partners are committed to enhancing laboratory preparedness and response to public health threats and works to improve the capability and capacity of member laboratories, in their response to biological, chemical, radiological threats, and to other public health emergencies.

Board 254. Ranking Infectious Disease Risks to Support Public Health Prioritization in the European Union

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Background: In the past century, extensive change in environmental and societal conditions has led to important alterations in risks posed by infectious pathogens. Based on the number of emergence events of new or newly introduced pathogens in the area, Europe has been identified as a hot spot of infectious disease emergence. Future global changes can reasonably be expected to further affect these emergence risks. As the societal impact of future disease risks will not only depend on pathogen characteristics, but also on the anticipation of future disease risks and subsequent preparedness, there is a need for methodologies to prioritise infectious diseases over the entire spectrum of transmission pathways. In this ongoing project we will develop such a methodology. **Methods:** The methodology used for ranking is a multicriteria analysis. We specify a limited number of criteria and infer criteria-weights based on expert opinion. Rank-scores for pathogens are obtained by assigning one level within each criterion, transforming the level-values to a natural scale and applying a linear model with the criteria-weighting. Specific tasks of the project include: pathogen selection, criteria development, attribution of ranking-levels to criteria, assigning weights to criteria, and defining a summary measure for the ranking. The methodology will be iteratively improved and applied in studies by EU Member States as well as in a pan-European study. **Results:** The main result of interest from the methodology is the overall relative ranking of pathogens and the methodology to generating the ranks. This ranking will identify-amongst others-relevant (groups of) pathogens to focus on with priority. Member states will gain insight in their expected challenges for infectious diseases. Furthermore, aggregation of data from individual member states will provide an overview of priority infectious diseases at the EU-level. **Conclusions:** Infectious disease ranking and prioritization have been done before using different methodologies, providing valuable insight but comparing different studies is difficult. This project will develop a general framework for infectious disease prioritization and apply the framework to EU member states, thereby supporting EU Member States in their preparedness planning.

Board 255. Ebola Virus Disease Outbreak Management System for Case Management, Contact Tracing, and Symptom Monitoring in Tennessee

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Background: The Tennessee Department of Health (TDH) identified the need for a comprehensive outbreak management system, flexible for any disease and scalable for any size of outbreak. TDH constructed a database model to support case management, contact tracing, and symptom monitoring of contacts in the Research Electronic Data Capture (REDCap) web application, developed at Vanderbilt University. In October 2014, TDH expanded preparedness and planning activities for Ebola Virus Disease (EVD) and determined a targeted outbreak management system would be needed. **Methods:** The Epidemiology Branch of the Operations Section in the Incident Command Structure was tasked with revising the model database for EVD. Three categories of persons for investigation were identified: cases, contacts with high or low risk exposures, and travelers with low but not zero risk of exposure. The main database, Ebola Surveillance and Case Management, was designed to capture the following: initial interviews with the cases and contacts, follow-up healthcare visits, laboratory results, exposure setting details, and the links between cases, contacts, and exposure settings. A separate, secondary database for symptom monitoring was established for contacts and travelers. Hardcopy forms were developed to match the electronic forms, assembled with training guidance, and distributed to the Tennessee public health offices. **Results:** TDH developed the hardcopy forms, guidance, and a web-based data system for use by local public health offices in the event of a response to EVD. Initial training was first provided to the local public health officials regarding guidance on the immediate monitoring of travelers with low but not zero risk of exposure. Additional trainings for the fever and symptom monitoring of travelers were delivered via live webinars later in October. These trainings also covered the real-time data entry into REDCap and the investigation protocols for cases and contacts. Automated daily reports and an up to date visual dashboard enhanced communication with partners and health leadership throughout the course of the response. **Conclusions:** The Tennessee Department of Health has a developed a flexible and scalable outbreak management system in REDCap, tailored for use by public health entities, in response to Ebola Virus Disease.

Board 256. A Multi-site Knowledge, Attitude and Practice Survey of Ebola Virus Disease in Nigeria

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Background: The 2014 Ebola Virus Disease (EVD) outbreak was characterised by fear, misconceptions and irrational behaviours. We conducted a knowledge, attitude and practice survey of EVD in Nigeria to inform institution of effective control measures. **Methods:** Between July 30th and September 30th 2014, a cross sectional study on knowledge, attitude and practice (KAP) of Ebola Virus Disease (EVD) was undertaken among adults of the general population and healthcare workers (HCW) in three states of Nigeria, including Kano, Cross River and Bayelsa states. Demographic information and data on KAP were obtained using a self-administered standardized questionnaire. The percentage KAP scores were categorised as good and poor. Independent predictors of good knowledge of EVD were ascertained using a binary logistic regression model. **Results:** Out of 1035 study participants with median age of 32 years, 648 (62.6%) were males, 846 (81.7%) had tertiary education and 441 (42.6%) were HCW. There were 218, 239 and 578 respondents from Bayelsa, Cross River and Kano states respectively. The overall median percentage KAP scores and interquartile ranges (IQR) were 79.46% (15.07%), 95.0% (33.33%) and 49.95% (37.50%) respectively. Out of the 1035 respondents, 470 (45.4%), 544(52.56%) and 252 (24.35%) had good KAP of EVD defined using 80%, 90% and 70% score cut-offs respectively. Independent predictors of good knowledge of EVD were being a HCW (Odds Ratio-OR-2.89, 95% Confidence interval-CI of 1.41-5.90), reporting "moderate to high fear of EVD" (OR-2.15, 95% CI-(1.47-3.13) and "willingness

to modify habit" (OR-1.68, 95% CI-1.23-2.30). **Conclusion:** Our results reveal suboptimal EVD-related knowledge, attitude and practice among adults in Nigeria. To effectively control future outbreaks of EVD in Nigeria, there is a need to institute public sensitization programmes that improve understanding of EVD and address EVD-related myths and misconceptions, especially among the general population.

Board 257. Public Knowledge, Perception and Source of Information on Ebola Virus Disease—Lagos, Nigeria; September, 2014

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Background: The first ever outbreak of Ebola virus disease (EVD) in Nigeria was declared in July, 2014. It was among the West Africa EVD outbreak declared as Public Health Event of International Concern (PHEIC) by World Health Organization (WHO). In Nigeria, level of public knowledge, perception and adequacy of information on EVD were unknown. We assessed the public preparedness level to adopt disease preventive behavior during the EVD outbreak in Nigeria, which was premised on appropriate knowledge, perception and adequate information. **Methods:** We enrolled 5,322 respondents in a community-based cross-sectional study in Lagos, Nigeria. We used interviewer-administered questionnaire to collect data on socio-demographic characteristics, EVD-related knowledge of the cause, mode of transmission, prevention and health seeking behaviour, perception and source of information. We performed univariate and bivariate data analysis using Epi-Info software setting p-value of 0.05 as cut-off for statistical significance. **Results:** Mean age of respondents was 34 years (± 11.4 years), 52.3% were males. Forty one percent possessed satisfactory general knowledge; 44% and 43.1% possessed satisfactory knowledge on mode of spread and preventive measures, respectively. Residing in EVD cases districts, male respondents and possessing at least secondary education were positively associated with satisfactory general knowledge (p-value: 0.01, 0.001 and < 0.001 respectively). Seventy one percent perceived EVD as a public health problem while 61% believed they cannot contract the disease. Sixty two percent and 64% of respondents will not shake hands and hug a successfully treated EVD patient respectively. Only 2.2% of respondents practice good hand-washing practice. Television (68.8%) and radio (55.0%) were the most common sources of information on EVD. **Conclusions:** Gaps in EVD-related knowledge and perception exist. We conducted focused public health communication and education that raised knowledge level, promoted desired positive behaviour, corrected misconception and discouraged stigmatization.

Board 258. Chikungunya in Georgia: Preventing Local Transmission Through Rapid Response, 2014

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Background: In December 2013 local transmission of Chikungunya was first detected in the Americas. Transmission of the virus in the Caribbean brought the threat of travel-related cases and local transmission to the U.S. In June 2014, the Georgia Department of Public Health (DPH) was notified of several travelers returning from the Caribbean with suspect infections. Concern mounted quickly as competent mosquito vectors, Aedes aegypti and Aedes albopictus, exist in the state. DPH epidemiologists promptly developed a Chikungunya Response Plan (CRP) to facilitate rapid detection and prevent local transmission in Georgia. **Methods:** A guide for public health staff statewide, the CRP included information on disease background, laboratory testing, mosquito avoidance, questionnaires, case report forms, and media talking points. Protocols were developed to fill gaps in local response where mosquito control programs were non-existent. A physician guidance document was disseminated statewide. Local public health staff was trained to triage new suspect cases and field questions from concerned parties. To track suspect cases throughout Georgia, an electronic case investigation log was created in our web-based disease reporting system. **Results:** In the first 2 weeks of the response, the CRP was made available as DPH epidemiologists were investigating 19 travelers with suspect infections, of which 9 were later laboratory confirmed. Subsequently, suspect case-patients and travel companions have been quickly identified, tested if appropriate, and educated on mosquito avoidance. As of March 17, 2015 there have been 30 confirmed travel-related cases identified and no local transmission documented in Georgia. **Conclusions:** Despite the presence of competent mosquito vectors and a significant number of confirmed Chikungunya infections, the rapid development and dissemination of the CRP along with a collaborative effort to identify and investigate suspect cases statewide has facilitated the prevention of local transmission in Georgia. Although local transmission may occur in the future, case investigation protocols, widespread education, and collaboration with mosquito control partners will continue to support rapid and efficient response while helping to minimize the number of secondary cases.

Board 259. Perception, Attitude and Acceptability of Ebola Virus Screening Among Travelers at the Murtala Muhammed International Airport, Lagos, Nigeria

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Background: The epidemic of Ebola virus disease in Nigeria followed importation through an infected air passenger from a West African country with ongoing epidemic on 23 July 2014. Screening is one of the control measures for prevention, early detection and containment of Ebova virus outbreak. Screening measures are based on symptoms and risk assessment and can be adapted for air, land, and sea points of departure and arrival. The aim of this study was to determine the knowledge, attitude and acceptability of Ebola Virus screening among travelers at the Murtala Muhammed International Airport in Nigeria. **Methods:** A descriptive cross-sectional survey of 480 travelers selected by time location sampling technique was carried out using a pre-tested self-administered semi structured questionnaire in February 2015. Information on demographics, knowledge about Ebola Virus, acceptability and willingness to be screened were sought. Knowledge, perception and attitude were rated as good of poor using point scales assigned to responses, respectively. Data were analysed using descriptive

statistics, Chi square and multiple logistic regression at 5% level of significance. **Results:** Mean age of the participant was 33.5±12.3years. Most, 94.6% have heard about Ebola virus screening while 83.8% had heard about the Ebola virus disease. Those who had good knowledge were 294 (61.3%), good perception, 264 (55.0%) and good attitude to screening, 55.0%. Main sources of information on Ebola virus included internet 400(83.3%), newspaper 366 (76.3%) and radio 341 (71.0%). Being male (p=0.004), married (p=0.039) and allowing self to be screened believing that Ebola virus screening was for individual's safety (p=0.029) were found to be significantly associated with good perception of screening. Being a male (OR=1.6; 95% CI=1.1-2.3) and departing passenger (OR=1.6; 95% CI=1.0-2.2) were predictors of good perception of screening. Being comfortable with screening using the infrared thermometer (OR=2.9; 95% CI=1.4-5.8) and allowing self to be screened believing it is for individual's safety (OR =2.7; 95% CI =1.2-6.3) were predictors of good attitude. **Conclusions:** The good knowledge of the Ebola virus disease and screening among air travellers is encouraging. Health education on radio and inclusion in newsprint especially made available during flights are suggested to improve the perception and attitude of passengers to screening.

Board 260. Stuck at Home During a Public Health Emergency? There's an App for That!

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Background: The *Resource Response* mobile application is designed to help state and local health departments connect community resources to households that may need to stay home during infectious disease outbreaks. Outbreaks are unpredictable and untimely events for which people may not have time to prepare. If individuals' basic needs are met, they may be more likely to comply with public health recommendations to stay home. The United States is expected to have 200 million smartphone users by 2017; the exponential growth of smartphone use can be leveraged to connect households to the local health department and community partners. **Methods:** We developed the prototype *Resource Response* application using the Grails framework; it will be hosted using the Heroku cloud application platform. We designed the prototype with simplicity, compatibility across platforms, and the ability to preserve confidentiality as essential characteristics. **Results:** During outbreaks, health departments can distribute the application to affected households to input requests for items such as groceries, diapers, and medication refills, as well as needs related to housing, school, or communication with employers. Health departments can use this information to facilitate connections with resources from community partners --including businesses, schools, charitable foundations, community and faith-based organizations, and mental health programs. The community partners will be able to view an aggregate list of needs and input information about resources that they can provide. The application will produce daily reports for the health departments and provide data for program evaluation. **Conclusions:** By facilitating engagement with community partners, the prototype *Resource Response* application can enhance public health preparedness. This application may help health departments quickly organize resources to support people who need to stay at home for extended periods of time during infectious disease outbreaks.

Board 261. Local Health Department Measles Outbreak Response: Use of the Public Health Incident Command System

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Background: Between July 7 and 16, the Sedgwick County Health Department (SCHD) and the Kansas Department of Health and Environment (KDHE) investigated and reported 11 confirmed cases of measles in Sedgwick County, Kansas. The cases were linked and considered part of a larger outbreak that occurred in May and June in the Kansas City area. **Methods:** Because the number of cases and contacts of this highly contagious illness escalated quickly during the first week of the investigation, on July 14, SCHD activated the Public Health Incident Command System (PHICS) to structure outbreak response and designate more people and resources towards the effort. SCHD preparedness staff used existing templates and protocols to document activities and assign standardized ICS positions. **Results:** During the first week of PHICS, 16 people within SCHD were assigned positions. The largest PHICS section was Operations which included Investigation and Quarantine/Immunization Task Forces and a Communications Branch manning the newly established public measles hotline. Other activated sections included Planning, Logistics and Finance. Meetings occurred with PHICS and state health staff. Documentation included check in/out, ICS 214 Activity Logs, Incident Action Plans, communications log, and entry of measles reports into case management software. Epidemiologists conducted in-person interviews of cases and contacts at homes and by telephone. Nurses visited the homes of quarantined and/or isolated cases and contacts daily and documented vital signs, gave immunizations and immune globulin shots, and collected specimens as needed. On July 19, a Measles Point of Dispensing (POD) site was opened at SCHD for the public to receive MMR vaccine. When activity began to decrease on July 22, PHICS was scaled back and by August 6, ten staff remained in PHICS positions in three sections. Demobilization of PHICS occurred on August 26, two incubation periods from the date the last confirmed case was infectious. **Conclusions:** The use of PHICS created clear operational objectives and strengthened incident management for all staff, especially those who were unfamiliar with disease investigation and containment. PHICS allowed SCHD to quickly put in place disease containment measures which contributed to timely resolution of the outbreak.

Board 262. Evaluating Mass Influenza Vaccination Clinics in Puerto Rico, 2013-2014

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Background: Puerto Rico (PR) routinely conducts mass influenza vaccination clinics. In response to high rates of influenza activity and deaths during the 2013-14 season, PR increased the number and frequency of planned clinics from 8 (originally planned for October - April) to 14 (conducted from October - December). The influenza outbreak and clinics received heavy media attention causing increased demand for vaccination; a total of 74,087 vaccinations were administered in the 14 clinics. Clinics were separated into special population (SP) (e.g. elderly and handicapped) and general population (GP) sub-clinics. Two clinics were visited to evaluate clinic flow, patient characteristics and patient satisfaction in order to inform future mass vaccination clinics. **Methods:** Data were stratified

by clinic location, sub-clinic type, and clinic station. To assess patient flow, total time to complete the vaccination process and time spent at each clinic station was collected. Post-vaccination surveys were administered to assess satisfaction and patient characteristics such as demographic and previous influenza vaccination information. **Results:** A total of 6,246 vaccines were administered in the two clinics visited. Preliminary results indicate the average time to complete the vaccination process was 17:38 (mm:ss). The average time for SP patients was 17:92, and the average time for GP patients was 16:65. Patients spent an average of 6:15 at triage and 4:27 at vaccination stations. 75% of surveyed patients had never attended a mass vaccination clinic. While 57% received an influenza vaccination at some point in the past, only 28% received one the previous year. 99% of patients at the two clinics reported being satisfied or extremely satisfied with the clinic. **Conclusions:** Mass vaccination clinics during the 2013-14 season in Puerto Rico were able to reach individuals who were not routinely vaccinated against influenza. Throughput in these clinics was relatively quick and patients were satisfied with their experiences. Increasing access to vaccinations during vaccine preventable disease outbreaks through mass immunization clinics can effectively reach large numbers of people who may otherwise not be vaccinated. These results can help assist public health officials when planning such clinics.

Board 263. Building Multi-agency Response Capacity to Emergent or Bioterrorism-related Zoonotic Disease Outbreaks in Georgia

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Background: The Georgia Department of Public Health (DPH) routinely conducts surveillance for notifiable zoonotic diseases, including those that are emergent or agents of bioterrorism. DPH and the Georgia Department of Agriculture (GDA) collaborate whenever sporadic cases of notifiable zoonotic diseases are identified in humans or animals to ensure appropriate case management and disease containment. While responses to these cases have been efficiently managed, DPH and GDA identified the need to develop a coordinated multi-agency response strategy for zoonotic disease outbreaks (naturally occurring or man-made) to include public health, agriculture and veterinary professionals, and emergency management partners. **Methods:** DPH collaborated with stakeholders (GDA, Georgia Emergency Management Agency, Georgia Veterinary Medical Association (GVMA), and others) through a series of meetings sponsored by the Atlanta Health Security Advisory Committee (HSAC) to determine agency response actions for the animal health/veterinary community following the detection of a zoonotic disease outbreak. Protocols for interagency notification and communication were developed. A series of drills and a tabletop exercise were conducted to test the notification and communication protocols and to discuss results and next steps. **Results:** Interagency notification protocols were tested through drills involving the HSAC and GVMA. GVMA facilitated a communications drill for membership statewide which directed participants to contact the DPH Surge for Public Health Emergency Response (SUPHER) phone system to receive information and instructions in response to a zoonotic disease outbreak exercise. More than 800 veterinarians throughout Georgia participated. A tabletop exercise for HSAC members and animal health stakeholders was held two weeks later to discuss drill results and identify additional multiagency response issues that must be addressed following a zoonotic disease outbreak. **Conclusions:** Georgia's novel approach to engage animal health professionals in zoonotic disease outbreak planning and response resulted in formalized interagency notification and communication protocols and identified state and federal animal laboratory testing facilities that may be called upon during a response.

Board 264. Ebola Virus Networks in the News: Transmission Dynamics in the West African Outbreak

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Background: The Ebola Virus outbreak in West Africa has been spreading through various pathways, such as through family, hospitals, or funerals, at differing rates. As of March 15th, 24,701 cases and 10,194 deaths have occurred in 9 countries. Knowledge of those transmission pathways and chains could help public health officials focus their prevention efforts where they are most needed. **Methods:** By reading through articles from news outlets including the Washington Post, New York Times, and WHO, data were gathered on 283 confirmed, probable, and suspected EVD patients in 7 countries. The data collected include age, sex, location, timing, healthcare worker status, survival, hospitalization, travel, means of exposure, and reproductive rate. **Results:** Of the 224 patients whose means of infection are known, 52.2% were exposed through family members or within the household, 26.8% through hospital settings, 14.3% through funerals, 8.9% through caring for others, 1.8% through sex, 1.8% through hazardous waste, and 0.4% presumably through a zoonotic event. Of all 283 cases, 4.6% were exposed in more than one setting, and exposure was not stated for 20.8%. When the number of new cases was stated, the average reproductive rate was 0.85, and when including inferred new cases it was 0.91. Of the 230 cases with known outcomes, 73.9% died and 26.1% recovered, while 53 cases have unknown outcomes. **Conclusions:** Household and family transmission was the most common, and patients who introduced the virus to their families had the highest reproductive rate. Family transmission would likely have been lower had ambulances and hospital space been more available, but without those services family members remained in close contact, and many chose to care for each other. Hospital transmission was fairly frequent in articles about healthcare workers, but once hospitalized or treated in ETUs patients suspected to have EVD generally had low reproductive rates. Funeral transmission was less frequent, but had the potential for large spreading events.

Lessons Learned from Recent Flu Preparedness Activities and Flu Season

Tuesday, August 25, 12:30 PM - 1:45 PM

Grand Hall

Board 265. Risk Investigation of Multiple Avian Influenza Viruses Based on Seroprevalence in Occupational Exposure Populations in China

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Background: China faces a high risk of avian influenza virus to human beings as a number of human infections of avian influenza viruses were detected, including H9N2, H5N1, H7N9, H10N8, H5N6, etc. The specific backyard mixed culture mode and live poultry consumption pattern in China increase the risk of producing novel reassortant viruses, which may induce an influenza pandemic. **Method:** A systematic and comprehensive seroprevalence study of H5N1, H9N2 and H6 influenza viruses were performed using 15,700 sera samples collected from live poultry market, poultry farm, backyard poultry farm, slaughter factory and nature reserve between 2009 and 2011. Hemagglutination Inhibition (HI) assay was used as primary assay and the result of Microneutralization (MN) assay is considered as the endpoint. **Results:** The seroprevalence of avian influenza H9N2 and H6N2 are 3.89% and 0.4%, respectively.

However, only two positive sera against H5N1 were detected in the 15,700 samples. For the H9N2 viruses in different lineages, the seroprevalence of A/Guangzhou/333/99 (333), one of the G9 lineage virus, is significantly higher than A/Chicken/AK4/Anhui/2011 (AK4), which is also belong to G9 lineage, and A/quail/Hong Kong/G1/97 (G1), which is belong to G1 lineage (p<0.0001). The seroprevalence of H9N2 in live poultry market, poultry workers and backyard exposure populations is significantly higher than butcher and nature reserve workers. The seroprevalence of 333 and G1 is higher in elder age groups and descends along with a decrease in age groups. From geographical point of view, positive samples of H9N2 viruses are detected in all 22 sample collecting provinces except Heilongjiang (n=280). The seroprevalence in South of China is significantly higher than North (p=0.002). Positive sera of H6N2 virus are detected in all sample collecting provinces except Henan, Jilin and Liaoning. **Conclusion:** This is the first time to report human infection of H6 avian influenza virus. From the seroprevalence point of view, the risk of occupational exposure populations infection of three major avian influenza viruses circulating in poultry is H9N2, H6 and H5N1 in order. The result of this study pointed out that the surveillance of avian influenza H9N2 and H6 viruses in exposure populations in China should be strengthened.

Board 266. Burden of Influenza-associated Deaths in the Americas, 2002-2008

R. Palekar, P-Y. Cheng, E. Aziz-Baumgartner, D. Iuliano, M-A. Widdowson; CDC, Atlanta, GA, USA

Background: Influenza disease is a vaccine-preventable cause of morbidity and mortality. The Americas have invested in influenza vaccines, but few estimates of influenza disease burden exist to justify these investments in Central and South America. We estimated influenza-associated deaths for 35 countries in the Americas during 2002-2008. **Methods:** Annually, countries in the Americas report registered deaths to PAHO/WHO. We used respiratory and circulatory (R&C) International Classification of Disease (ICD-10) codes from seven countries with distinct influenza seasonality and high-quality mortality data to estimate influenza-associated mortality rates by age group (0-64, 65-74, and ≥75 years) using a Serfling regression model or a negative binomial model. Next, we calculated the percent of R&C deaths attributable to influenza by age group in these countries and applied it to the age-specific mortality in 13 additional countries with good mortality data but poorly defined influenza seasonality. We then grouped the remaining 15 countries, with poor mortality data, into WHO mortality strata, and applied the age and mortality stratum-specific influenza rate as calculated from the other 20 countries, with good mortality data. Finally, we summed each country's mortality estimate to calculate an average total annual number and rate of influenza deaths in the Americas. **Results:** or the 35 countries in the Americas, we estimated an annual median influenza-associated mortality rate of 1.9/100,000 among <65-year-olds, 29.4/100,000 among those 65-74 years, and 151.4/100 000 among those ≥75 years. We estimated that annually between 40,880 and 160,270 persons (median 79,057) die of influenza-associated illness in the Americas region. **Conclusion:** Influenza remains an important cause of mortality in the Americas, especially among the elderly.

Board 267. Characterizing Influenza Cases in China's First Sentinel Severe Acute Respiratory Infection (SARI) Surveillance System, February 2011–June 2014

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Background: In December 2009, the recent influenza A(H1N1)pdm09 pandemic prompted China to establish its first severe acute respiratory infections (SARI) sentinel surveillance system. We present 3 years of epidemiologic and clinical data from 10 sentinel hospitals, located in 10 provinces throughout China. **Methods:** A SARI case among those >5 years of age was defined as admission to a surveillance hospital with acute onset of fever, cough or sore throat, and tachypnea (respiratory rate >=25) or dyspnea. Separate age-specific case definitions were developed for children aged <=5 years. We used a standardized case report form (CRF) to collect data on demographics, medical history and clinical presentation and course. We collected nasopharyngeal specimens from case-patients to test for influenza subtype by real-time reverse transcription PCR performed at influenza network laboratories. We analyzed data collected from February 2011 to June 2014. **Results:** During the study period, we identified 6922SARI cases and completed CRFs on 6008 (87%).Among SARI cases, 485 (7%) were influenza positive. Among influenza cases, CRF data were available for 430 (89%); 303(70%) were influenza type A and 127 (30%) were influenza B. The median age of influenza-positive SARI cases was significantly higher than influenza negative SARI cases (28 vs 17 years, respectively, p=0.001). Compared to patients without influenza, a greater proportion with influenza were >=65 years old (26% vs. 20%, p=0.001) and a smaller were<5 years old (32% vs. 39%, p=0.006). . Influenza positive patients were more likely than others to have at least one underlying chronic medical condition (38% vs. 29%, p<.001), the most common for both groups being cardiovascular disease, metabolic disease and chronic obstructive pulmonary disease. Mortality was higher among influenza positive than influenza negative patients (4.2% vs. 1.8%, p=0.001). **Conclusions:** Findings from China's first SARI sentinel surveillance system suggest that compared with influenza-negative SARI cases, influenza SARI cases were older, more likely to have an underlying chronic medical condition, and had higher mortality. Continued, expanded SARI surveillance will identify populations most at risk for severe influenza and seasonality by region to inform prevention and control efforts.

Board 268. Epidemiology of Childhood Influenza Illness in the Post-pandemic Period in Bangladesh: 2010-2014

N. Homaira[1], E. Azziz-Baumgartner[2], M. U. Bhuiyan[1], K. Islam[1], M. Rahman[1], Z. Rahman[1], M-A. Widdowson[2], M. Rahman[3], S. P. Luby[1,2], K. Sturm-Ramirez[1,2]; [1]Intl. Ctr. for Diarrhoeal Diseases Res., Bangladesh (ICDDR,B), Dhaka, Bangladesh, [2]CDC, Atlanta, GA, USA, [3]Inst. of Epidemiology, Disease Control and Res. (IEDCR), Dhaka, Bangladesh

Background: Data on the evolving epidemiology of influenza in the post-pandemic period is needed to guide policy decisions relating to country-specific appropriateness of vaccine formulation. Here we present hospital-based epidemiological and virological surveillance data of influenza-associated childhood respiratory illness in the post-pandemic years. **Method:** During August 2010-July 2014, we conducted respiratory illness surveillance in four tertiary hospitals located in four dispersed locations of Bangladesh. Once every two weeks in the outpatient department (OPD) and once every week in the inpatient department (IPD), surveillance physicians collected nasal and throat swabs from all children aged <5 years, who presented with any two symptoms including fever, cough or difficulty breathing. Respiratory specimens were tested for influenza viruses using real-time RT-PCR. **Results:** We enrolled 3454 children with acute respiratory symptoms, 300 (9%) were positive for influenza; 26 in 2010, 63 in 2011, 61 in 2012, 96 in 2013 and 54 in 2014 (11% of the OPD specimens and 4% of the IPD specimens).

Among the 300 influenza positive children, 31 were aged <6 months, 61 were 6-12 months and 208 were 1-4 years. Among the influenza positive specimens 69% were positive for influenza A and 31% for influenza B. More than 70% of the influenza A positive specimens were positive for influenza A/H3... In 2010 33% of the influenza A positive children were infected with influenza A (H1N1) 2009, in 2011 7%, in 2012 84%, in 2013 22% and in 2014 none. A total of 28% of the children aged<6 months, 17% aged 6-12 months and 29% aged 1-4 years were infected with of influenza A (H1N1) 2009. Influenza A/H3 and A (H1N1) 2009 co-circulated throughout the year with increased detection rate between May-August in our surveillance population. **Conclusion:** The data suggest that the influenza A positive children in our surveillance were predominantly infected with influenza subtype A/H3. In addition majority of these children belong to age-group under current influenza vaccine recommendation. Children of Bangladesh may benefit from a standard trivalent influenza vaccine but year-long circulation may make timing of influenza vaccine a challenge.

Board 269. Comparison of the Seasonality of Influenza A and B in Thailand, 2009-2014

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Background: Although influenza is considered a perennial disease in tropical climates, standard seasonality indices have not been calculated. We used data from 11 sentinel sites in Thailand to describe the seasonality of influenza A and B (2009-2014). **Methods:** A convenience sample of up to 10 cases of influenza-like illness (ILI) was enrolled each week per site and a throat or nasopharyngeal swab tested by real-time reverse transcription polymerase chain reaction. The total influenza A and B positive specimens each week was adjusted for the actual number of specimens collected and the proportion of influenza cases by type was calculated by dividing the weekly total by the total number of influenza A and B specimens identified over the putative influenza season (beginning week 22, June). The Gini coefficient, ranging from 0 for an equal distribution throughout the year to 1 for an unequal distribution, was calculated for each influenza type, and 95% confidence intervals (CI) were computed using bootstrapping. The start and end of the actual season each year for each influenza type was defined as the first week in which the cumulative proportion of positive specimens exceeded 10% and 90%, respectively. **Results:** Between 2009 and 2014, 15,910 ILI cases were tested and 3398 (21%) were positive, 2070 (61%) of which were influenza A and 1331 (39%) were influenza B. The median Gini coefficient for influenza A and B across the five years was 0.54 (range, 0.30-0.67) and 0.51 (range 0.38-0.76), respectively, and the 95% CI excluded 0 for both influenza types across all years, indicating significant seasonality. The median week that signaled the start of the influenza season was similar for influenza A (week 31, range 29-37) and B (week 30, range 23-53) and 50% of influenza A and B specimens were accumulated in a median of 12 (range 7-17) and 13 (range 10-37) weeks, respectively. The median duration of the influenza A season (29 weeks, range 19-34) was similar to influenza B (30 weeks, range 18-46). **Conclusions:** Although influenza in tropical Thailand is transmitted year-round, both influenza A and B showed similar seasonality, although the start of the influenza B season was variable. This standardized method can be used to compare the seasonality of influenza between zones, as well as monitor seasonal trends over time and between influenza types.

Board 270. Lessons Learned During the Influenza Pandemic of 2009-2010 in Kazakhstan

S. Aubakirova; Dept. for Consumer Protection, Astana, Kazakhstan

In 2009, a new virus subtype A/H1N1/09/California/ spread widely throughout the country causing another influenza pandemic, just like it did in more than 136 other states across the globe. **Methods:** Descriptive analysis of influenza routine surveillance data. **Results:** In July 2009 first 12 cases were detected in Kazakhstan among children of Astana. Selected throat and nose swabs of the patients were examined in the laboratory of Astana by PCR, which within 12 hours identified the virus as influenza A/H_1N_1-09. Today, the experience gained in managing the 2009 influenza A/H_1N_1-09 epidemic prioritizes the importance of measures such as isolation and treatment of patients, medical monitoring of the contacts, daily checkups (active visits) of people in risk groups, arrangement of health posts in schools and morning screenings in preschool institutions, preventive treatment with antiviral medicines, vaccination campaigns against influenza, personal hygiene (cough hygiene, hand-washing), as well as mandatory recommendation to wear masks not only in medical institutions, but also in places of potential contact with a large number of people (drivers of public buses, cashiers in malls). In the absence of an influenza vaccine during the July 2009 pandemic, the use of antiviral drug Tamiflu in pregnant women with flu symptoms has dramatically reduced all forms of complications and mortality among pregnant women. An important component of managing an influenza epidemic is selecting a correct stance in working with the media. The main purpose of a communication campaign must be to develop common understanding and to properly present the situation. Communication measures should enhance public confidence and be a key contributor to the success of all interventions. **Conclusions:** It was considered epidemiologically unreasonable to quarantine healthy individuals, cancel cultural events in educational institutions, close borders, and introduce body temperature control at the airport, request healthy people to wear masks outside of hospital facilities, or interrupt school training.

Board 271. Epidemiologic, Virologic and Clinical Characteristics of Adenovirus-associated Respiratory Illness at Five US Military Hospitals, 2009-2014

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Background: Adenovirus is a cause of influenza-like illness (ILI) among children and adults. The burden of ILI due to adenovirus is not known. Moreover, characterization of the epidemiology, virology and clinical characteristics of adenovirus-associated respiratory illness is needed. **Methods:** An observational study of febrile ILI (i.e., fever, respiratory symptoms and/or sore throat) among otherwise healthy 0-65y subjects at five US military hospitals is ongoing. Nasopharyngeal specimens are tested by single reaction PCR for influenza, rhinovirus, and adenovirus. Adenovirus-positive specimens were further subjected to multiplex assay for co-infecting viral pathogens. **Results:** From 11/2009-05/2014, a total of 1536 cases of ILI were enrolled. Of these, 43 (2.8%) were positive for adenovirus. The median age of cases was 3.4 (range: 0-41) yrs. Three cases were hospitalized, including 1 child and 2 adults. Type information

was available for 33 (76.7%) cases. The most frequent subtype isolated was type C (n= 21) followed by B3 (n=9) and one each of E4a, D46 and A. Type C infections were noted to be significantly more common in children (P<0.01). Rates of co-infection were high and substantially higher in children than adults (66% vs. 38%; p=0.23), although the difference was not statistically significant. Co-infections included influenza (32%), rhinovirus (27%), and RSV (23%). Symptoms were generally mild, regardless of type, and most commonly included cough (90%), fatigue (79%), rhinorrhea (74%), loss of appetite (71%) and sore throat (64%). However, children with non-type C infection were more likely to report sore throat (p=0.05) and hoarseness (p=0.06), compared to those with type C. **Conclusions:** In otherwise healthy individuals, adenoviruses are infrequent causes of ILI. Particularly among children, adenovirus is associated with other respiratory viruses. Non-type C infections tended to be more severe, suggesting type-specific differences in virulence and/or host response to infection.

Board 272. Comparison of the Fall 2013 and Spring 2014 Waves of the Avian Influenza A(H7N9) Outbreak of Human Infections in China

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Background: Novel avian influenza A(H7N9) was first detected in China in March 2013. To date, two waves of human infections have occurred. We compared the epidemiologic and virologic characteristics of the outbreak's first two waves. **Methods:** Wave 1 (W1) included laboratory-confirmed H7N9 cases with illness reported from March 31-September 30, 2013. Wave 2 (W2) included cases reported from October 1, 2013-September 30, 2014. Doctors and local public health staff reported demographic, clinical, and epidemiologic data for case-patients to China Information System for Disease Control and Prevention. The Chinese National Influenza Center conducted genomic sequencing and antigenic analysis on viruses isolated from human and environmental specimens across both waves. **Results:** There were 134 case-patients in W1 and 44 deaths (CFR: 33%); W2 had 306 case-patients and 128 deaths (CFR: 42%, P=0.08). Twelve provinces reported cases in W1 and 14 in W2, 4 of which were new. In W1, Zhejiang, Shanghai and Jiangsu provinces had the most H7N9 cases (80%) compared with Guangdong and Zhejiang (66%) in W2. The number of townships reporting at least one H7N9 case expanded from 112 in W1 to 268 in W2; only 9 reported cases in both. The median age of patients in W1 was older than in W2: 61 (3-91) years vs. 57 (1-88) years, respectively (p=0.03). Also, the median age at death was older in W1 than W2: 66.5 (27-91) years vs. 63.0 (20-86) years (p=0.04). Men accounted for the majority of patients in both waves (70% vs. 69%, p=0.80). Few patients were aged <15 years in both waves (4.5% vs. 6.2%, p=0.47).The majority of patients in both waves had contact with live birds (83% vs. 84%, p=0.76), and most had visited live-poultry markets (75% vs. 78%, p=0.53). Of 78 viruses isolated from humans and 52 from the environment, no new known substitutions were identified comparing W1 and W2 on the critical binding position of the virus and receptor. **Conclusions:** The epidemiology and virology of the W1 and W2 A(H7N9) outbreak in humans was similar. However, case-patients in W2 were younger and had a lower age at death. W2 had more than twice as many patients as W1, and involved new administrative regions, suggesting a geographic shift and expansion of the outbreak. Maintaining vigilant surveillance throughout China is required to monitor and control this ongoing epidemic.

Board 273. Effectiveness of Using Standard Case Definitions for Influenza-like Illness in the Republic of Kazakhstan During the Epidemic Seasons of 2010-2011 and 2012-2013

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Introduction: Since 2008, the Republic of Kazakhstan performs the year-round sentinel surveillance (SS) for influenza-like illness (ILI). The purpose of this study was to refine the standard case definition to achieve greater preciseness in ILI patients sampling for epidemiological and laboratory influenza surveillance in Kazakhstan. **Methods:** We analyzed clinical and laboratory data for the period from week 40 to week 18 of 2010-2011 and 2012-2013 seasons from 5 sentinel cities, where different standard case definitions (SCD) proposed by the WHO/Europe were used (the "old" one, effective until 2011, i.e. body temperature ≥38oC and cough and/or sore throat; and the "new" one, in effect since 2011, i.e. body temperature ≥38oC and cough). The study was performed using EpiInfo 3.3.2, calculations focused on sensitivity, specificity, comparison of positive and negative predictive values (PPV and NPV), the odds ratio (OR), P-value of symptoms, and of a complex of symptoms. **Results:** The 2010-2011 season data demonstrated that where the "old" SCD was used for the ILI, the symptom 'cough' produced a high sensitivity (91%) and NPV of 89%, but a low specificity (23%), and PPV of 27% which is below average, OR - 3.0, P-value - 0.009. Exclusion of the 'sore throat' symptom reduced the sensitivity to 32.8% but increased the specificity to 74%; exclusion of 'cough' negatively impacted the sensitivity reducing it to 9%, and the PPV to 1%. Where the "new" SCD for ILI was used in 2012-2013 season, exclusion of the 'sore throat' symptom resulted in sensitivity of 61%, specificity - 52%, PPV - 40%, NPV - 72%, OR - 1.71 and P-value - 0.02; exclusion of all other symptoms apart from the 'body temperature ≥38.0°C' and 'cough' resulted in sensitivity of 27%, PPV - 38%, and NPV - 67%. Exclusion of the 'sore throat' from the list of mandatory symptoms had a positive impact on sensitivity and PPV, yet the amount of samples was not affected. **Conclusions:** An attempt to use an SCD for ILI which excludes all non-essential symptoms can have a negative impact both on the amount of samples collected, and the number of PCR (+) tests.

Board 274. Use of Rapid Influenza Diagnostic Tests: Impact on Treatment and Health Outcomes of Hospitalized Influenza Cases

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Background: While rapid influenza diagnostic test (RIDT) results assist clinicians in treatment decisions, due to low sensitivity of the tests, exclusively relying on RIDT results may compromise decisions to use antivirals and timeliness of treatment. Decisions to forego or delay treatment with antivirals based upon negative RIDT results

may be particularly problematic among patients hospitalized with influenza or influenza-like illness (ILI). **Methods**: The New York State Department of Health's Emerging Infections Program participates in CDC FluSurv-NET by conducting active population-based surveillance for all laboratory-confirmed influenza cases hospitalized in the eight Albany area counties. To ascertain all cases, hospital laboratories are encouraged to submit both positive and negative RIDT specimens for hospitalized patients to the Wadsworth Center (WC) for PCR testing. We present results comparing the use of antivirals and disease severity among hospitalized patients initially diagnosed negative by RIDTs and later confirmed as PCR+ by the WC to patients initially diagnosed positive. **Results:** During the 2013/14 season, in the eight Albany area counties, a total of 523 hospitalized influenza cases were identified. Of these, 180 (34.4%) initially tested negative by RIDT at the local hospital lab but were later confirmed as PCR+ at the WC. Medical chart reviews showed that 18.9% of the RIDT-/PCR+ patients were treated with antivirals compared to 83% of patients initially testing positive for flu. ICU admissions did not differ between the two groups. RIDT-/PCR+ patients were more likely to die (6.7%) compared to initially positive patients (3.2%). RIDT-/PCR+ patients were also more likely to be hospitalized for 6+ days (37.8%) versus 26.4% among those initially positive patients. **Conclusions:** The high proportion of patients who were rapid negative upon hospital admission but later confirmed to have influenza, supports the recommendation that the decision whether to administer antivirals should be based on clinical presentation, underlying health factors and other epidemiologic factors of patients with suspected influenza, and not exclusively on rapid test results. Initiating antiviral treatment should not be delayed pending confirmatory testing results.

Board 275. Human Infection with a Novel, Highly Pathogenic Avian Influenza A (H5N6) Virus: Virological, Pathological and Clinical Findings

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Background: No human infection with avian influenza A (H5N6) virus was reported previously. Here, we report the virological, pathological and clinical findings of a fatal human infection with a novel H5N6 virus. **Methods:** We obtained and analyzed clinical, epidemiological, virological and pathological data from the patient. RT-PCR, viral culture and sequencing were conducted for determination of causative pathogen. Hematoxylin-Eosin (H&E) and immunohistochemistry (IHC) stains were performed for pathological evaluation of autopsy tissues. **Results:** The patient presented with fever, severe pneumonia, leucopenia and lymphopenia, developed septic shock and ARDS, and died at day 10 after illness onset. Novel reassortant avian-origin influenza A (H5N6) viruses were isolated from throat swab, trachea aspirate and autopsy tissues from the patient. The HA gene belonged to Clade 2.3.4.6 H5N1, with six internal genes closely related to Clade 2.3.2.1. NA was most closely related to avian influenza A (H6N6) virus. The virus had multiple basic amino acid motif in HA cleavage site indicating HPAI virus. The receptor-binding site of HA contained 226-228 QRG which suggested that the virus preferentially bound avian-like receptor (α2,3-SA). The molecular markers associated with increased pathogenecity in mammalian were detected including L89V, G309D, R477G, I495V, D701N in PB2, and D92E in NS1.The virus predominantly replicated in lung and trachea, and caused major damage in lung tissue, but also detected in extrapulmonary tissues. **Conclusions:** A novel HPAI H5N6 virus with the backbone of H5N1 virus acquired NA gene from H6N6 virus was first identified, and caused human infection with severe respiratory disease.

Board 276. Dynamic Re-assortment of Novel Influenza A (H7N9) with Circulating Influenza Viruses in Guangdong, China, 2013-2014

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Background: On March 30, 2013, a novel influenza A (H7N9) virus was detected in Eastern China. Although the first Guangdong H7N9 human case was detected on August 10, 2013, Guangdong identified 109 between September 2013 and September 2014. To characterize the virus and its transmissibility, we sequenced and analyzed environmental H9N2 strains circulating in Guangdong, in addition to H7N9 isolates from Guangdong patients. **Methods:** We sequenced isolates from the index case, four patients diagnosed from August to December 2013, and seven H9N2 environmental isolates collected from April to June 2013. Phylogenetic trees were drawn for eight influenza gene segments: hemagglutinin (HA), neuraminidase (NA), nucleoprotein (NP), polymerase (PA), matrix (M), nonstructural (NS), polymerase basic 1 (PB1) and 2 (PB2) proteins with MEGA software using Generalized Time Reversible GTR+G model. To assess robustness of individual node on phylogenetic tree, a bootstrap resampling process was used (1000 replications) with the neighbor-joining approach. We compared the sequence from our patients with those from environmental isolates and patient isolates from other provinces. **Results:** Phylogenetic analysis of the H7N9 virus from the first patient showed that HA, NA, PA and M genes shared high sequence similarity with other H7N9 viruses from Eastern China, while the four internal genes NS, NP, PB1 and PB2 were more closely related to local circulating H9N2 viruses. Similar re-assortment patterns were also found in isolates from Guangdong's other patients. For the isolates from these other patients, in addition to re-assortment of NS, NP, PB1 and PB2 genes with local circulating virus, there were mutations in these four genes such that the sequence more closely resembled the local H9N2 viruses. Further, the PA gene also shared high similarity with local H9N2 viruses. **Conclusions:** Guangdong's index patient's isolate's external genes shared high similarity with the H7N9 virus from the East, suggesting the virus was imported and then re-assorted with local H9N2 viruses. Sequencing from the other patients' isolates showed that novel H7N9 virus has likely reasserted with local H9N2 viruses and then transmitted within Guangdong. Continued virologic analyses will increase understanding of outbreak spread.

Board 277. Significance of Phenotypic and Genotypic Characteristics of Influenza Viruses Identified in the Republic of Moldova

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Background: The epidemic process of influenza morbidity in 2013/2014 season has been manifested by regional geographical spread, medium intensity - 14.70/0000, absence of lethal cases, low impact on the health system. Influenza vaccine coverage of the groups with increased risk of infection has accounted for 83%. **Methods:** During the 2012/2014 period in the NIC Moldova in collaboration with Influenza Center of Institute "Cantacuzino", Bucharest and the WHO CC on Influenza, London were isolated in MDCK cells cultures and identified by HAI test 45 influenza viruses: 10 - A(H1N1)pdm, 24 - A(H3N2, and 11 - influenza B virus from patients with presumptive clinical diagnosis ILI, ARI, and Pneumonia. **Results:** Dominant influenza viruses during 2012/2013 influenza season were A(H1N1)pdm (48 %), and during 2013/2014 season - influenza A(H3N2) (95 %) viruses. Strains studied by HAI test

were not significantly different from antigenic variants of reference influenza viruses and are considered similar to A/California/7/2009 H1N1pdm and A/Texas/50/2012 H3N2, B/Florida/60/2008 - B/Victoria-lineage and B/Massachusetts/02/2012 - B/Yamagata-lineage influenza viruses respectively. The phylogenetic trees demonstrated that influenza viruses A(H1N1)pdm fall into genetic group 6C (common substitution D97N in gene HA1), influenza viruses A(H3N2) - genetic group 3C.3 (common substitutions N145S, V223I in gene HA1, and D158N in gene HA2 - resulting in the loss of a potential glycosylation site) and influenza B viruses - genetic groups 2 (common substitutions T121S, T75N, T181A, D196N in HA gene), and 3 (common substitutions S150I, N165Y, G229D, D196N). All isolates of influenza viruses in neuraminidase inhibition assay were sensitive to neuraminidase inhibitors: Oseltamivir and Zanamivir and were similar to those included in vaccine formula recommended by WHO. **Conclusions:** Obtained results demonstrate that the segment regarding the highlight and evaluation of the phenotypic and genotypic properties of influenza viruses has an important significance for the Republic of Moldova in the context of policy on influenza vaccine use, optimization of the treatment management and prophylaxis of mentioned infections, prognosis of the epidemic process and significant reduce of the negative impact on the health system.

Board 278. Application of the World Health Organization (WHO) Case Definition for Suspect Influenza A(H5N1) Case Detection in the Primary Health Setting, Indonesia: Big Effort, Low Yield

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Background: In virus-endemic areas of Indonesia, influenza A(H5N1) cases are often only detected after illness has progressed to require hospitalization in a tertiary health facility, thereby triggering laboratory testing. Few cases have been detected in primary health settings, resulting in treatment delay. We applied the WHO case definition for suspect A(H5N1) to respiratory illnesses in primary health facilities in an area endemic for A(H5N1) virus in birds to assess if it could improve case detection. **Methods:** From 2011-2014, all patients meeting the case definition for influenza-like illness (ILI) in 4 primary health centers in East Jakarta were enrolled. A questionnaire was administered with clinical and A(H5N1) exposure questions per the WHO suspect A(H5N1) case definition (unexplained acute respiratory illness with fever (T>38 ºC) and cough, shortness of breath or difficulty breathing AND experienced one or more exposures). Exposures included close contact with an A(H5N1) case; exposure to birds, their remains, or contaminated environments; consumption of raw or undercooked poultry products in an area where A(H5N1) infections were reported; or close contact with a confirmed A(H5N1) infected animals. Respiratory specimens were collected from all ILI cases and tested for influenza viruses by RT-PCR. Proportion positive for A(H5N1) virus and proportion that met the WHO suspect case definition were calculated. **Results:** Of 6,334 ILI cases enrolled, 17% were positive for influenza A, of which 56% were positive for A(H3) and 44% were positive for A(H1N1pdm09), with none positive for the H5 subtype. However, 39% of ILI cases met the WHO suspect H5N1 case definition. Exposures mostly reported by ILI cases were consumption of undercooked poultry products (35%), visits to live poultry markets (15%) and owning poultry (14%). **Conclusions:** The WHO case definition was applied in a primary health setting, resulting in identification of many individuals with both ILI and A(H5N1) exposures, but no detection of A(H5N1) infection despite enrolling and testing >6000 outpatients. Possible explanations include that human A(H5N1) infection may be rare or that mild A(H5N1) infections may be rare. However, increased testing for A(H5N1) in an outpatient setting may result in earlier detection in some case-patients.

Board 279. Establishing the Sentinel Surveillance System for Severe Acute Respiratory Infections in Lebanon, 2014: Better Understanding the Epidemiology of Influenza

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Background: In context of the epidemic and pandemic preparedness for influenza in the Eastern Mediterranean Region, Lebanon has been supported to establish a sentinel surveillance for Severe Acute Respiratory Infections (SARI). Objectives of SARI surveillance in Lebanon are to: better understand the epidemiology of influenza, detect outbreaks, identify seasonality and circulating respiratory virus strains, and contribute to the regional and international influenza networks. Here we highlight the implementation process. **Methods:** The process followed consisted of four phases. First phase was the selection of hospital sentinel sites. The sites were selected according to its geographic distribution, representativeness, and sustainability of conducting surveillance at the site. Sites were visited and assessed using a standardized questionnaire filled on-site and gathering information on human and laboratory capacity, turnover of patients that meet the SARI case definition, and willingness of the site to enroll. A focal point was designated for each site mission of which is to aid in implementing the surveillance process. Second phase is the formulation of a national protocol and establishment of an expert group with the oversight function. Third phase is the training of the involved staff on proper case finding, data collection, specimen collection, data analysis, laboratory testing, and indicator monitoring. Fourth phase is the procurement of necessary supplies and equipment for the sites and the national influenza center. **Results:** Phases one and two of the process have already been accomplished. Twelve hospitals were selected as sentinel sites and a focal point was identified for each site. An expert group meeting was conducted and the national protocol was discussed. Another meeting is scheduled for final consensus. Phase three has been scheduled, where all focal points will be trained on SARI surveillance protocol. The fourth phase has been initiated and almost all supplies needs have been identified. **Conclusion:** Implementation of a sentinel surveillance for SARI in Lebanon will contribute to enhancing the national public health capacity for detection, prevention and effective response to any emerging respiratory disease threats in addition to better understanding the epidemiology of influenza.

Board 280. Has H7N9 Spread Beyond China? An Assessment Based on Lessons Learned from H5N1

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Background: Low-pathogenic avian influenza (LPAI) A(H7N9) [H7N9] virus emerged in China in February 2013 and has caused over 450 cases of human infection; however, no autochthonous human or poultry cases of H7N9 have been reported outside of mainland China. In contrast, when highly-pathogenic avian influenza (HPAI) A(H5N1) [H5N1] re-emerged in China in 2003, >30 human cases were detected in Vietnam and Thailand within 12 months and poultry outbreaks were reported in six countries in Southeast Asia. It remains unclear if the lack of reported H7N9 infection among humans or poultry outside mainland China represents a lack of spread or lack of detection. **Methods:** We assessed key epidemiologic and virologic characteristics of H7N9 and H5N1. Using H5N1 as a historical example, we sought to predict future spread of H7N9 in Southeast Asia. We described human and poultry surveillance data from Vietnam, Cambodia, Laos, and Thailand to assess the likelihood that H7N9 infections in these countries would have gone undetected during the period of highest H7N9 virus circulation in China. **Results:** H5N1 and H7N9 viruses can cause severe disease in humans, do not transmit easily from person-to-person, and human infections are frequently related to poultry exposures. However, H7N9 infections in humans typically occur in older individuals compared to H5N1 infections. Using national surveillance systems for respiratory infections in humans, Vietnam identified four (>2,500 specimens tested from sentinel and non-sentinel platforms for influenza) Cambodia eight (3,849 specimens from sentinel surveillance tested for influenza), and Laos (2,248 specimens tested for influenza), and Thailand (>4,800 specimens tested for influenza) zero H5N1 human infections from April 1, 2013-May 30, 2014. During that same period, Vietnam, Cambodia, Laos, and Thailand detected no cases of H7N9 in poultry. **Conclusions:** Surveillance systems in Southeast Asia are able to detect cases of H5N1 and should likewise be sufficiently sensitive to detect H7N9 infections in humans. Although we cannot rule out the potential occurrence of human H7N9 disease in Southeast Asia, substantial spread of H7N9 with human infection is unlikely to have occurred in Vietnam, Thailand, Cambodia, and Laos as of October 2014.

Board 281. Severe Acute Respiratory Infections in Border Populations in Southern Arizona, 2010-2014

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Background: The Border infectious Disease Surveillance program has conducted surveillance for Severe Acute Respiratory Infections (SARI) on the U.S.-Mexico border since 2009. Here we describe the characteristics of patients in Southern Arizona during 2010-2014. **Methods:** Patients admitted to 5 large acute care hospitals that met the SARI case definition were enrolled. A SARI case was defined as temperature ≥100°F or reported fever with history of cough, sore throat or shortness of breath in a hospitalized person. A case report form was completed with demographics and clinical details. Nasopharyngeal swabs were collected and tested for respiratory viruses by reverse transcription polymerase chain reaction. **Results:** From October 2010- September 2014, we enrolled 332 SARI patients. The majority of cases were male (52%) and white non-Hispanic (48%). The median (range) age was 63 (0-97) years, with 47% aged ≥65 years and 5.2 % aged <5 years. During hospitalization, 51 (22%) of 230 patients required tracheal intubation, 120 (40%) of 297 patients were admitted to ICU, and 28 (10%) of 278 died. Of the 309 cases tested for viral pathogens, 16% (n=49) were positive for influenza viruses, 8% (n=24) for human metapneumovirus (HMPV), 6.5% (n=20) for parainfluenza viruses, 5.8% (n=18) for coronavirus, 4.5% (n=14) for rhinovirus, 3.6% (n=11) for respiratory sincycial virus (RSV), 2.3% (n=7) for coxsachievirus, 1% (n=3) for adenovirus. Among the 49 influenza positive specimens, 76% were influenza A (19 H3N2, 17 H1N1pdm09, and 1 not subtyped) and 24% (n=12) were influenza B. Influenza activity was between October-April except for the 2013-2014 season where four cases of influenza virus were isolated in May, June and July. Eleven cases that died had a pathogen identified (3 coronaviruses, 3 influenza viruses, 2 HMPV, 2 parainfluenza viruses, 1 rhinovirus). Among cases with influenza vaccination history, 56% (n=138/245) self-reported vaccination within one year of the onset of the illness. **Conclusion:** Influenza was a frequent cause of SARI in hospitalized patients in Southern Arizona. Monitoring respiratory illness in border populations will help us better understand the causes and identify appropriate prevention strategies.

Board 282. Measured Voluntary Avoidance Behavior During the 2009 A/H1N1 Epidemic

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Background: The World Health Organization and other public health bodies have emphasized an important role for "distancing" or non-pharmaceutical interventions. Interpersonal contacts play a critical role in infectious disease transmission, and recent advances in epidemiological theory suggest a central role for adaptive human behavior with respect to changing contact patterns. If individuals perceive that contact with others carries a high enough risk of infection, they may voluntarily take action to avoid unnecessary public contacts. However, this theory of avoidance has remained largely untested, except for in specific cases that make it difficult to extrapolate back to the broad population. Neglecting this important human-pathogen feedback can lead to overestimation of the benefits of social distancing policies. **Methods:** We test whether the American public engaged in voluntary avoidance behavior during the 2009 A/H1N1 epidemic using time-use data from the American Time Use Survey. We estimate a fixed effects regression model of daily time spent at home on A/H1N1 prevalence in the US between 2008-2010. We control for health status, socioeconomic and demographic characteristics, day of week, and weather. We then construct two sets of probabilistic age-structure contact matrices: one set based on the time use data during the epidemic period (April-December) in each year 2003-2012, and another based on the pre-epidemic period (January-April). We simulate a set of SIR models based on each contact matrix and compare the attack rates of the two time periods in each year. **Results:** We find that Americans voluntarily reduced their time spent in public places by approximately 30 minutes during the 2009 A/H1N1 swine flu, which reduced the total number of infections by approximately 16%. We show that the mixing patterns in 2009 yield the lowest number of total cases relative to if the epidemic had occurred in an of the other ten years. **Conclusions:** Our empirical results suggest that neglecting voluntary avoidance behavior in epidemic models may overestimate the public health benefits of public social distancing policies.

Board 283. Triple Combination Antiviral Drug Therapy Against H3N2 Variant Influenza Virus

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Background: Vaccines are normally an effective safeguard against seasonal influenza but may be inadequate if a novel influenza emerges. When prevention of influenza is compromised, medical intervention rests on treatment of active infections with antivirals. Our objective was to test the triple combination antiviral drug (TCAD) therapy against a novel H3N2 variant virus carrying genes from avian, swine, and human origins. TCAD therapy has previously shown to be effective against seasonal and H5 influenza strains. We hypothesized that TCAD therapy_ consisting of three drugs with different mechanisms of action and functioning at distinct points in the virus lifecycle_would produce synergistic antiviral activity against A/Indiana/11/2011 (H3N2v) virus. **Methods:** In this study, we assessed the *in vitro* antiviral activity of single, double, and triple combinations of amantadine (AMT), oseltamivir carboxylate (OSC), and ribavirin (RBV) against H3N2v using CPE inhibition assays in MDCK cells. Synergy is assessed in dual combinations of drugs and in triple combinations using fixed concentrations of AMT. **Findings:** Each drug combination was tested in 96-well plates seeded with MDCK cells. A control experiment with drugs in the absence of virus was also performed. TCAD therapy achieved a therapeutic effect with lower doses of component drugs compared with monotherapies of antivirals as single agents. **Conclusions:** This study supports that combination therapy offers a broad spectrum treatment option, as seen against other seasonal and avian strains, and could potentially play a role in pandemic preparedness. Author Note The views expressed in this research are those of the authors and do not necessarily reflect the official policy or position of the Department of the Navy, Department of Defense, or the U.S. Government. Approved for public release; distribution is unlimited. This research has been conducted in compliance with all applicable federal regulations governing the protection of human subjects in research. U.S. Government Work (17 USC 105). Not copyrighted in the U.S.

Board 284. Influenza Surveillance Networks and Response to Seasonal Influenza in Brazil, 2013

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Background: After the pandemic there is a need to adapt the strategy of influenza surveillance in Brazil and makes the necessary deeper knowledge of the clinical, epidemiological and etiological cases of SARI since a variety agents, among others beyond influenza are responsible for most of these cases and its occurrence can occur in clusters of cases that deserve specific and timely interventions. The Brazil currently has 79 municipalities sentinels for influenza (ILI and SARI) and Universal Surveillance the SARI cases hospitalized - online system; Hospitalization and Mortality (Delay) and Outbreak investigation. **Methods:** Descriptive study of influenza cases reported to the National Information System for Notifiable Diseases adapted to collect online data (Sinan and Sivep-gripe) from January at December, 2013. The samples (nasopharyngeal aspirates or combined swabs) were collected at SU and hospitals and a nationally standardized form was used to assess clinical and epidemiological information. The clinical materiaI tested for respiratory viruses in immunofluorescence and influenza detection by Real Time RT-PCR. **Results:** Until Epidemiological Week (EW) 52 of 2013, a total of 16,856 samples were collected at the SU. From these, 21.3% (3,583) were positive for influenza or another respiratory virus. At the beginning of the year, the majority of positive samples were from North and Northeast regions and until EW 52, about 36,134 universal SARI cases were notified. These, 16.4% (5,935) were influenza. The predominant viral type was Influenza A (H1N1)pdm09, with 62.9% (3,733) positivity, with increased activity from EW 12. Influenza B was identified in 1,337 cases (22.5%), whereas influenza A H3N2 was detected in 669 cases (11%). Influenza A was not subtyped in 198 cases (3.3%). São Paulo state presented the larger number of SARI cases with a total of 2,760. Until the EW 52, a total of 4,328 deaths by SARI had occurred, from which 955 (22%) were caused by influenza, the mortality rate due to influenza was estimated in 0.49/100.000 inhabitants. In 65.0% of deaths at least one risk factor was identifiedy. **Conclusion:** The epidemiological data of 2013 influenza cases subsidized information to the vaccination strategy in 2014 and these data were important to guide control and prevention measures against influenza in Brazil.

Board 285. Laboratory Control of Influenza in the Republic of Armenia, 2009-2014

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Background: In 2010, a national sentinel laboratory system for influenza was established by the Armenian Ministry of Health. Surveillance is conducted at three laboratories: The National Center for Disease Control and Prevention (NCDCP) laboratory in Yerevan and branch laboratories in the Syunik and Lori marzes (administrative districts). The NCDCP laboratory functions as the national influenza reference laboratory. All influenza cases from the branch laboratories are confirmed at the NCDCP laboratory. Year-round surveillance is conducted with the objective to identify circulating influenza strains, understand the patterns of respiratory illness, and provide early detection of new viruses with a pandemic potential. **Methods:** Nasal and throat swabs were collected from each patient with suspected influenza infection using disposable sticks. Specimens were immersed into a sterile 0.5 mL vial with transport medium and transferred to the NCDCP laboratory in refrigerated bags at 2-8°C. Specimens were tested using one step rRT-PCR. Briefly, RNA was extracted using a QIAamp viral RNA mini kit (GmbH, Germany) and RNesay mini kit (GmbH, Germany). One step rRT-PCR was carried out using the AgPath kit (Applied Biosystems, USA) and Superscript III platinum One Step qRTPCR System (Invitrogen, USA). Specimens were tested for influenza A and B. Specimens positive for influenza A were further subtyped for A/H1N1, A/H3, A/H1, A/H5, and A/H1p. Primers and probes were provided by the US Centers for Disease Control and Prevention. **Results:** In 2009-2014, specimens from 1,598 patients with suspected influenza infection were analyzed. Influenza was confirmed by rRT-PCR in 523 of the patients. Of the positive cases, 499 (95.4%) were influenza A, 15 (2.8%) were influenza B, and 9 cases (1.7%) were unable to be subtyped. Amongst influenza A viruses, 496 (99.4%) were H1N1 and 3 (0.6%) were H3. **Conclusions:** From 2009-2013, influenza A/H1N1 and influenza B viruses were the two major types of influenza in circulation. In 2014, the major type of influenza was A/H3. The most vulnerable age groups were 1-11 and 22-31. Peak years for influenza cases were 2009 (October - December), 2011 (January - April), 2013 (February - April) and 2014 (February - March). Positive confirmation of samples from various clinics ranged from 19%-54% (average 31%).

Board 286. Flu on Call: Improving Access to Antivirals During a Severe Pandemic

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Background: The impact of a severe influenza pandemic could be overwhelming to hospital emergency departments, clinics, and medical offices if large numbers of ill people simultaneously seek care. In addition, antiviral treatment for influenza works best if started within 48 hours after symptoms arise. Surge on healthcare facilities may delay receipt of antiviral treatment and thus contribute to increased morbidity and mortality during a severe pandemic. **Methods:** The Centers for Disease Control and Prevention (CDC), in collaboration with the Association of State and Territorial Health Officials (ASTHO), the National Association of County and City Health Officials (NACCHO), the Council of State and Territorial Epidemiologists (CSTE), the Association of Poison Control Centers (AAPCC), and the United Way Worldwide/2-1-1 , and other partners, launched the Flu on Call™ project to explore the acceptability and feasibility of using a coordinated network of triage telephone lines during a pandemic. The goals of Flu on Call™ are to: improve access to antiviral prescriptions for ill persons, provide an alternative to face-to-face provider encounters, and increase appropriate use of medical resources during a severe pandemic. As part of this effort, the integration and coordination of poison control centers (PCC) and 2-1-1 help lines are being explored. A series of exercises and simulations were conducted during 2012 - 2014 with centers participating in a pilot effort to test feasibility and acceptability. **Results:** Results from exercises have demonstrated that Flu on Call™ can be feasible, acceptable, and effective in providing an alternative to face-to-face provider encounters during a severe pandemic. Clinicians at PCCs correctly provided advice and access to antivirals to more than 90% of callers and callers had a very high level of satisfaction (> 95%) with their experience during these simulations. Additional findings will be provided. **Conclusions:** Utilizing a network of triage lines that can safely provide care to the public may be an important tool for increasing accessibility to antiviral medications for ill persons and reducing medical surge during a severe pandemic. Innovative methods to rapidly provide access to countermeasures during a severe pandemic will likely be needed during a future emergency.

Board 287. Global Mortality Impact of the 1957-1959 Influenza Pandemic

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Background: Epidemiological descriptions of the 1957 influenza pandemic are particularly scarce, although this pandemic is often used as reference in pandemic planning scenarios. Here we characterize geographic variation in the mortality impact of the 1957 influenza pandemic in 27 countries and augment our study using highly detailed historic mortality records for Chile, where pandemic-related mortality was highest. **Methods:** We used age- and cause-specific deaths to estimate the excess mortality burden of the pandemic in 27 countries of Europe, Asia-Pacific and the Americas and assessed the relationship between influenza-related mortality and socio-economic factors. We used more detailed city- and regional-level data from Chile to investigate how this relationship fared on a smaller spatial scale. **Results:** Respiratory excess mortality rates associated with the 1957 pandemic varied 88 fold across the 27 countries studied, with a mean of 1.09 deaths per 10,000 (95% CI 0.70-1.48), and highest rates found in Chile. Infant mortality rates and GDP were the best predictors of flu-related mortality in all age and age-specific data (72% of variance explained). Detailed data from Chile indicate a ~10-fold variation in pandemic-related mortality across the 25 administrative provinces, with higher baseline mortality rates predictive of influenza severity (R2=41.8%; P=0.02). Excess mortality rates increased sharply post school-age, but we found no evidence of reduced mortality amongst seniors. **Conclusions:** Our study is the first to provide a global estimate of the mortality impact of the 1957 pandemic grounded in data and placing this pandemic below the 1918 pandemic but well above the 2009 pandemic. We find considerable geographic variation in excess mortality rates between countries, strongly linked with socio-economic status, but the relationship weakens on a smaller spatial scale. Chile experienced the worst pandemic impact ever reported, notably 3-5 times that of previously reported estimates from wealthier nations in North America or Europe, suggesting that global estimates need to rely on information from multiple countries and regions.

Board 288. Influenza Surveillance Networks and Response to Seasonal Influenza in Brazil, 2013 and 2014, Advances and Challenges

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Background: After the pandemic (2009) there is a need to adapt the strategy of influenza surveillance in Brazil and makes the necessary deeper knowledge of the clinical, epidemiological and etiological cases of SARI since a variety agents, among others beyond influenza are responsible for most of these cases and its occurrence can occur in clusters of cases that deserve specific and timely interventions. The Brazil currently has 79 municipalities sentinels for influenza (ILI and SARI) and Universal Surveillance the SARI cases hospitalized - online system. **Methods:** Descriptive study of influenza cases reported to the National Information System for Notifiable Diseases adapted to collect online data (Sinan and Sivep-gripe) from 2013 and 2014. The samples (nasopharyngeal aspirates or combined swabs) were collected at sentinel and hospitals and a nationally standardized form was used to assess clinical and epidemiological information. The clinical materiaI tested for respiratory viruses in immunofluorescence and influenza detection by Real Time RT-PCR. **Results:** In 2013 and 2014 a total of 37,494 samples were collected at the sentinel and from these, 20.8% (7,797) were positive for influenza or another respiratory virus. And Universal Surveillance the SARI cases hospitalized in 2013 and 2014 were notified a total of 54,622, these 14.1% (7,729) were influenza - in 2013 the predominant viral type was Influenza A (H1N1)pdm09, with 62.9% (3,733) positivity and 2014 were influenza A H3N2 was detected in 1,042 cases (58.1%). In 2013 and 2014 were notified a total of 6,646 deaths by SARI (Universal Surveillance), from which 1,281 (19.3%) were caused by influenza and the mortality rate due influenza was estimated in 0.64/100.000 inhabitants, accumulated in these two years. In 65.0% of deaths at least one risk factor was identifiedy. **Conclusion:** The epidemiological data of influenza surveillance in 2013 and 2014 show the advances in Brazil through this data capture new model surveillance. The timely capture of data of an influenza, to knowledge of the seasonality of the virus and strengthen surveillance and assistance to health is crucial and a challenge in a country with different geographical and climatic regions such as Brazil.

I1. Vector-Borne Diseases

Tuesday, August 25, 3:30 PM - 5:00 PM
Centennial Ballroom I

Jamestown Canyon Virus as an Emerging Cause of Human Disease in Minnesota

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Background: Jamestown Canyon virus (JCV) is a mosquito-borne virus that is widely distributed throughout North America, but rarely reported as a cause of human disease. JCV is a member of the California serogroup of bunyaviruses and is likely transmitted to humans through the bite of an infected *Aedes* sp. mosquito. The clinical spectrum of human disease is not known but the typical presentation, which includes fever, headache, fatigue, and in severe cases, meningitis or encephalitis, is similar to other arboviruses. Previous studies have identified the virus in Minnesota in mosquitoes and white-tailed deer, although the enzootic maintenance cycle has not been fully described. Minnesota detected its first human case in 2013. **Methods:** In 2014, the Minnesota Department of Health Public Health Laboratory (PHL) began using an internally developed EIA assay specific to JCV on serum and CSF specimens submitted for other arboviral testing. It was suspected that prior to the development of this assay positive results were being missed due to the relatively poor sensitivity of a broader California group IFA in detecting JCV. **Results:** From May through October of 2014, the PHL performed the JCV IgM EIA on 84 samples from 61 unique patients. Of these 84, 10 (11.9%) specimens from seven patients were preliminary positives for JCV. Confirmatory testing using plaque reduction neutralization (PRNT) was performed, with four specimens (40%) from three patients confirming as JCV and four specimens (40%) from two patients confirming as La Crosse encephalitis. One patient was negative for all arboviruses by PRNT, and one is pending. The confirmed JCV patients range in age from 15 to 62, and two of the three were male. Illness onsets were from late May to early August. Clinical presentation included fever (3/3), fatigue (3/3), myalgia/arthralgia (3/3), and headache (2/3). One patient developed encephalitis. All three patients were likely exposed in Minnesota. **Conclusions:** Detection of JCV virus infections in humans has increased with the implementation of routine testing of arboviral specimens submitted to the PHL, providing further evidence of the virus as an emerging cause of human disease in Minnesota. It is expected that with continued testing and increased awareness of JCV as a cause of human disease, cases will continue to be identified.

Unveiling the Burden of Dengue and Dengue-like Illnesses Through Enhanced Fatal Case Surveillance in Puerto Rico

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Background: Dengue is an acute febrile illness (AFI) that is difficult to distinguish from other AFIs, thus diagnostic testing is required to correctly diagnosis patients. Despite endemicity throughout the tropics, fatal dengue cases are still misdiagnosed and underreported. Conversely, non-dengue AFIs may be misdiagnosed as dengue. To quantify the incidence of fatal dengue and other causes of fatal AFI in Puerto Rico during 2010-2012, enhanced surveillance to detect fatal cases of dengue-like AFI was established. **Methods:** Hospital nurse epidemiologists were routinely queried for recent dengue-like deaths, tissue specimens and blood specimens were collected by forensic pathologists during autopsy of patients that died after a dengue-like illness, and death certificates were systematically reviewed for the word "dengue" or symptoms of a dengue-like AFI. Blood specimens were tested for evidence of infection with dengue virus (DENV) and *Leptospira* species bacteria. Tissue specimens were tested for evidence of infection with DENV and *Leptospira* spp. by PCR and immunohisochemistry, and other pathogens based on histopathology. **Results:** In total, 310 fatal dengue-like cases were identified; most had at least one blood (91%) or tissue (57%) specimen available. An etiologic agent was identified in 119 (38%) cases, the most common of which was DENV (58; 0.52 deaths/100,000 residents/year). Of the DENV-positive fatal cases, 51 (88%) were not reported to health authorities and 33 (57%) did not have "dengue" on the death certificate. Other identified etiologic agents included *Leptospira* spp. (34), *Staphylococcus* spp. (4), *Streptococcus* spp. (4), influenza virus (3), *Neisseria meningitidis* (1), and *Burkholderia pseudomallei* (1). **Conclusions:** This study indicates that fatal dengue is under recognized and underreported in Puerto Rico. Uses of this surveillance system included case-control studies to identify risk factors for fatal dengue and leptospirosis. Investigation of the melioidosis case demonstrated endemicity in Puerto Rico. After introduction of chikungunya virus (CHIKV) in 2014, four CHIKV-associated fatal cases were detected. To better understand the burden of dengue deaths and identify under recognized causes of AFI, similar protocols should be initiated in other regions where dengue is endemic.

Climate Change and Chikungunya Transmission in Europe: A Preparedness Priority in Europe

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Background: Following its introduction in Europe, Aedes albopictus has spread throughout many areas of the Mediterranean basin. In 2007, the mosquito mediated an outbreak of Chikungunya, with nearly 200 people infected. The extent to which climate changes will alter the distribution range of Aedes albopictus and possibilities for Chikungunya transmission in Europe remain important questions for public health. **Methods:** Ecological niche modelling was conducted to assess the climatic suitability for Aedes albopictus and Chikungunya. The impact of climate change on the climatic suitability for Chikungunya transmission was then modelled based on the A1B and B1 climate scenarios for 2011-2040, 2041-2070 and 2071-2100 (modelling work is in progress to develop projections under IPCC RCP 4.5 and RCP6 climate scenarios). Regions at risk were compared with regions deemed to have the lowest adaptive capacities in Europe, based upon a previous ECDC study. **Results:** Climate change will likely lead to shifts in the climatically suitable areas for Aedes albopictus and for Chikungunya virus transmission in Europe. Relatively speaking, climate change impacts are projected to increase in central Western Europe, such as France, Belgium and Luxembourg, and Germany. The currently suitable Mediterranean regions are projected to remain this way, with the exception of the southernmost areas of Europe which could become too dry. When considering adaptive capacities alongside projected impacts, some areas within the Pannonian Basin in East-Central Europe (comprising parts of Hungary, Croatia, Slovakia, Serbia, Slovenia and Romania), had the highest overall risk profile due to an increase in projected impacts and lower anticipated adaptive capacities. **Conclusions:** Understanding preparedness priorities for vector-borne disease necessitates assessments of how climate changes may

affect suitable climates for disease transmission, as well as consideration of a broad range of other factors such as disease introduction risks and the adaptive capacities and underlying health status of populations at-risk. This assessment may be used to assist preparedness planners by providing information about where measures such as enhanced vector-surveillance, information-raising, and vector control activities could prove helpful.

Clinicopathologic Characteristics and Immunolocalization of Viral Antigens in Chikungunya-associated Fatal Cases—Puerto Rico, 2014

R. S. Levine[1], W-J. Shieh[1], T. M. Sharp[1], D. M. Blau[1], J. V. Torres[2], A. Rivera[1], J. Perez-Padilla[1], D. Thomas[3], J. Cadez Velazquez[3], J. Bhatnagar[1], D. Ng[1], M. K. Keating[1], E. Hunsperger[1], J. Munoz-Jordan[1], D. Sanabria[2], J. E. Staples[1], M. Fischer[1], B. Rivera Garcia[3], H. S. Margolis[1], S. R. Zaki[1]; [1]CDC, Atlanta, GA, USA, [2]Forensic Sci. Inst. of Puerto Rico, San Juan, PR, USA, [3]Puerto Rico Dept. of Hlth., San Juan, PR, USA

Background: Chikungunya virus (CHIKV) disease-related deaths are uncommon and usually occur in neonates exposed intrapartum, older adults, or people with underlying medical conditions. We describe the epidemiology and histopathologic findings for patients who died and had evidence of acute CHIKV infection during a large outbreak in Puerto Rico in 2014. **Methods:** We identified patients who died following an acute febrile illness and had CHIKV RNA identified by reverse transcription polymerase chain reaction (RT-PCR) in a pre-mortem serum specimen, or in serum or tissue specimens collected at autopsies. Immunohistochemical staining for CHIKV antigens was performed on available post-mortem fixed tissues. Data from available medical records, autopsy findings, family interviews, and diagnostic test results were compiled using a standardized chart abstraction form. **Results:** We identified 26 patients who died in Puerto Rico during May-December 2014 and had laboratory evidence of acute CHIKV infection. Median age was 61 years (range: 6 days-85 years) and 16 (62%) were male. All patients had underlying medical conditions, the most common being hypertension (54%), diabetes (46%), and obesity (35%). Median day of death post-illness onset was 6 (range: 1-28) for the 18 (69%) cases where this data was available. Of 21 cases with post-mortem tissues available for evaluation, 10 (48%) had CHIKV antigen detected in fixed tissue. Common histopathologic findings included intraalveolar hemorrhage and edema. Viral antigens were observed in multiple organs, predominantly in mesenchymal tissues and cells of the mononuclear phagocytic system. **Conclusions:** CHIKV RNA was detected in the serum and tissues of patients who died during a chikungunya outbreak in Puerto Rico. All of the patients had comorbid conditions and most were older adults. Half of the patients evaluated had viral antigens detected in post-mortem tissues. Evaluation of autopsy tissues from patients infected with CHIKV provides evidence on the pathologic consequences of the disease that cannot be gained by diagnostic laboratory testing alone. This investigation underscores the importance of enhanced surveillance, autopsies, and tissue-based diagnostic testing in understanding mortality associated with an emerging infectious disease.

Outbreak of Phlebovirus Infection in Lombardia, a Northern Italy Region, in Summer 2013

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Background: An outbreak of Phlebovirus in Lombardia region (Northen Italy) during the period 1 June-30 November 2013 is described. **Patients and Methods:** CSF and plasma or serum samples from 22 patients (age 37-98) with a suspected Phlebovirus were investigated. Sera and CSF were tested with an indirect immunofluorescence test (IIFT) Sandfly fever virus Mosaic 1 IgG and IgM EUROIMMUN (Lubeck-Deutschland) that allows the simultaneous detection of antibodies against four viral serotypes Sandfly Sicily virus (SFSV), Sandfly Naple virus (FSNV), Sandfly Toscana virus (TOSV) and Sandfly Cyprus virus (SFCV). Sera were also tested with a neutralization test with two sandfly strains: a TOSV isolated in Bologna area and another strain isolated from a flebotomus in Brescia area. **Results:** Phlebovirus IgM were detected in 8 patients, IgM and IgG were detected in 10 patients and IgG only were detected in 4 patients. Neutralizing antibodies were detected in 15 patients: in 5 both strains were neutralized, in 6 only BS strain and in the remaining 4 only TOSV strains. Among the patients, 4 had a history of travel in endemic areas (3 in Southern Italy and 1 in Romania) in the 2 weeks before the onset of symptoms, while the remaining 18 patients had no history of travel, suggesting the local acquisition of the infection. The regional center for Arbovirus vectors control confirmed an increasing density of the vector (Phlebotomus) in the Lombardia region and the appearance of the vector in areas previously free from sandflies. **Conclusion:** As far as we know, autochthonous Phlebovirus infections were not previously reported north to the Po River. Thus, is shown circulation of Phlebovirus in Northen Italy (beyond Central and Southern Italy) belonging to different strains. Modification of sandflies ecology niches as a result of climatic changes have a direct impact on the epidemiology of associated human diseases.

The Factors Contributing to Seven Hundred Percent Increase in Malaria Incidence in Thailand-Lao PDR-Cambodia Border Province, Ubonratchathani Province, Thailand, 2014

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Background: On 22 June, 2014 Bureau of Epidemiology detected that Malaria incidence in Ubonratchathani Province has been immensely increased in year 2014, 7 times more than 5-year median of the Province The objectives of study are to describe magnitude and epidemiological characteristic of the outbreak, identify risk in term of environment, vector and human host and recommend further control measures. **Methods:** Malaria surveillance data were reviewed, laboratory data was retrieved from 8 hospitals in most affected districts, and patient records were reviewed. Case-control study was conducted to identify risk factors contributing the outbreak. Demographic and risk behavior data of the 155 cases and 233 controls in 6 highest- malaria incidence villages in 2 districts were interviewed. Univariate and Multivariate analysis were done. Mosquito and larva survey were done in 3 areas (communities, tourism area and forest entry). Interventions which have been done since January, 2014 were collected by interviewing public health officers, National park officers and villagers. **Result:** There were 2711 malaria cases cumulative (case-population ratio = 188.69 case per 100,000) without death case reported in Ubonratchathani province in year 2014. The highest incidence was in May 2014. Male to female ratio was 19:1. Most of them (89%) were 15 - 54 years old and 91% was living along the Thailand-Lao-Cambodia border around Phu-Jong-Na-Yong National park.P. vivax was 53.33%, P.falciparum was 44.99% and mixed type was 1.68%. From Univariate analysis, there were 2 factors which statistically significantly associate to malaria infection including having history of going into the forest (OR = 3.90 (95% CI 2.33 - 6.70)) and having malarial member in his family (OR =1.98 (95% CI 1.31 - 3.00)). Two hundred sixty two mosquitoes

were trapped. Of those, 64.9% was anopheles. There were only 2 species of suspected vectors, An.philippinesis and An.barbirostris, found in 2 villages. **Conclusion:** The major causes of the outbreak were entering and staying over-night in the National Park for seeking forest product and logging.

I2. Vaccine-Preventable Diseases

Tuesday, August 25, 3:30 PM - 5:00 PM
International Ballroom North

Efficacy of Inactivated Trivalent Influenza Vaccine Among Children in Rural India: A Three-year Randomized Controlled Trial

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Background: Influenza vaccine efficacy (VE) is not well characterized for children in developing countries. **Methods:** We conducted a household-randomized, controlled, participant/observer-blinded study in 3 villages in north India to measure the VE of inactivated trivalent influenza vaccine (IIV3) among children 6 months through 10 years of age. Children were given 1 (6 mos - 8 yrs) or 2 (9 and 10 yrs) doses of IIV3 or a control [inactivated poliovirus vaccine (IPV)] during 3 periods that began in Nov 2009, Oct 2010, and Oct 2011 with follow-up to May 2012. Weekly home visits identified subjects with febrile acute respiratory illness from whom nasopharyngeal samples were tested for influenza by real-time reverse transcription polymerase chain reaction. The primary outcome was laboratory-confirmed influenza virus infection (1st episode per year) among those receiving IIV3 versus those receiving IPV for assessment of direct or total protection. **Results:** In the modified intention to treat analysis (received at least 1 vaccine dose) in 2009/10, influenza was found in 151 of 1572 (9.6%) in the IIV3 group and 206 of 1633 (12.6%) in the IPV group for a VE of 25.6% [95% confidence interval (CI) 6.8 to 40.6]. The vaccine did not include influenza A(H1N1)pdm09 which emerged in 2009 and against it no efficacy was seen [VE14.5% (CI -20.4 to 39.3)]. Influenza A(H1N1)pdm09 was not present in sufficient numbers to estimate its VE in years 2 and 3. VE in 2010/11 was 42.5% (CI 25.9 to 55.4, influenza in 100/1617 (6.2%) in IIV3 group and in 177/1712 (10.3%) in IPV group) and in 2011/12 to May 2012 was 74.2% (CI 57.8 to 84.3, influenza in 20/1670 (1.2%) in IIV3 group and 81/1786 (4.5%) in IPV group). Influenza A(H3N2) only occurred sufficiently for evaluation in 2010/11 and its VE that year was 66.9% (CI 51.3 to 77.5), it was matched to vaccine. VE against influenza B in 2009/10, 2010/11 and 2011/12 was 32.5% (CI 11.3 to 48.6), 7.2% (CI -35.5 to 36.5), and 76.5% (CI 59.4 to 86.4) respectively. Influenza B viruses were predominantly B/Victoria-like (58%) and matched vaccine. **Conclusions:** Influenza was a common cause of febrile illness among children in rural villages in India. VE varied by virus type and year. Influenza vaccine can reduce the burden of disease among children in a developing country. Support U01 IP000177 Centers for Disease Control and Prevention, USA

Reduction in HPV Precursor Incidence in Connecticut Between 2008 and 2013

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Background: With vaccine licensing in 2006, human papillomavirus (HPV) related cervical disease caused by HPV types 16 and 18 became vaccine preventable. Baseline data from Connecticut (2008-2009) showed that in women 18-39 years old, 44% of all biopsied lesions graded cervical intraepithelial neoplasia (CIN) 2 and higher were caused by types 16 and 18. In women 21-24 years, 47% of CIN2+ were caused by types 16 and 18. **Methods:** CT is one of five Emerging Infections Program sites in which enhanced surveillance for CIN2+ has been conducted from 2008 to the present. In CT, basic surveillance is conducted statewide. We examined changes in CIN2+ incidence in CT from 2008 (baseline) to 2013 by age group (21-24, 25-29, 30-34, 35-39), age groups for whom routine screening continues to be recommended. **Results:** In 2008, there were 2102 cases of CIN2+, incidence 513.7 per 100,000. From 2008 to 2013, overall incidence decreased by 21.5% ($p<0.01$). By age group, only women 21-24 years had a statistically significant decrease ($p<0.05$), from 835.7/100,000 population to 450.0, a 46.2% decrease. The decrease in this age group began in 2010 and had reached 32.9% by 2012. The decrease in 21-24 year olds was similar for those with CIN 2 or CIN2/3 compared to those with CIN3 and higher (42.8% vs 46.4%, $p=0.69$). **Conclusion:** The decrease in CIN2+ incidence in 21-24 year old women in CT in 2013 is greater than would be predicted based on vaccination rates in this group alone (<50% had a first dose by age 17 years based on NIS Teen). Possible hypotheses to explain the decrease include herd immunity, cross-protection, reduced rates of detection due to new less frequent PAP smear screening guidelines introduced in 2012, and under-reporting compared to 2008. Given that clearly reduced incidence only has occurred thus far in 21-24 year olds, the age group in our analysis most likely to have directly benefitted from a vaccine that began to be used only in late 2006, we believe our surveillance data support clinic based studies that suggest substantial early and ongoing impact of HPV vaccine.

Varicella Seroprevalence of Beijing Residents in 2012

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Background: In 2012, in response to challenge of the continuous outbreaks caused by break-through varicella cases in schools, a booster vaccination was recommended by Bejing CDC to children in Beijing who had single dose vaccination. In mid-2012, before change of varicella immunization strategy, a seroepidemiolgical survey was carried out in Beijing to glean the VZV seroprevalence in the one-dose era and compare with of anti-VZV IgG antibodies (anti-VZV) and the risk for VZV infection in different age groups, which will provide basis on developing better immunization strategy. **Methods:** A cross-sectional serum epidemiology survey was carried out in June 2012 by Beijing CDC in the capital of China. We designed a multistage stratified random sampling method to recruit subjects of ten age groups. The sample size was expected to reach 2 000 people. For comparing with historical serological data , we used same laboratory testing method(ELISA) but different type of reagents to evaluate blood samples collected from another seroepidemiological survey of Beijing residents in 2008 to assess the differences and trends of anti-VZV seroprevalence in the past 4 years. **Results:** The adjusted overall anti-VZV seropositivity of Beijing residents in 2012 was 84.5%. Geographic region (P=0.062) and household registration (P=0.150) distribution didn't show difference.

Age specific seropositivity increased nearly steadily from 22.2% in < 1 yr of age to 93.7% in ≥30 yr of age (P<0.001 for trend test), however with a fluctuation (50.4%) in 5-9 yr of age. The adjusted overall anti-VZV IgG seropositivity in 2012 didn't showed growth comparing with 2008 (84.5% vs. 83.5%, P=0.899). Two age groups' sex-adjusted seropositivity increased (< 1 yr of age: from 6.3% in 2008 to 22.2% in 2012, P=0.019; 1-4 yr of age: from 27.6% in 2008 to 57.2% in 2012, P = 0.006). **Conclusion:** Moderately high anti-VZV seroprevalence has been achieved of Beijing residents and maintain stable in the single-dose indication and voluntary vaccination era. A government funded vaccination program that includes catch-up vaccination for children, adolescents and adults need consideration in the near.

Clinical Characteristics of Vaccinated and Unvaccinated Pertussis Cases—United States, 2010-2012

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Background: Despite high acellular pertussis vaccine coverage, 48,277 pertussis cases were reported in the US in 2012. Many cases occurred in vaccinated people, showing that vaccination does not eliminate risk of disease. However, to understand the full impact of pertussis vaccination it is important to also consider the effect of vaccination on disease severity. **Methods**: To assess whether severe pertussis symptoms or complications are more common among case-patients who are not up to date (nUTD) for pertussis vaccinations for age, we analyzed data on cases meeting the CSTE probable or confirmed case definition in patients aged ≥ 3 months reported through Enhanced Pertussis Surveillance/Emerging Infections Program Network in 2010-2012. Case information was collected at 6 sites through physician and patient interview and vaccine registries. Cases were stratified by age and odds ratios (OR) calculated to compare clinical characteristics in up to date (UTD) or nUTD case-patients (Tdap received vs. not for adults ≥ 20 years). The combined effect of antibiotic treatment timing and vaccination was assessed with logistic regression. **Results**: The analysis included 10,092 pertussis case-patients (median age 11 years, range 0-99). Of case-patients 3 months-19 years old, 81% were UTD; of adults, 45% had received Tdap. UTD status was protective against severe disease (seizure, encephalopathy, pneumonia, or hospitalization; 2.9% of cases) in children 7 months-6 years old (OR 0.37, 95% CI 0.22-0.61) and against post-tussive vomiting in persons aged 19 months-64 years (OR 0.72, 95% CI 0.64-0.80). Using logistic regression, both UTD status (adjusted OR (aOR) 0.72, 95% CI 0.64-0.80) and antibiotic treatment within 1 week of symptom onset (aOR 0.60, 95% CI 0.53-0.68) were independently protective against vomiting in persons 19 months-64 years old. **Conclusions**: UTD case-patients 7 months-6 years old were less likely than nUTD patients to have severe disease, demonstrating that pertussis vaccination reduces disease severity. Post-tussive vomiting, which can accompany severe coughing fits, was also less frequently reported in UTD case-patients. This effect was independent of antibiotic treatment timing, showing that both rapid treatment and completion of the pertussis vaccination schedule reduce post-tussive vomiting.

Epidemiology of Bacterial Meningitis Among Bangladeshi Children <5 Years, 2005-2013

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Background: Bacterial meningitis is a major cause of morbidity and mortality in children <5 years globally; a large proportion of episodes are vaccine-preventable. Bangladesh introduced *Haemophilus influenzae* type b (Hib) vaccine in 2009 and will introduce 10-valent pneumococcal conjugate vaccine (PCV10) in late 2014. We describe etiology and risk factors for bacterial meningitis prior to PCV10 introduction. **Methods:** Data were collected from 4 hospitals during 2005-2013. Illnesses requiring hospitalization meeting WHO-defined clinical signs and symptoms among children 2-59 months with blood or cerebrospinal fluid (CSF) collected were defined as suspected meningitis cases. Probable meningitis cases also had CSF showing either 1) leukocytosis (>100 cells/mm^3) or 2) leukocytosis (10-100 cells/mm^3) AND either elevated protein (>100 mg/dl) or decreased glucose (<40 mg/dl). Confirmed meningitis cases had detection of a meningitis pathogen from CSF or blood through culture, PCR or antigen testing or had a pathogen identified from blood AND a discharge diagnosis of meningitis. We calculated frequencies of etiologic agents and assessed associations between demographic and socio-economic factors and having probable and confirmed meningitis. **Results:** Among 13,059 cases identified through surveillance, 11,213 (86%) were suspected, 1,079 (8%) probable and 767 (6%) confirmed bacterial meningitis. Among culture-confirmed meningitis cases (n=399), the most common etiologies were *Streptococcus pneumoniae* (163, 48%), Hib (81, 24%), and *Neisseria meningitidis* (11, 3%); Hib cases declined 92% (2005-2008 average: 18.75 cases to 2010-2013 average=1.5 cases) after Hib vaccine introduction. Greater number of household members (aOR=1.92, p <0.001) and non-hygienic latrine type (aOR=1.56, p <0.001) were independently associated with developing confirmed and probable bacterial meningitis while older age (aOR=0.45, p <0.001), father's higher education level (aOR=0.6, p=0.003), and full receipt of DPT or pentavalent vaccine, proxy for care-seeking behavior (aOR=0.7, p=0.009), were protective. **Conclusions:** Potentially vaccine-preventable bacterial meningitis comprises over half of all Bangladesh meningitis cases. Continued surveillance is needed to monitor the impact of PCV10 after introduction.

Adult Measles Outbreaks Associated with Endemic H1 and Imported D8 Measles Viruses in Beijing, China

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Background: Beijing is the capital city of China. Following the 2010 SIA, the incidence of measles in Beijing reached a historic low level in 2012. However, in 2013, outbreaks of measles occurred in Beijing. **Methods:** The epidemiology characterization were investigated and analyzed. Serum samples and throat swabs were collected and tested for measles IgM (Verion Serion ELISA kits , Germany) or Measles virus genes by real time RT-PCR (real time RT-PCR kits, Shuoshi, Jiangsu, China) to do the laboratory diagnosis. Sequence determinations and phylogeny analyses based on N450 nucleotide sequences were performed. **Results:** Between January and December of 2013, 1,233 suspected measles cases

were reported and investigated. In total, 563 confirmed measles cases were reported, which represented a 6-fold increase from 2012. Most cases were among adult migrant workers, local adults, and their children. Among cases, 22.8% (80) were younger than 8 months, 11.5% (65) were 8 months to 14 years of age, and 65.7% (370) were 15 years of age or older and defined as adult cases. The median age of the adult cases was 23.5 years (range 15 to 70 years), and 87.6% of adult cases had unknown measles vaccination histories. Four hundred sixty eight real time RT-PCR positive samples were used for genotyping. A total of 45.6% (257/563) of measles cases from 14 of 16 districts or counties was genotyped. Among 257 genotyped cases, 84.0% were endemic genotype H1, 15.2% were imported D8, and 2 were imported D9. We found that Beijing D8 viruses had 99.8%-100% nucleotide homology with viral sequences from patients diagnosed in Russia, France, Canada, Thailand, Denmark, Germany and other locations, using WHO MeaNS matches search approach. Genotype D8 viruses were associated with at least 2 adult measles outbreaks that occurred in different large clothing wholesale markets and lasted from March to July. These outbreaks were confined to adults with no transmission to children. **Conclusions:** A measles resurgence occurred in Beijing in 2013. Endemic H1 and imported D8 viruses were associated with the resurgence and with adult outbreaks. Adult cases pose a challenge for measles elimination. Because migrant workers were disproportionately affected in the outbreaks, offering these workers measles vaccine may be an effective strategy.

I3. Surveillance I

Tuesday, August 25, 3:30 PM - 5:00 PM

International Ballroom South

Ebola Knowledge, Attitudes, and Practices Among Community Members in Three Low-incidence Counties: Liberia, September 2014

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Background: Initial visits to southeastern Liberia identified gaps in Ebola preparedness. As preparedness activities scale up to fill these gaps, accompanying health messages should address local Ebola-related knowledge, attitudes and practices (KAP). To develop targeted messages, we conducted KAP surveys in three low-incidence counties with ongoing preparedness efforts. **Methods:** We administered surveys in a nonprobability sample of residents within 20 districts across three counties, after initial <13 case reports per county but before Ebola Treatment Unit (ETU) construction. Selected districts already had or expected to have cases. Surveys assessed knowledge of Ebola transmission; perceptions of severity, treatment types, and survivors; and anticipated practices. We considered knowledge questions correct if consistent with the Liberia Ministry of Health Ebola messaging. We analyzed data using Chi-square tests. **Results:** Of 271 total participants, 43.2% were female and 64.3% had a middle school education or higher. Half of participants correctly answered >15 of 17 questions regarding Ebola transmission (range = 2-17). Of these questions, the lowest proportion of correct answers involved whether Ebola can be transmitted by bushmeat (74.5%). Fears included Ebola patients (93.7%), people living with Ebola patients (93.3%), ETUs (58.3%), and Ebola survivors (47.6%). Among 158 participants afraid of ETUs, the main fear was that family visits would not be allowed (n=111; 70.3%; $P < 0.001$). However, most respondents who feared ETUs would still seek treatment for themselves (89.9%) or family members (75.3%). **Conclusions:** Our survey found that Ebola transmission knowledge was high and was accompanied by fear of Ebola patients and their families. Attitudes toward new ETUs and future survivors might be improved with preemptive treatment-related messaging that also acknowledges and validates community members' fears.

Centralizing and Mapping Surveillance Data During the 2014 West African Ebola Virus Disease Outbreak

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Background: The Ebola Virus Disease (EVD) outbreak that began in March 2014, continues to spread within the affected West African countries and led to autochthonous cases in Spain and the United States. We present a centralized source of data encompassing situational context and disease spread as response to public concern over this outbreak. Non-traditional, or 'innovative' resources have become increasingly integral to timely disease surveillance. Here, online media reports and other 'innovative' data sources were collected, organized, and disseminated through a centralized outbreak timeline website (healthmap.org/ebola). **Methods:** The HealthMap automated system collects online information about infectious disease events 24/7. The automated system assigns disease, location, and species associated with the alert. Public health analysts review these categorizations. The West Africa EBV outbreak's specialized map and e-mail alert system includes the most pertinent breaking news alerts, which are posted to the timeline website. Additionally, subscribers can receive daily email mailers with the breaking news alerts along with alerts providing more contextual background on the progression of the outbreak. Finally, we provide case count projections based on WHO data using the IDEA model described by Fisman et al. (2013). **Results:** HealthMap's Ebola timeline site has received more than 600,000 unique page views since its creation. Ebola alerts coming into the system appear to follow a temporal clustering pattern around official report releases and milestone events. At times of significant media reporting of other world news, the number of unique Ebola alerts entering the database wanes. In this way, the system may not be an accurate representation of the true progression of the outbreak, and the situation on the ground. **Conclusions:** The outbreak timeline website provides a centralized source of official, media, and 'innovative' information on the 2014 West African EVD outbreak. This tool may help to inform the general public and communicate outbreak response methods and protocols. The timeline website's goal is to provide fact- and science-based information to as broad an audience as possible.

The Georgia Ebola Active Monitoring System for Travelers from Ebola-affected Countries—2014-2015

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Background: Monitoring emerging infectious disease outbreaks requires innovative and rapid implementation of new surveillance systems. The West African Ebola epidemic resulted in CDC's recommendation that all travelers to the U.S. from Ebola-affected countries undergo active monitoring for 21 days to allow for early detection of potential imported

Ebola disease to allow timely treatment and reduce the potential for spread. Georgia Department of Public Health (DPH) epidemiologists and technical staff collaborated to develop an Ebola Active Monitoring System (EAMS). **Methods:** EAMS was rapidly developed and implemented in six days within the existing notifiable disease reporting system. EAMS enables DPH and district epidemiologists to create an account for each traveler and track his/her temperature, symptoms, and travel plans during their monitoring period. Low risk travelers (according to CDC's exposure risk categorization) enter their own monitoring information online. Travelers with some/high risk undergo direct active monitoring daily via live video and epidemiologists enter their information. EAMS notifies epidemiologists of reported symptoms via immediate automated email alerts, enabling early management of possible cases. The system summary screen displays real-time traveler status and allows early identification of travelers who fail to report. **Results:** As of February 19, 2015, 799 travelers were monitored (average 103 daily); 20 were referred for medical evaluation. Of these, seven were diagnosed with influenza, six with viral upper respiratory infections, and seven with other diagnoses. Five travelers were tested for Ebola; all were negative. Less than 7% of travelers failed to report daily, all received follow-up. Seventeen travelers with some or high risk exposures were directly monitored; all were asymptomatic. Since early 2015, CDC also uses EAMS to monitor their staff who live in Georgia. **Conclusions:** EAMS makes it possible for two DPH epidemiologists to monitor >100 travelers each day and easily share information among state and federal Stakeholders and to facilitate rapid risk assessment and response as needed. The success of EAMS illustrates the return on DPH's preparedness investment in retaining technical staff to work with epidemiologists to meet urgent surveillance needs.

USAID-EPT-PREDICT — A New Approach to Preventing Pandemics and Targeting Control by Detecting Potentially Zoonotic Pathogens Before They Spill over from Wildlife

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Background: Reactive attempts to control viral diseases with wildlife host origins, like HIV/AIDS, influenza, SARS and Ebola are inefficient. Here we describe a new proactive approach to address the challenge of emerging infectious diseases that should reduce morbidity and mortality as well as reduce their economic burden. **Methods:** Our USAID-funded PREDICT Consortium has worked with 59 government ministries to conduct a comprehensive zoonotic pathogen surveillance program, advancing One Health capacity and infrastructure in 20 countries in emerging infectious disease hotspot regions. Following modeling and risk assessment, high-risk human-animal-environment interfaces were selected for investigation of viral spillover from wildlife hosts to humans and their food animals. Environmental, host, and behavioral data were collected, and samples screened for viral families that contain known zoonoses, using novel high-efficiency consensus PCR that is readily deployable in developing countries and high throughput sequencing. **Results:** In addition to detecting over 100 known pathogens, we discovered over 700 new viruses, more than doubling the number of known mammal viruses. We are now combining these discoveries with data on rates and types of human-wildlife contact and likely pathogenicity to assess risk and inform mitigation strategies. We have trained 2,500 government personnel and human and animal health workers, and equipped, supplied, and trained staff in 31 diagnostic laboratories globally to safely process and test samples for viral pathogens. We have established multidisciplinary collaborations and established systems for data sharing and interpretation across ministries. The PREDICT Consortium has trained its local partners to safely and humanely sample more than 55,000 wild primates, bats, rodents, and other wildlife (including bushmeat) at these high-risk human-wildlife interfaces. **Conclusions:** We focus our work where environments, human behaviors, and market systems are changing in ways conducive to the spillover of viruses among hosts. We have characterized pathogens of epidemic potential, and facilitate targeting of intervention strategies to reduce the risk of disease emergence in known EID hotspots.

An Evaluation of Psychological Distress and Social Support of Survivors and Contacts of Ebola Virus Disease Infection and Their Relatives in Lagos, Nigeria —2014

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Background: Starting in 2014 an outbreak of Ebola Viral Disease (EVD) in West Africa started to affect Guinea, Liberia, Sierra Leone and Nigeria. Research conducted during EVD outbreaks focussed on clinical manifestations and aspects of the epidemiology of EVD. We set out to determine the prevalence and pattern of psychological morbidity and social support among the survivors, relatives and contacts of EVD. **Methods:** A descriptive cross-sectional study among survivors, contacts and their first-degree relatives. A socio-demographic questionnaire was used to measure the socio-demographic characteristics while General Health Questionnaire was used to assess psychological distress. The Oslo social support scale (OSS) was used to assess patients' social support base. **Results:** The most frequently occurring psychological distress were "Not been able to concentrate on what you are doing" (37.6%) and "Lost much sleep over worry" (33.3%). Only 23 (19.7%) of the participants reported "Can count on less than 2 people for help for serious problem". Loosing a relation to the EVD outbreak (OR=6.0, 95% CI, 1.2 - 32.9), and been a health worker (OR=0.4, 95% CI, 0.2 - 0.9) were significantly associated with psychological distress of "feeling unhappy or depressed". Not loosing a relation (AOR=0.1745, 95% CI, 0.0357 - 0.8532) remained an independent protective factor against the psychological distress of "feeling unhappy or depressed". Having no tertiary education (AOR=0.2234, 95% CI, 0.0829 - 0.6024) and loss of a relation (AOR=0.0995, 95% CI, 0.0357 - 0.0165) remained independent predictors of protection against psychological distress of "not been able to concentrate". **Conclusions:** We concluded that survivors and contacts of EVD or their relatives develop psychological distress. Loss of a family member and having no tertiary education were independently associated with psychological distress. We recommended that mental health specialist be part of the case management team of the response to EVD outbreak. The clinical teams managing EVD patients should be trained on recognition of psychological distress among the patients. A mental health specialist should follow up the survivors/contacts with increased risk.

Seasonal Influenza Forecasting in Military Populations

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Background: Seasonal influenza forecasts could guide allocation of vaccine and other medical resources, and risk communication. We used comprehensive US military medical surveillance data to develop and test influenza-like illness (ILI) forecasting models. **Methods:** We obtained ILI data from the Defense Medical Surveillance System, the central repository of medical encounter data for the military health system. The dataset covered 2000-2013, and included: de-identified demographic, diagnostic, and location data for all ILI encounters, as defined by previously validated ICD-9 code sets, at US-based facilities, for military members and their dependents; and the total number of encounters (ILI and non-ILI) weekly per facility. We calculated weekly ILI incidence as the percentage of ILI among all encounters per facility. Candidate predictors included previous ILI incidence, regional CDC-reported ILI activity, and local NASA- or NOAA-reported climatological data. We applied 2 forecasting approaches: Method of Analogues (MOA; using a novel multi-dimensional extension to external predictors), to forecast ILI incidence and total ILI cases per season; and Predicting Infectious Diseases Scalable Model (PRISM), a novel data-mining method we reported previously, to forecast peak ILI incidence week. We aggregated data by state. MOA and PRISM used 2000-2010 and 2006-2010 data, respectively, for model development, with 2011-2013 reserved for testing. **Results:** There were 68,934,506 ILI encounters at 968 facilities; further analysis excluded territories and 10 states with sparse data. In 4-week-ahead MOA forecasting with dew point as external predictor, mean root-mean-square error across states was 12% (s.d.=5%) and 12% (6%) for peak incidence and total cases, respectively. Using PRISM with a 4-to 6-week-ahead window and epidemiological and climatological predictors, sensitivity, specificity, and positive and negative predictive value were 0.61, 0.99, 0.60, and 0.99, respectively. **Conclusions:** Using comprehensive medical event data, these novel approaches achieved accurate ILI forecasting (compared to previous studies) with 4-6 week lead time. We plan to integrate prospective forecasting into ILI surveillance, and compare ILI dynamics between civilian and military populations.

I4. Antimicrobial Resistance

Tuesday, August 25, 3:30 PM - 5:00 PM

Centennial Ballroom II

The Impact of an Educational Intervention Among Drug Sellers in Pharmacies on Antibiotic Dispensing Practices for Acute Respiratory Illness, a Pilot Study in Dhaka City, Bangladesh

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Background: Improper antibiotic use has raised global concern of antimicrobial resistance. In Dhaka, Bangladesh 48% of respondents with acute respiratory illness (ARI) reported using pharmacies as their first point of care. We evaluated the impact of an educational intervention for drug sellers at pharmacies to promote proper antibiotic dispensing. **Methods:** From June 2012–December 2013, we investigated drug sellers' antibiotic dispensing practices for ARI before and after an educational intervention (day-long training based on standard ARI management and antimicrobial resistance) in 100 randomly selected pharmacies in Dhaka. Research assistants visited the pharmacies acting as relatives of ARI patients, presenting 1 of 6 predefined clinical scenarios (for pediatric and adult cases: acute onset of cough with runny nose; cough with fever; respiratory distress) without any prescription. They recorded antibiotic dispensing at baseline and at 1 and 6 months after intervention. Drug sellers were consented but unaware of this role play. As per proper antibiotic dispensing, drug sellers should not dispense antibiotics for any of these pediatric or adult ARI scenarios without examining the patient. **Results:** The intervention reduced improper antibiotic dispensing for 2 pediatric scenarios (cough with runny nose and cough with fever) according to pharmacy visits at 1 month (38/192; 20%) and 6 months (39/188; 21%) compared to baseline (67/200; 34%) ($p<0.05$). For the same 2 scenarios in adults, antibiotic dispensing was lower after 1 month (88/192; 46%) and 6 months (75/187; 40%) compared to baseline (98/200; 49%), but the trend was not significant. Improper antibiotic dispensing for adult respiratory distress increased at 1 month (64/96; 67%) and 6 months (73/93; 78%) after intervention (baseline: 45/100; 45%) ($p<0.05$). For pediatric respiratory distress, antibiotic dispensing initially decreased (8/96; 8%) compared to baseline (14/100; 14%), but was not sustained at 6 months post-intervention (16/93; 17%). **Conclusions:** A positive change in antibiotic dispensing was observed after intervention for the pediatric ARI scenarios except respiratory distress. Further studies in Bangladesh are needed to determine if educational interventions can have sustaining positive impact on antibiotic dispensing.

Development of an Electronic Bidirectional Public Health Information Exchange to Control Extensively Drug-resistant Organisms (XDROs)

W. E. Trick[1], M. Lin[2], M. Driscoll[1], R. Cheng-Leidig[3], A. S. Tang[3], W. Gao[1], E. Runningdeer[3], A. Arwady[3], R. Weinstein[1]; [1]Cook County Hlth. & Hosp. System, Chicago, IL, USA, [2]Rush Univ. Med. Ctr., Chicago, IL, USA, [3]Illinois Dept. of Publ. Hlth., Chicago, IL, USA

Background: Carbapenem-resistant Enterobacteriaceae (CRE) are resistant bacteria for which treatment options are limited; there have been several high profile clusters of infection, some with serious consequences. Historically, the process for sharing patient-specific CRE information was communication between healthcare providers during direct facility-to-facility patient transfer. Such communication was inconsistent and even with maximum compliance, would only impact an estimated 20% of patient sharing episodes because most is indirect (e.g., a patient goes home before admission to another hospital). In Illinois, authorized healthcare facility infection preventionists can access patient-specific CRE information through the XDRO registry. The registry was developed in response to an emerging CRE problem and is based on mandated reporting by hospitals, long-term care facilities and laboratories. **Methods:** The Illinois Department of Public Health (IDPH) and Chicago Centers for Disease Control & Prevention Epicenter launched the web-based registry in November 2013. CRE entered into the system are searchable through manual patient-specific queries, enabling inter-facility communication. We are automating transmission of admission data at pilot hospitals using de-identification software, which enables rapid notification of facilities that admit a patient found in the XDRO registry. **Results:** During the first 12 months (November 1, 2013-October 31, 2014) there were 1,557 CRE reports submitted from 115 acute care hospitals, 5 long-term

acute care hospitals, 46 skilled nursing facilities, 7 reference laboratories, and 2 clinics. On average, 30 unique facilities queried the registry each month. During the first month of automating the admission feed, one pilot hospital received two notifications about CRE registry patients; for both, the colonization status had been unknown by the infection control department. **Conclusions:** Guided by a consortium that included a state and local public health agency task force, key experts, and a non-profit informatics entity, we deployed a statewide XDRO registry that included automated bidirectional information exchange. The legal, technical, and collaborative underpinnings of the system enable rapid incorporation of future emerging XDROs.

A Summary Index for Antimicrobial Resistance in Food Animals in the Netherlands

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Background: The Dutch government has set targets for reduction of antimicrobial usage in food animals, stipulating a 50% reduction in usage (on a weight basis) in 2013 as compared to 2009 and a 70% decrease in 2015. To evaluate the impact of this policy for public health, antimicrobial resistance (AMR) is monitored for several pathogenic and commensal bacteria (including *E. coli* and *Enterococcus* spp.) in food animals as well as foods. A summary index of AMR in the food chain was developed based on these data, in order to comprehensively report the impact of reducing antimicrobial usage in food animals on AMR in food-related isolates to parliament. **Methods:** Scientists and policy makers contributed to the definition of a set of criteria to evaluate existing monitoring systems and relevant antimicrobial agents. Data on AMR in selected isolates from four animal species (broiler chickens, slaughter pigs, veal calves and dairy cattle) were obtained from 2009-2012. Aggregation of data was based on weighted averages, with weights reflecting the clinical relevance of antibiotics as elicited from a panel of clinical microbiologists, epidemiologists, pharmacologists, veterinarians and clinicians. **Results:** Monitoring for resistance in commensal *Escherichia coli* best met the required criteria. Antimicrobial classes selected for inclusion in the summary index were therapeutically important substances(3rd/4th generation cephalosporins and quinolones) and high usage substances (tetracyclines and penicillins). Resistance to critically important antimicrobials was less prevalent than to high usage antimicrobials. Therefore, a weighted average was preferred. Weighted AMR prevalence was highest in broiler chickens, followed by pigs and veal calves; and low in dairy cattle. There was a significantly decreasing trend in the summary index for all food animal species from 2009-2012, coinciding with decreased usage. **Conclusions:** Reducing AMR in food animals is a key policy objective in many countries around the world. This study shows that active monitoring of resistance among commensal bacteria can inform about the impact of such policies, and that detailed data can be aggregated to summary indices that are meaningful and interpretable for policy makers.

Antimicrobial Treatments for *Clostridium difficile* Infection in the Outpatient Setting in Maryland: Implications for Stewardship

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Background: While *Clostridium difficile* infection (CDI) is increasingly diagnosed in outpatient settings, information on outpatient treatment is limited. We examined outpatient treatment of Maryland CDI cases, including consistency with Society for Healthcare Epidemiology of America (SHEA) and Infectious Diseases Society of America (IDSA) treatment guidelines. **Methods:** We reviewed 2013 CDI surveillance data from 11 Maryland counties collected as part of the Emerging Infections Program. Data collected for CDI patients included clinical setting at time of stool collection, white blood cell count, and underlying conditions. Information extracted for assessing CDI treatment adherence included antibiotic, route of administration, dosage, frequency, and dates of administration. Treatment adherence was assessed based on SHEA-IDSA guidelines. Disease severity was assessed using a modified Charlson Comorbidity Index as well as SHEA-IDSA guidelines. **Results:** Of 657 patients with treatment data, 264 were treated as outpatients with 16% receiving vancomycin and 85% receiving metronidazole. Of the outpatients who received vancomycin, 36% received 125mg qid, 43% received 250mg qid, and 5% received 500mg qid, while 17% did not have dosage documented. Among outpatients, 71% were classified as mild/moderate (Charlson score 0-4) and 29% were classified as severe (Charlson score ≥ 5). Of mild/moderate cases of CDI, 13% received vancomycin and 89% received metronidazole. Among severe CDI cases, 23% received vancomycin and 77% received metronidazole. Of mild/moderate CDI outpatients, 88% received the recommended antibiotic for treatment compared to 23% of severe CDI outpatients. Guideline adherence occurred in 48% of mild/moderate CDI outpatients and 4% of severe CDI outpatients. **Conclusions:** Adherence to SHEA-IDSA treatment guidelines for mild/moderate CDI is low and adherence to treatment guidelines for severe CDI is even lower. Importantly, vancomycin is often prescribed for outpatients in higher than recommended dosages, which have been shown to be no more effective than the recommended dose. Treatment with the inappropriate drug or dose could potentially negatively impact patient outcomes and promote antibiotic resistance.

Critical or Fatal Illness Caused by Community-associated *Staphylococcus aureus* (CA-SA) Infection—Minnesota (MN), 2005-2013

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Background: Methicillin-resistant and susceptible SA (MRSA and MSSA) can cause critical illness and death. We characterized the clinical and molecular characteristics of CA-SA in MN to further understand severe SA disease epidemiology. **Methods:** MDH initiated reporting of severe CA-SA in 2005, defined as culture-confirmed SA infection in a person with fatal illness or ICU admission and no healthcare-associated risk factors. Submitted isolates underwent PFGE typing and toxin PCR testing. **Results:** 135 cases were reported during 2005-2013: 61 (45%) MRSA, 74 (54%) MSSA. Twenty nine (48%) MRSA and 39 (53%) MSSA patients were male. MRSA and MSSA median age was 36 and 17 years, respectively (p=0.02). MSSA case proportion increased during 2005-2013 (1df, p=0.047). Multifocal infections occurred in 31 (23%) cases: 20 MRSA, 11 MSSA. Pneumonia was common: 34 MRSA, 23 MSSA cases. Eighteen (30%) MRSA and 19 (26%) MSSA cases died (p=0.65). Of 37 fatal cases, 25 (68%) involved pneumonia: 13 MRSA, 12 MSSA. Three MRSA and 20 MSSA had TSS; 5 MRSA and 12 MSSA had endocarditis; 21 MRSA and 13 MSSA had skin-related infections. Septic arthritis, meningitis, and internal abscesses also occurred. 52 MRSA and 59 MSSA isolates were characterized. Of MRSA isolates, 42 were USA300, 1 USA400, 5 USA100 and 1 USA200. The proportion of USA300

MRSA did not change over time. Of MSSA isolates, 12 were USA200, 7 USA600, 5 USA1000, 4 USA300, 3 USA400, 2 USA100, 2 USA700, 2 USA1200, 1 USA1100, 1 USA900, 1 USA800. Three MRSA and 19 MSSA had no defined USA group. MRSA and MSSA toxins included PVL, SEK, SEQ, TSST-1, and SEA-SED. PVL, SEK, and SEQ were present together in 69% of USA300 MRSA isolates. USA200 MSSA contained TSST-1 (12), TSST-1 and PVL (1), and TSST-1 and SEA (5). Nineteen MSSA isolates did not have these toxins, although, of these, 5 (26%) were fatal. USA300 ($p<0.01$) and USA400 ($p=0.03$) cases more commonly involved pneumonia than other clonal groups. USA200 cases more commonly involved TSS ($p<0.01$). **Conclusion:** Both MRSA and MSSA caused severe infections, including pneumonia, which was often fatal. MSSA appeared to increase in later years, and there was more diversity in strain types. USA300 MRSA infection was common. Ongoing surveillance can be informative for vaccine development and other control measures.

Can the Past Inform the Current Response to Cephalosporin-resistant *Neisseria gonorrhoeae*? A Comprehensive Review of Prior Public Health Responses to Gonococcal Antimicrobial Resistance

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Background: Gonorrhea prevention and control rely on prompt and effective treatment. However, gonorrhea treatment has been complicated by bacterial acquisition of resistance to each antimicrobial recommended for treatment. Resistance to cephalosporins, the backbone of the only remaining recommended regimen, is a real threat; its emergence could undermine prevention and control efforts. To inform public health responses to cephalosporin-resistant gonorrhea, a comprehensive literature review was conducted to assess the effectiveness of prior public health responses to *N. gonorrhoeae* resistance in the US. **Methods:** Using a key word search and review of article reference lists, the medical literature and government reports were reviewed for descriptions of outbreaks of and/or public health responses to the emergence of penicillinase-producing *N. gonorrhoeae* (PPNG) (1970s–1980s) and quinolone-resistant *N. gonorrhoeae* (QRNG) (2000s). **Results:** Thirty-one relevant articles (20 related to PPNG and 11 to QRNG) were found. During PPNG outbreaks, responses focused on containment and included some combination of the following: enhanced surveillance and case finding, including increased gonorrhea screening, testing all clinical samples for penicillinase; detailed interviews of patients and active tracing of recent sexual partners; community and provider education; and changes in treatment guidance. Data from California, Florida, New York and Washington suggested that if outbreaks were detected quickly, aggressive measures achieved containment. In each location, however, containment was short-lived: the number of PPNG cases increased (often sharply) within several years. As QRNG emerged, responses focused instead on changing treatment guidelines to no longer recommending fluoroquinolone use in affected locations and populations. Following guideline changes, the QRNG prevalence may have decreased, but quickly increased within 3 years. **Conclusions:** Enhanced surveillance and rapid containment efforts might slow the emergence of cephalosporin-resistant gonococci, however, the effects may be short-lived. Other tools and interventions, such as new diagnostics, antimicrobials and/or a vaccine, will be needed to effectively respond to cephalosporin-resistant *N. gonorrhoeae*.

I5. Foodborne Diseases I

Tuesday, August 25, 3:30 PM - 5:00 PM

Centennial Ballroom III

Quantitative Microbial Risk Assessment of Salmonellosis for Owners of Backyard Poultry Flocks, Seattle, Washington

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Background: The practice of urban chicken farming has been gaining popularity in major US cities nationwide; however, these urban farmers may be unaware of the zoonotic risks associated with animal rearing. Over the past 20 years, more than 45 outbreaks in the US have been linked to baby poultry purchased to supply backyard flocks. Using the Quantitative microbial risk assessment (QMRA) methodology we set out to estimate the risk of salmonellosis from backyard flocks. **Methods:** From June 1-Oct 1 2014 we recruited a convenience sample of 50 backyard flocks in the Seattle Metropolitan area. Flock owners were video recorded while providing routine care to their birds and video notational analysis performed to estimate the rate of contamination and possible self-inoculation. Hand swabs were collected before and after routine care to estimate *Salmonella* transfer. A series of environmental swabs were collected from the interior of the coop to estimate environmental *Salmonella* contamination. A 62-item survey was also completed by flock owners reviewing animal inventory and husbandry practices, as well knowledge, attitude and practices of the flock owners related to *Salmonella*. Using CrystalBall® software and exposure frequencies identified in the study a quantitative microbial risk assessment was performed modeling scenarios of high and low environmental contamination. **Results:** Flock owners on average owned 5 hens, with a range of 2-18 hens. On average poultry caretakers touched potentially contaminated poultry surfaces including the interior of the coop, bird feed and feeding equipment, eggs, and chickens 13.0 +/- 5.2 times while conducting their poultry care routine. Potential sources of self-inoculation involved touching the face, touching the mouth directly and placing fingers in the mouth as well as kissing chickens and was observed on average 1.2 +/- 1.6 times during poultry care routines. Cross-contamination was measured by the number of times flock owners wiped their hands on their clothing, held birds close to their person and wore flock shoes in the house. These situations were noted 1.9 +/ 1.9 times per routine. **Conclusions:** Our modeled risk of *Salmonella* exposure in backyard poultry suggests value in preventive measures. Such measures include personal protective equipment and hand hygiene.

Outbreak of *Salmonella* Newport Infections Linked to Cucumbers—United States, 2014

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Background: *Salmonella* causes approximately 1 million foodborne infections and 400 deaths annually in the United States. In August 2014, PulseNet, the national molecular subtyping network for foodborne disease surveillance, detected a multistate cluster of *Salmonella* Newport

(*S*N) infections with an indistinguishable pulse-field gel electrophoresis pattern. This strain has previously been linked to tomatoes from the Delmarva Peninsula of the Eastern US. We investigated to identify the source and prevent further illnesses. **Methods:** A case was defined as an illness with the outbreak strain with onset from 5/20/2014-9/30/2014. Information was collected on travel, restaurant, and food exposures in the 7 days before illness onset using a structured questionnaire. Reported food frequencies were compared to the 2006-2007 FoodNet Population Survey. A non-regulatory traceback was performed to identify the source of food items consumed in illness sub-clusters. Whole genome sequencing (WGS) was conducted to further characterize relatedness of *Salmonella* isolates. **Results:** A total of 275 cases from 29 states and DC were identified; 34% (48/141) were hospitalized and 1 death was reported. A significantly higher percentage of ill persons consumed cucumbers in the week before illness onset than expected, (62% vs. 46.9%, p=0.002). Traceback of 8 illness sub-clusters led to a common cucumber grower in the Delmarva region of Maryland. WGS analysis showed that genetic sequences of clinical isolates from MD and DE were highly related but distinct from a NY sub-cluster. **Conclusion:** Epidemiologic and traceback evidence suggest cucumbers were a major source of illness in this outbreak. This is the first multistate outbreak of *S*N infections linked to a produce item from the Delmarva Peninsula other than tomatoes, suggesting an environmental reservoir may be responsible for recurring outbreaks.

Tracing *Brucella suis* Infection in a Human, Oregon, 2013

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Background: Oregon is considered Brucella free; there are feral swine populations in the state, but routine surveillance has not identified any animals with brucellosis. Human brucellosis is rare in Oregon. Since 1991, 18 human cases have been reported: 13 confirmed and five presumptive. Of the confirmed cases, five were identified as *Brucella melitensis* and only one as *B. suis*. We report the first case of *B. suis* in Oregon acquired in Tonga more than three years before the onset of illness. **Methods:** A case of brucellosis was reported in a 26-year-old man from Tonga in July of 2013. We interviewed the case and inspected the farm where the patient had purchased a live pig. The Centers for Disease Control and Prevention (CDC) biotyped the patient's *Brucella* isolate. The National Veterinary Services Laboratory (NVSL) performed whole genome sequencing (WGS) and single nucleotide polymorphism (SNP) testing of the patient's isolate and also 7 isolates requested from the New Zealand Animal Health Laboratory from patients with a history of residence on Tonga. **Results:** The patient had not traveled out of the state or consumed any pork products from Tonga since moving to the U.S. three years before illness onset. The patient had purchased pigs from the same Oregon farm three times before illness onset. The farm was part of a larger operation that produced and sold luau pigs, but did not custom-slaughter them. Routine slaughter surveillance for *Brucella* from the blood of cull sows originating from the operation had been collected over the past 10 years, including 25 over the past 12 months; none were positive for Brucella by NVSL. CDC confirmed the patient's isolate as *B. suis* biovar 1. WGS and SNP analyses indicated close clustering of the Oregon isolate with all isolates from Tonga and indicated that the patient was not infected from a U.S. source by biotype and genotype. **Conclusion:** We report a case of *B. suis* biovar 1 from an individual whose exposure occurred at least three years prior to his onset of illness. The average incubation period for brucellosis is 2--10 weeks, but can be as long as six months, according to the literature. Brucellosis should be considered in the differential diagnosis of compatible illness in immigrants, regardless of time since immigration.

Climate Change Blunts Progress Reducing Infectious Diseases Attributable to Unsafe Water and Sanitation in China

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Background: Despite China's rapid progress improving water, sanitation and hygiene (WSH) infrastructure and access, in 2011, 471 million people lacked access to improved sanitation, and 401 million people to household piped water. Infectious diseases are sensitive to changes in climate, particularly temperature, and WSH conditions. **Methods:** To explore possible impacts of climate change on these diseases in China in 2020 and 2030, we coupled estimates of the temperature sensitivity of diarrheal diseases and three vector-borne diseases, temperature projections from global climate models using four emissions pathways, WSH-infrastructure development scenarios and projected demographic changes. The change in the burden of diarrheal diseases, malaria, dengue fever, and Japanese encephalitis in China—expressed in DALYs per 1,000 population—was estimated in response to projected changes in temperature in China in 2020 and 2030 using a standard comparative risk assessment approach. Projected changes in disease burden were analysed alongside changes in China's demographics and urbanization, and uncertainty in both future climate conditions and future WSH infrastructure development were explored. The impact of climate change was summarized as a 'development delay', which expresses the additional time (in months) that China would be required to continue to provide infrastructure improvement, health investments, and other efforts in order to attain the burden of WSH-attributable disease predicted under a scenario without the impact of climate change. **Results:** China is anticipated to warm 1.0°C by 2020 and a 1.39°C by 2030 under RCP 8.5. Urbanization, WSH improvements, and China's demographic transition will cause the burden of WSH-attributable disease to decrease substantially between 2008 and 2030. However, by 2030, climate change is projected to delay China's historically rapid progress toward reducing the burden of WSH-attributable infectious disease by 8-85 months. **Conclusions:** This development delay provides a key summary measure of the impact of climate change in China, and in other societies undergoing rapid social, economic, and environmental change where a significant health burden may accompany future changes in climate even as the total burden of disease falls due to non-climate reasons.

Genotypic and Epidemiologic Trends of Norovirus Outbreaks in the United States, 2009-2013

J. Vinje[1], L. Barclay[1], N. Gregoricus[1], H. Shirley[2], D. Lee[2], E. Vega[1]; [1]CDC, Atlanta, GA, USA, [2]AREF, Atlanta, GA, USA

Background: Noroviruses are the leading cause of epidemic acute gastroenteritis in the United States. Since 2009, norovirus outbreak laboratory surveillance in the US has been conducted using CaliciNet which is a surveillance network of state and local public health laboratories coordinated by CDC. To better understand epidemiologic and genotypic trends of norovirus outbreaks in the United States, we describe and analyze data reported to CaliciNet from September 2009 to August 2013. **Methods:** Nucleotide sequences of small regions of the VP1 gene (region C and region D, and epidemiologic data (outbreak date, city or county, setting, transmission, number sick, and age of patients) were downloaded from the national CaliciNet database. All norovirus outbreak data and

investigation results were uploaded by certified state and local public health laboratories. The P2 region of specimens from 43 GI.6 outbreaks was amplified using the Qiagen One-Step RT-PCR Kit. **Results:** A total of 3,960 norovirus outbreaks were reported to CaliciNet. Of the 2,895 outbreaks with a known transmission route, person-to-person and foodborne transmission were reported for 2,425 (83.7%) and 465 (16.1%) of the outbreaks, respectively. A total of 2,475 (62.5%) of outbreaks occurred in long term care facilities (LTCF) followed by 389 (9.8%) in restaurants and 227 (5.7%) in schools. A total of 435 (11%) outbreaks were typed as GI and 3,525 (89%) as GII norovirus. GII.4 viruses caused 2,853 (72%) of all outbreaks, of which 94% typed as either GII.4 New Orleans or GII.4 Sydney. In addition, three non-GII.4 viruses, GII.12, GII.1, and GI.6, caused 528 (13%) of all outbreaks. Several non-GII.4 genotypes (GI.3, GI.6, GI.7,GII.3, GII.6, and GII.12) were significantly more associated with foodborne transmission (P < 0.05; OR: 1.9 - 7.1). Phylogeographic analysis identified three major dispersions from two geographic locations responsible for the GI.6 outbreaks from 2011 - 2013. **Conclusions:** Our data demonstrate the cyclic emergence of new (non-GII.4) norovirus strains, and several genotypes are more often associated with foodborne outbreaks. These surveillance data can be used to improve viral foodborne surveillance and help guide studies to develop and evaluate targeted prevention methods such as norovirus vaccines.

Astrovirus and Sapovirus in Children Under Five Years of Age with Acute Diarrhea in Guatemala

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Background: Acute diarrheal illness (ADI) is a key cause of morbidity in Guatemalan children and viral infections are believed to be a significant etiology. Astrovirus and sapovirus are two viral etiologies that are important in other regions but their epidemiology is unknown in Central America. **Methods:** To examine the role of these viruses in ADI, we used an ongoing health facility-based surveillance for children aged <5 years in two Guatemalan departments (Santa Rosa and Quetzaltenango). ADI cases were defined as children <5 years of age presenting with ≥3 loose/liquid stools within a 24 hour period and an onset <14 days. Individuals were hospitalized patients and outpatients in both sites. Stool samples from ADI cases were tested for astrovirus, sapovirus and norovirus using multiplex RT and qRT-PCR, with rotavirus tested by ELISA. Additionally, *Shigella* sp. and C*ampylobacter* sp. were recovered by culture. No *Salmonella* was recovered during this period. **Results:** From January-August 2014, a total of 460 children met the case definition, and 425 (92%) were enrolled. Of these, 240 provided stool samples, of which 6 (3%) tested positive for astrovirus and 21 (9%) tested positive for sapovirus, accounting for approximately 12% of hospital and 6% of ambulatory cases. In general we have found that children with more severe diarrheal cases as with rotavirus attend the hospital facilities rather than community services. Other significant etiologies among these cases included rotavirus (25%), norovirus (10%), *Shigella* sp. (5%), and *Campylobacter* sp. (8%). The results of pathotypes of *Escherichia coli* and intestinal parasites are not presented here as the analysis has not been completed. Coinfections were detected with astrovirus and rotavirus (n=2) and with sapovirus and rotavirus (n=5). **Conclusions:** This is the first report of astrovirus and sapovirus infections in the country and indicates that astrovirus and sapovirus may be important causes of diarrheal disease in Guatemala.

I6. Late Breakers I

Tuesday, August 25, 3:30 PM - 5:00 PM
Centennial Ballroom IV

See page 257.

Modeling

Tuesday, August 25, 5:00 PM - 6:15 PM
Grand Hall

Board 289. Modeling Triple-diffusions of Infectious Diseases, Information, and Preventive Behaviors Through a Metropolitan Social Network—An Agent-based Simulation

L. Mao; Univ. of Florida, Gainesville, FL, USA

Background: A typical epidemic often involves the transmission of an infectious disease, the flow of information regarding the disease, and the spread of human preventive behaviors against the disease. These three processes diffuse simultaneously through human social networks, and interact with one another, forming negative and positive feedback loops in the complex human-disease systems. Few modeling work, however, have been devoted to coupling all the three diffusions together and representing their interactions. **Methods:** To fill the knowledge gap, this article proposed a new conceptual framework for such a triple-diffusion. A spatially explicit agent-based model was implemented to simulate the triple-diffusion process in a metropolitan area of 1 million people. The agent-based approach, network model, behavioral theories, and stochastic processes were used to formulate the three diffusions and integrate them together. **Results:** Compared to the observed facts, the model results reasonably replicate the trends of influenza spread and information propagation. **Conclusions:** The model thus could be a valid and effective tool to evaluate information/behavior-based intervention strategies. Besides its implications to the public health, the research findings also contribute to network modeling, systems science, and medical geography.

Board 290. The Economics of Pandemic Prevention: SARS, Ebola and New Strategies to Mitigate Disease Emergence at Source

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Background: Emerging infectious diseases (EIDs) can cause significant economic impacts as well as morbidity and mortality. Despite this, there are few analyses of the economic incentives to prevent and control pandemics. **Methods:** We analyzed the economics of strategies to prevent them at very early stages of spread. Given the continual rise in the number of new EIDs each decade, global efforts to deal with pandemics are similar to the mitigation vs. adaptation approaches to address climate change. We used economic modeling from climate change work to analyze mitigation of pandemics (prevention of their origins from animals) vs. adaptation (business as usual surveillance and outbreak control programs). We assessed mitigation strategies to

underlying drivers of disease emergence, specifically targeted to West Africa and Ebola emergence, and to reducing land use change as a driver of EIDs (the USAID-funded IDEEAL project). **Results:** Our results suggest that there is an urgent window to execute coordinated global pandemic control programs such as the IHR, with optimum efficiency achieved within the next 27 years. Mitigating disease emergence by reducing the impact of underlying drivers (e.g. the FAO-OIE-WHO 'One World One Health' approach) is more cost effective than business as usual. Our economic analysis of Ebola control shows that modest pre-outbreak investments to build capacity for early response, could have reduced economic damages significantly. Finally, mitigating emergence by reducing deforestation rates in tropical emerging disease 'hotspots' could follow 'ecosystem services' approaches to value tropical forests for conservation by including the health costs of diseases associated with deforestation. This approach can be used to inform local government, industry and village stakeholder groups to help reduce the negative health impacts of land use change. **Conclusions:** Our economic modeling suggests that efforts to mitigate against pandemic emergence (e.g. reducing their underlying drivers) will be more cost-effective in the long-term than our current global strategies. Furthermore, they may have collateral benefits for conservation and sustainability in developing countries.

Board 291. Estimation of MERS-Coronavirus Reproductive Number and Case Fatality Rate for the Spring 2014 Saudi Arabia Outbreak: Insights from Publicly Available Data

M. S. Majumder[1,2], C. Rivers[3], E. Lofgren[3], D. Fisman[4]; [1]Massachusetts Inst. of Technology, Cambridge, MA, USA, [2]Computational Epidemiology Group, Boston Children's Hosp., Harvard Med. Sch., Boston, MA, USA, [3]Virginia Tech, Blacksburg, VA, USA, [4]Univ. of Toronto, Toronto, ON, Canada

Background: Middle East Respiratory Syndrome Coronavirus (MERS-CoV) was initially recognized as a source of severe respiratory illness and renal failure in spring 2012. Prior to 2014, MERS-CoV was mostly associated with sporadic cases of human illness, of presumed zoonotic origin, though chains of person-to-person transmission in the healthcare setting were reported. In spring 2014, large healthcare-associated outbreaks of MERS-CoV infection occurred in Jeddah and Riyadh in the Kingdom of Saudi Arabia. To date, the epidemiological information published by public health investigators in affected jurisdictions has been relatively limited. However, it is important that the global public health community have access to information on the basic epidemiological features of MERS, including basic reproduction number (R0) and best estimates of case-fatality rate (CFR). **Methods:** We sought to address these gaps using a publicly available line listing of MERS-CoV cases. R0 was estimated using the incidence decay with exponential adjustment ("IDEA") method, while period-specific case fatality rates that incorporated non-attributed death data were estimated using Monte Carlo simulation.**Results:** IDEA model fits suggested a higher R0 in Jeddah (3.5-6.7) than in Riyadh (2.0-2.8). The model accurately projected final size and end date of the Riyadh outbreak based on information available prior to the outbreak peak; for Jeddah, these projections were possible once the outbreak peaked. Overall case-fatality (spring 2012 to spring 2014) was 40%. Depending on the simulated temporal distribution of 171 deaths that were known to have occurred but were unlinked to available case data, through-outbreak CFR may have been higher, lower, or equivalent to pre-outbreak CFR. Notably, case-proportional distribution of unlinked deaths from 2012 to spring 2014 yielded a through-outbreak CFR that was significantly lower than pre-outbreak CFR. **Conclusion:** Notwithstanding imperfect data, inferences about MERS epidemiology important for public health preparedness are possible using publicly available data sources. The R0 estimated in Riyadh is similar to that seen for SARS, but R0 in Jeddah and CFR appear to be higher. These data suggest this novel virus should be regarded with equal or greater concern than the related SARS-CoV.

Board 292. The Global Distribution and Burden of Melioidosis, an Overlooked Emerging Infectious Disease

D. Limmathurotsakul[1], N. Golding[2], D. Dance[3], R. Kitphati[4], N. P. Day[3], S. Peacock[5], E. Bertherat[6], S. I. Hay[3]; [1]Mahidol Univ., Bangkok, Thailand, [2]Univ. of Oxford, Oxford, United Kingdom, [3]Oxford Univ., Oxford, United Kingdom, [4]Ministry of Publ. Hlth. Thailand, Bangkok, Thailand, [5]Univ. of Cambridge, Cambridge, United Kingdom, [6]World Hlth. Organization, Geneva, Switzerland

Background: Melioidosis is an emerging infectious disease of humans and animals throughout South and East Asia, Southern China, Northern Australia, the Indian subcontinent, regions of South America, various Pacific and Indian Ocean islands, and some countries in Africa. The causative organism is the Tier 1 select agent and environmental Gram-negative bacillus *Burkholderia pseudomallei*. In northeast Thailand, melioidosis causes more than 1,000 deaths per year, which is now comparable to deaths from tuberculosis, and exceeds those from malaria, diarrheal illnesses and measles combined. There is a striking lack of accurate information on the worldwide burden of melioidosis. **Methods:** In this study, we undertook an exhaustive assembly of all available records of human and animal melioidosis and the presence of *B. pseudomallei* in the environment worldwide, and used a formal modelling framework to construct a global risk map of melioidosis. We then paired the resulting risk map with longitudinal information from melioidosis cohort and whole-population studies to infer the public health burden of melioidosis in 2012. **Results:** We predict melioidosis to be ubiquitous throughout the tropics, with local spatial variations in risk influenced strongly by the presence of the organism in the environment, soil type, rainfall, temperature and the degree of sanitation and urbanization. Using geospatial statistical models, we predicted new areas and countries where melioidosis is probably endemic but under-diagnosed (such as India, Bangladesh, Indonesia and Philippines) or never reported (such as Gabon, Seychelles, Guatemala and Cuba). We predicted that there are more than 100,000 people died of melioidosis each year. This is probably due to a combination of the lack of specific clinical features of melioidosis, microbiology facilities and familiarity with the organism, insufficient preventive measures, use of inappropriate antimicrobials and inadequate supportive care. **Conclusions:** We anticipate that this new risk map and burden estimates will provide a starting point for a wider discussion about the global impact of melioidosis and will help to guide improvements in disease diagnosis, preventive and treatment strategies and their economic evaluation.

Board 293. Estimating Etiology Distributions for Foodborne Disease Outbreaks with Missing Etiologies Using CART Analysis, 1998-2012

S. D. Johnson, D. Cole, L. Richardson, A. Vieira, S. Bennett, W. Gu; CDC, Atlanta, GA, USA

Background: Previous studies defined clinical profiles for groups of pathogens causing foodborne outbreaks by analyzing outbreak reports with complete clinical data; these profiles were used to identify characteristic features and determine the most likely pathogen group for outbreaks with missing etiologies. However, these methods faced challenges analyzing complex data from reports with frequently missing predictors. Tree-based modeling may be a better tool to define profiles from complex data and

to estimate etiology distributions of foodborne outbreaks with no etiology reported. **Methods:** We used a classification and regression tree (CART) analysis to model pathogen profiles of 6,963 foodborne outbreaks with known etiologies reported from 1998 through 2012. We used 14 clinical and demographic variables to develop profiles. We compared the classification accuracy of trees modeling profiles of up to 7 possible pathogen groups: norovirus, *Salmonella*-like (*Salmonella* spp. and *Shigella*), *Clostridium*, *Escherichia coli (E. coli* spp.*)*, *Staphylococcus*, *Campylobacter*, and *Bacillus.* We examined the performance of trees to classify 3,067 foodborne outbreaks missing etiologies into a single pathogen group. **Results:** The pathogen profiles could not distinguish between *Campylobacter* and the *Salmonella*-like group, nor *Bacillus* and *Staphylococcus*. Our final tree, comprised of profiles describing 5 pathogen groups, predicted 77% of outbreaks with known etiologies. Predictors of importance were percentage of cases reporting vomiting and fever, and median incubation and illness durations. Outbreaks with missing etiologies were assigned to norovirus (2032 outbreaks, 66%), *Clostridium* (464, 15%), a profile for both *Salmonella*-like pathogens and *Campylobacter* (310, 10%), a profile for both *Staphylococcus* and *Bacillus* (256, 8%), and *E. coli* (5, 0.2%). **Conclusion:** CART analysis is an efficient method for analyzing complex data with missing information. Similar to foodborne outbreaks with known etiologies, norovirus was the most likely pathogen in outbreaks with missing etiologies. Although we were unable to assign all outbreaks to a single pathogen, our classification tree contributes insight into the likely etiologies of foodborne outbreaks lacking laboratory confirmation of pathogens.

Board 294. EPIPOI: A User-friendly Software for Inspecting Seasonality, Burden and Spatial-patterns of Epidemiological Time-series

W. J. Alonso, B. J. McCormick; Fogarty Intl. Ctr., NIH, Bethesda, MD, USA

Background: There is an increasing need to process and understand relevant information generated by the systematic collection of public health data. However, the analysis of such time series usually requires advanced modeling techniques, which are not necessarily mastered by staff, technicians and researchers working on public health and epidemiology. **Methods:** EPIPOI is freely available software developed using Matlab (The Mathworks Inc) that runs both on PC and Mac computers, and available at www.epipoi.info. Its friendly interface guides users intuitively through useful comparative analyses including the exploration and extraction of parameters describing trends, seasonality and anomalies and crucially, the comparison of spatial patterns in those parameters. Not least it provides an analytical environment where even advanced users can benefit through a high degree of control over model assumptions, such as those associated with detecting disease outbreaks and pandemics. **Results:** EPIPOI was able to handle complex analyses in an accessible way. It has already been used to assist researchers in a variety of contexts, from didactic use in public health workshops to the main analytical tool in published research. Examples of analysis with EPIPOI include several papers on diarrhea and influenza, and it is being used now to study in other causes of death. **Conclusions:** EPIPOI can have an important role in advancing knowledge in the epidemiological field by empowering a broader range of public health officials, researchers and students from all over the world to explore time series data using a number of sophisticated analytical and visualization tools. As such, it is expected to decentralize the production of such analyses from distant institutions, allowing the producers and organizers of the raw data to look at their own data themselves, providing novel understanding of patterns and processes of causes of morbidity and mortality.

Board 295. Ebola in West Africa: Impact of Exponential Growth on Case Fatality Estimates

Withdrawn at Author's Request

Board 296. Transmission Dynamics and Control of Ebola Virus Disease Outbreak in Nigeria, July to September 2014

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Background: The largest Ebola virus disease (EVD) outbreak to date is ongoing in West Africa, particularly in Guinea, Sierra Leone and Liberia. A total of 20 EVD cases (19 laboratory confirmed, one probable) have been reported in Nigeria, with no new cases reported since 5 September 2014. All 20 cases stemmed from a single importation from a traveller returning from Liberia on 20 July 2014. **Methods:** We analyse up-to-date epidemiological data of the Ebola virus disease outbreak in Nigeria as of 1 October 2014 in order to estimate the case fatality rate, the proportion of healthcare workers infected and the transmission tree. We also assess the epidemiological data for the EVD outbreak in Nigeria from 20 July to 1 October 2014, and use a dynamic disease transmission model to illustrate the effect of forceful interventions in rapidly containing the EVD outbreak in Nigeria. **Results:** The interventions included timely implementation of careful contact tracing and effective isolation of infectious individuals. We found a critical level of isolation effectiveness of infectious individuals estimated at about 60% with a mean time from symptom onset to diagnosis of one day, which is necessary to reduce the reproduction number below the epidemic threshold at R=1.0 and halt the spread of EVD. **Conclusions:** Our results indicate that Nigeria's quick and forceful implementation of control interventions was determinant in controlling the outbreak rapidly and avoiding a far worse scenario in this country.

Board 297. Estimating the Effective Reproduction Number, Ebola Virus Disease Epidemic, 2014

H. Nishiura[1], G. Chowell[2]; [1]The Univ. of Tokyo, Tokyo, Japan, [2]Georgia State Univ., Atlanta, GA, USA

Background: Interpreting the time-course of ongoing Ebola virus disease epidemic is of utmost importance to consider essential countermeasures and resources required to curb the epidemic. The effective reproduction number, R_t, greatly helps elucidating the time-dependent transmission dynamics. **Methods:** We sought to estimate the R_t in real time in order to assess the current status of the evolving outbreak across countries affected in 2014. Country-specific data reported from Guinea, Liberia and Sierra Leone to the World Health Organization were used. **Results:** R_t for the three countries lies consistently above 1.0 since June 2014. Country-specific R_t for Liberia and Sierra Leone have lied between 1.0 and 2.0. **Conclusions:** The transmission potential of Ebola virus disease appeared to be comparable to previously estimated values of the same disease in Central Africa. R_t<2 indicate that control could be attained by preventing over half of the secondary transmissions per primary case.

Board 298. Impact of Interventions on the Effective Reproductive Number of the 2014 West African Ebola Outbreak

M. S. Majumder[1,2], S. Kluberg[3,2], M. Santillana[4,2], S. R. Mekaru[2], J. S. Brownstein[2]; [1]Massachusetts Inst. of Technology, Cambridge, MA, USA, [2]Computational Epidemiology Group, Boston Children's Hosp., Harvard Med. Sch., Boston, MA, USA, [3]Boston Univ., Boston, MA, USA, [4]Harvard Univ., Cambridge, MA, USA

Background: The ongoing Ebola epidemic in West Africa is much larger and more widespread than any other in history. While previous outbreaks in small villages have burned out due to the depletion of susceptible individuals, this epidemic has already spread across entire countries, and thus can only be curtailed by reducing the effective reproduction number, R_E. The efficacy of specific interventions for an Ebola epidemic of this scale has not yet been studied. In this paper, we describe how various interventions have impacted R_E thus far. **Methods:** First, we modeled R_E over time for Sierra Leone and Liberia using an adaptation of the Incidence Decay and Exponential Adjustment (IDEA) model (where the discount factor d was held constant at 0). We then collected news stories of disease control interventions and "aggravating events" - namely, events that would likely cause an increase in effective contact rate and thus, an increase in R_E. We classified interventions into three categories: providing education, limiting contact rates, and strengthening healthcare systems. Using a serial interval of 18 days, we then charted R_E, control interventions, and aggravating events over time. In order to assess impact of interventions, we assumed that contact rate and R_E should remain constant in the absence of control measures. **Results:** The R_E curves differed substantially between the two countries. As expected, we found large increases in R_E following early aggravating events. Positive control interventions were generally followed by a sustained decrease in R_E, while aggravating events preceded a temporary increase or suppressed decrease in R_E. Certain classes of interventions appeared to be more effective than others. **Conclusion:** This qualitative analysis suggests that both disease control interventions and aggravating events have had quantifiable effects on Ebola transmission in West Africa. Control measures likely demonstrate a lasting effect because they are typically implemented at the country level, while negative events show a more transient effect because they tend to occur locally. By further improving our understanding of how interventions and aggravating events have influenced the outbreak to date, we hope to better inform decision-making and resource allocation in the months ahead.

Board 299. A Method for Calculating the Lifetime Risk Reduction of Infection Induced by Newly Implemented Vaccination Program

A. Endo, H. Nishiura; Graduate Sch. of Med., The Univ. of Tokyo, Tokyo, Japan

Background: Effectiveness of vaccination program is defined as the relative reduction in the risk of infection in vaccinated population compared with unvaccinated. When a new vaccination program is introduced, a part of population is usually not covered by vaccination and protected only by herd immunity. Such disparity in immunization program has a profound impact on age- and time-dependent transmission dynamics, leading to inequality in the benefit across generations. **Methods:** A mathematical model is employed to describe the time- and age-dependent effectiveness considering an introduction of a new vaccination program (e.g. pneumococcus or *Haemophilus influenzae* vaccination). We compute the force of infection, cohort risk and lifetime risk of infection, demonstrating that the age- and time-dependent population effectiveness of vaccination varies with time. **Results:** The incidence after introduction of a new vaccination program showed generation-specific reduction. The inequality of lifetime benefit across different generations was explicitly modeled as an equation. **Conclusions:** The lifetime risk reduction of infection due to a new vaccination program was mathematically modelled. Any country attempting a new vaccination program could refer to the proposed formula to anticipate generation gaps even in advance of implementing vaccination program.

Board 300. Mortality Patterns of the 1957 Influenza Pandemic in Maricopa County

A. J. Cobos[1], C. G. Nelson[1], M. Jehn[1], G. Chowell[2,3]; [1]Arizona State Univ., Tempe, AZ, USA, [2]Div. of Intl. Epidemiology and Population Studies, Fogarty Intl. Ctr., NIH, Bethesda, MD, USA, [3]Georgia State Univ., Atlanta, GA, USA

Background: While research has quantified the mortality burden of the 1957 influenza pandemic in the United States, little is known about how the H2N2 virus spread locally in Arizona, an area where the dry climate was promoted as reducing respiratory illness transmission yet tuberculosis prevalence was high. **Methods:** Using archival death certificates from 1954 to 1961, this study quantified the age-specific seasonal patterns, excess-mortality rates, and transmissibility patterns of the 1957 pandemic in Maricopa County, Arizona. By applying cyclical Serfling linear regression models to weekly mortality rates, the excess-mortality rates due to respiratory and all-causes were estimated for each age-group during the pandemic period. The reproduction number was quantified from weekly data using a simple growth rate method and generation intervals of 3 and 4 days. Local newspaper articles from *The Arizona Republic* were analyzed from 1957-1958. **Results:** Excess-mortality rates varied between waves, age-groups, and causes of death, but overall remained low. From October 1959-June 1960, the most severe wave of the pandemic, the absolute excess-mortality rate based on respiratory deaths per 10,000 population was 17.85 in the elderly (≥65 years). All other age-groups had extremely low excess-mortality and the typical U-shaped age-pattern was absent. However, relative risk was greatest (1.90) among children and young adolescents (5-14 years) from October 1957-March 1958, based on incidence rates of respiratory deaths. Transmissibility was greatest during the same 1957-1958 period, when the mean reproduction number was 1.08-1.11, assuming 3 or 4 day generation intervals and exponential or fixed distributions. **Conclusions:** Maricopa County largely avoided pandemic influenza from 1957-1961. Understanding this historical pandemic and the absence of high excess-mortality rates and transmissibility in Maricopa County may help public health officials prepare for and mitigate future outbreaks of influenza.

Geographic Information Systems (GIS)

Tuesday, August 25, 5:00 PM - 6:15 PM

Grand Hall

Board 301. Evaluation of Neighborhood-level Risk Factors on *Campylobacter* Infection Using Geographically Weighted Regression – FoodNet

J. Y. Huang[1], R. M. Hoekstra[1], O. L. Henao[1], D. Cole[1], K. J. Scherzinger[2], N. Oosamanally[3], B. Shiferaw[4], S. McGuire[5], T. E. Libby[6], M. McMillian[7], A. R. Vieira[1]; [1]CDC, Atlanta, GA, USA, [2]New Mexico Emerging Infections Program, Albuquerque, NM, USA, [3]Georgia Dept. of Publ. Hlth., Atlanta, GA, USA, [4]Oregon Publ. Hlth. Div., Portland, OR, USA, [5]New York State Dept. of Hlth., Albany, NY, USA, [6]California Emerging Infections Program, Oakland, CA, USA, [7]Tennessee Dept. of Hlth., Nashville, TN, USA

Background: *Campylobacter* is the second most common laboratory-confirmed infection reported to the Foodborne Diseases Active Surveillance Network (FoodNet). We conducted neighborhood-level analyses to better understand relationships between *Campylobacter* infection rates and demographic and environmental factors. **Methods:** FoodNet conducts population-based active surveillance for laboratory-confirmed *Campylobacter* infections in 10 US sites. We used 2010 incidence data from 9 FoodNet sites; information on race, ethnicity, income, home ownership, high school or college education, and population density from the US Census; and number of cattle and poultry farms from the Homeland Security Infrastructure Program. All factors were analyzed at census tract level. We used zero-inflated Poisson (ZIP) regression to select variables for inclusion in geographically weighted regression (GWR) models that adjust for geography by residence of each case (either county or region of state). For each site, we used GWR to model the relationship between *Campylobacter* incidence and factors found to be significant predictors in the ZIP models. **Results:** Factors significantly associated with *Campylobacter* incidence for varied by site, resulting in different variables being selected for each site-specific GWR model. For most models, *Campylobacter* incidence increased as income, number of poultry farms, and population density increased, and as percentage of population with education, number of cattle farms, percentage of Hispanic, and percentage of home owner occupancy decreased. GWR identified specific areas within each site where factors were more or less influential in the models. **Conclusions:** The incidence of *Campylobacter* infection varies geographically and our methods provide insights into regionally-relevant factors that might be associated with infection. This analysis highlighted site-level differences in the relationship between *Campylobacter* incidence and other factors. Neighborhood-level analyses that link multiple data sources can help characterize subpopulations at higher risk for *Campylobacter*.

Board 302. Geographic Expansion of High Lyme Disease Incidence Foci in the United States

K. J. Kugeler, J. D. Forrester, P. S. Mead; CDC, Fort Collins, CO, USA

Background: Lyme disease (LD) is a tickborne zoonosis with a highly focal geographic distribution. Residents of 14 states account for >95% of the ~30,000 LD cases reported annually in the United States. Over the last 20 years, case counts have increased steadily, with some evidence of expansion into neighboring areas. To better quantify and track the geographic distribution of human LD cases, we sought to develop a simple but robust method for defining counties of high risk. **Methods:** LD has been a nationally notifiable condition since 1991. Counties with high LD incidence were identified using SaTScan cluster detection software, with a maximum possible cluster size of 25% of the US population (minimum size: one county). County-level data on confirmed LD cases reported 1998-2012 were aggregated into 5-year intervals (1998-2002, 2003-2007, 2008-2012), offset by U.S. county population figures. Significance of clusters was determined according to likelihood ratio tests and Monte Carlo hypothesis testing (n=999). Relative risk (RR) was defined as the observed number of cases divided by expected number of cases based on a discrete Poisson probability distribution. Counties designated as high incidence were: 1) part of a defined, statistically-significant cluster of elevated risk (α=0.05), and 2) had a county-specific RR $\geq$ 2.0. **Results:** Two major foci of largely contiguous counties met the high incidence county designation in each time period: one in the Northeast and one in the north-central US. Over time the number of high incidence counties in the Northeast doubled from 90 during 1998-2002, to 130 during 2003-2007, to 182 during 2008-2012. During the same time periods, the number of high incidence counties in north-central states also nearly doubled, from 40 to 67 to 78. The centroid of high incidence counties in the Northeast moved to the west and north, whereas the centroid in the north-central states remained relatively stable over time. **Conclusions:** We describe a simple yet statistically robust measure to objectively quantify counties with high incidence of human LD. Using this measure based on human disease information rather than entomologic metrics, the geographic expansion of LD over time is apparent. This method can be used to quantify future geographic expansion of high Lyme disease incidence foci.

Board 303. Mapping Recent Chikungunya Activity in the Americas

A. Anyamba[1], R. Jepsen[1], J. L. Small[1], K. J. Linthicum[2], S. C. Britch[2], J-P. Chretien[3], J. L. Sanchez[3], C. J. Tucker[1]; [1]NASA Goddard Space Flight Ctr., Greenbelt, MD, USA, [2]USDA /ARS Ctr. for Med. and Vet. Entomology, Gainesville, FL, USA, [3]DoD Armed Forces Hlth. Surveillance Ctr. (AFHSC), Silver Spring, MD, USA

Background: The risk of vector-borne diseases is increasing due to changes and variability in the global climate, and increasing global travel and trade. The recent chikungunya activity in the Western Hemisphere and its spread throughout the Americas illustrates the ability for a vector-borne disease to spread rapidly. Location-based disease data are spotty and disease outbreak data are often incomplete and difficult to access. In our continuing efforts to establish better outbreak data records and provide near real-time outbreak assessments, we present a compilation of geo-referenced reports of recent chikungunya activity in the Americas. **Methods:** Web-searching tools were thoroughly exploited to find named locations reporting chikungunya cases from January to September 2014. We compiled and summarized reports from ProMed Mail, HealthMap and the U.S. Centers for Disease Control and Prevention. Each disease report location was geo-coded using GIS mapping software by identifying the latitude and longitude of each disease report location by place name (approximate home town or county, region or country). We also recorded additional information fields including Report Date, End Date, Suspected Cases, Confirmed Cases, Imported Cases, and Deaths. **Results:** In general the distribution maps indicate an increase in the number of outbreak locations over time. This may be a result of improved disease surveillance as the outbreak was recognized, improved case detection, or better diagnostics and documentation. The maps also provide a spatial-temporal timeline of the spread and intensification of chikungunya activity in the Americas during this time period. **Conclusions:** The compiled geo-referenced data records for chikungunya in the Americas are going to complement existing comprehensive geo-referenced data records for chikungunya

in the Eastern Hemisphere for modeling purposes. However, problems associated with this methodology of data mining for disease report data include: 1) unknown accuracy of reported case data; 2) case underreporting in some areas; and 3) limited information on location where human cases were exposed to likely mosquito vectors. Nevertheless, such databases are crucial to the study of disease-climate relationships, and ultimately to disease prevention.

Board 304. Spatial and Temporal Analysis of *Campylobacter* spp. and *Salmonella* spp. in England

R. Elson; Publ. Hlth. England, London, United Kingdom

Background: *Campylobacter* spp. and *Salmonella* spp. are common gastrointestinal infections in England. This study set out to examine geographical differences (and similarities) between the two infections with a view to informing public health interventions. **Methods:** Data from a large sentinel surveillance study of human infections of *Salmonella* spp and *Campylobacter* spp. carried out between 2004 and 2007 was analysed using statistical tools in commercially available GIS software and freely available spatial statistics software. Several approaches were used to determine the optimum scale of analysis and scan window size. Independent variables, including deprivation levels, ethnicity and urban/rural split were also examined. **Results:** statistically significant clusters of high and low rates for both pathogens were detected. Statistically significant spatial clusters generated by both pieces of software mapped closely. Levels of deprivation and residence in rural areas or on town fringes may influence rates of infection. **Conclusions:** This study demonstrates geographical differences in the rates of two common gastrointestinal infections in England and provides a framework to perform routine spatial and temporal analyses of surveillance data.

Board 305. Software to Facilitate Remote Sensing Data Access for Infectious Disease Surveillance and Forecasting

M. C. Wimberly, M. DeVos, J. Hu, C. L. Merkord, Y. Liu; South Dakota State Univ., Brookings, SD, USA

Background: Increased understanding of the ecological effects of climate and land use change on emerging diseases has highlighted the need to integrate environmental monitoring with disease surveillance. Satellite remote sensing is a critical source of environmental data that provides consistent, repeatable measurements across nearly the entire surface of the Earth. However, disciplinary and technological barriers still limit its widespread application in the public health arena. To bridge this gap, we have developed the Epidemiological Applications of Spatial Technologies (EASTWeb) software tool to provide health scientists with automated and customizable access to remote sensing data. **Methods:** EASTWeb is an open-source, client-based application that connects to online data archives and automatically acquires, processes, and summarizes remote sensing datasets. A variety of environmental summary statistics are produced and stored in a relational database that can be easily linked to a geographic information system (GIS) for further analysis of geocoded epidemiological data. EASTWeb is programmed using JAVA for user interface development and overall system control. Spatial analyses are carried out using the GDAL open source geospatial library. PostgreSQL is used to store and manipulate the resulting data summaries. **Results:** The current version of EASTWeb computes environmental indicators that are relevant to the surveillance and forecasting of vector-borne and zoonotic diseases. They include meteorological variables such as air temperature and precipitation, vegetation indices, and estimates of soil moisture and evapotranspiration. EASTWeb has been utilized to support malaria early warning in the Ethiopian highlands and West Nile virus risk forecasting in the northern Great Plains of the US. **Conclusions:** EASTWeb has the potential to facilitate broader utilization of remotely-sensed environmental data for disease surveillance and forecasting. The next version of EASTWeb, currently under development, will incorporate more data sources, allow greater customization through an improved user interface, and include expanded documentation to make the software more accessible to health scientists engaged in geospatial analysis of epidemiological data.

Board 306. Is Listeriosis Really Sporadic in England?

R. Elson; Publ. Hlth. England, London, United Kingdom

Background: Listeriosis is a rare but serious infection in England and disproportionately affects the elderly, immunocompromised and pregnant women. Most cases are deemed sporadic. Previous studies have indicated that levels of social deprivation may be an important driver in terms of predisposition to infection. Social deprivation is not uniform across the England and geographic variation in rates of listeriosis have not been examined. **Methods:** Laboratory confirmed cases of *L. monocytogenes* in England and Wales reported to enhanced surveillance between 2001 and 2014 were summed at local authority, medium and lower super outputs areas and spatially joined to 2011 census data. The data did not include pregnancy associated cases or those linked to known clusters. Data was analysed using tools in commercially available GIS software and in freely available spatial statistics software. Multiple approaches were used to determine the optimum spatial scale for analysis. **Results:** Statistically significant higher rates of infection were detected by the commercially available software. These were primarily in urban areas in the northwest and northeast of England. Clusters detected by the freely available software were not statistically significant but largely mapped well to areas with high incidence rates. **Conclusions:** Geography may play a part in determining predisposition to listeriosis. This may be related to social deprivation, rates of chronic illnesses or differences in food consumption patterns or food distribution networks. These findings can inform public health interventions.

Board 307. Mapping Insecticide Resistance in Malaria Vectors: Latest Updates from IR Mapper®

M. P. Hadi[1], E. O. Juma[1], H. Pates Jamet[2]; [1]Vestergaard Frandsen EA Ltd, Nairobi, Kenya, [2]Vestergaard Frandsen Inc, Washington, DC, USA

Background: The emerging and rapid spread of resistance to major classes of public health insecticides threatens current malaria vector control efforts. Deployment of the most appropriate tools needs to be informed by up-to-date data on insecticide resistance in target malaria vector species. Launched in 2012, IR Mapper® (www.irmapper.com) is an online geospatial mapping platform built on a systematic review of peer reviewed, published literature to visualize insecticide resistance trends in *Anopheles* vectors. **Methods:** IR Mapper® was built using ArcGIS for JavaScript API platform. The platform is updated monthly with newly published data from peer reviewed scientific publications on phenotypic (WHO susceptibility test and CDC bottle assay data) and resistance mechanisms (target site and overexpressed metabolic enzymes) data. Additional data meeting standard WHO or CDC test criteria from PMI, National Malaria Control Programs, and other reputable sources are also included. The filter tools on IR Mapper® enable filtering by year, vector species, insecticide class, and resistance mechanisms. **Results:** As of January 2015, IR Mapper® consisted of 9,433 unique field records from 57 countries and 48 *Anopheles* species or species complexes. 81.5% of countries have reported resistance to at least one of the four classes of insecticides; 76.0% have reported testing of resistance mechanisms. Filtering by time period highlighted that three times more reports of

insecticide resistance in *Anopheles* were reported between 2000 and 2014 compared with the previous 45 years. IR Mapper® also revealed data gaps notably for two high malaria burden countries: Democratic Republic of Congo and Nigeria. For instance, there were 59 reports of insecticide resistance testing in DRC, which is estimated to account for 34.1% of global malaria cases compared to 850 reports of monitoring in Benin with estimated 5.2% of global cases. **Conclusion:** While insecticide resistance testing has increased in recent years, IR Mapper® is able to identify where data gaps on insecticide resistance exist in malaria vectors. IR Mapper® is a useful tool for visualizing temporal and spatial trends in *Anopheles* insecticide resistance and associated resistance mechanisms in order to inform evidence based decision making of vector control interventions.

Strengthening Public Health Systems

Tuesday, August 25, 5:00 PM - 6:15 PM
Grand Hall

Board 308. Advances in Influenza Surveillance in Latin America and the Caribbean, 2010-2014

R. Palekar[1], M. Cerpa[2], E. Aziz-Baumgartner[1], T. D'Mello[2], O. Bilbao[2], W. Clara[1], S. Mirza[1], A. Moen[1], M-A. Widdowson[1], S. Aldighieri[2], M. Espinal[2]; [1]CDC, Atlanta, GA, USA, [2]Pan American Hlth. Organization, Washington, DC, USA

Background: The 2009-influenza A(H1N1) pandemic highlighted gaps in influenza surveillance in the 33 PAHO/WHO Member States in Latin America and Caribbean (LAC). Specifically, there was limited information available on cases, especially severe cases, and virologic and clinico-epidemiologic data were not linked at the individual level, both of which challenged rapid assessment of the pandemic threat and public health decision-making. **Methods:** During 2010-2014, PAHO/WHO and partners worked to address gaps in influenza surveillance in LAC. Efforts were focused on implementation of widespread sentinel surveillance for severe acute respiratory infection (SARI) with integration of virologic and clinic-epidemiologic data. Activities included the revision and dissemination of operational surveillance guidelines, establishment of common data reporting mechanisms, training of staff in sentinel sites and strengthening of influenza laboratory capacity. **Results:** During 2010-2013, there was a 14% increase in the number of samples analyzed for influenza by LAC labs (n=227,246 in 2013); a 7% increase in voluntary participation in (n=28 labs in 2013) and perfect concordance on (n=26 labs in 2013) the WHO Influenza External Quality Assurance Program; and a 30% increase in the number of NICs reporting weekly virologic data to PAHO (n=19 NICs in 2013) for ≥60% of the year. During 2010-2014, PAHO developed four influenza training courses with didactic and activity components, which were used to train >150 public health professionals from >25 LAC countries. In LAC in 2013, >90 SARI sentinel sites, from 19 countries, were conducting routine influenza surveillance and >15 countries submitted SARI data to PAHO for ≥60% of the year. In 2014, to promote regional sustainability and collaboration, the America's respiratory disease network, SARInet (www.sarinet.org), was launched. **Conclusions:** Through capacity building and establishment of a formal network, increased timely epidemiologic and virologic data on severe influenza disease are available. The utility of these data, to decision-makers in LAC, to inform prevention and control measures, might increase the likelihood of surveillance system sustainability.

Board 309. Enhancing Notifiable Disease Surveillance Systems in Middle-income Countries to Improve Detection of Possible Intentional Biological Events

C. Hanou, J. C. Lay, C. Bautista, B. L. Smoak; Walter Reed Army Inst. of Res., Silver Spring, MD, USA

Background: The Governments of Azerbaijan (AJ) and Georgia (GG) have been working with Walter Reed Army Institute of Research (WRAIR), the Defense Threat Reduction Agency's Cooperative Biological Engagement Program (CBEP), and other US agencies since 2005 to enhance their notifiable disease surveillance systems and outbreak detection and response capabilities, with particular focus on pathogens with bioterror potential (PBP). **Methods**: Classroom-based trainings in epidemiology were provided to public health care workers (PHCWs) using a train-the-trainer approach. Each Ministry of Health (MoH) updated their case definitions for nine PBPs to a three-tiered approach and developed surveillance guidelines for PBPs. Both countries converted from a paper-based system to an electronic one, implementing the Electronic Integrated Disease Surveillance System (EIDSS), a software program developed with funding from CBEP. Five EIDSS system performance assessments, three in AJ and two in GG, were conducted. PHCWs used EIDSS data to analyze disease patterns within their countries. Each country created data quality and surveillance indicators to monitor the performance of their notifiable disease surveillance systems. **Results**: In each country, over 150 PHCWs were trained in basic surveillance and outbreak investigations, and 25 were taught analytic epidemiology. Both countries have legally approved revised case definitions while AJ has also approved new surveillance guidelines. As PHCWs gain experience in analyzing electronic data and assessing the system, quality and timeliness of reporting in EIDSS have improved. In AJ, analysis of EIDSS data on brucellosis, a high priority disease for the MoH, allowed them to determine expected values and evaluate algorithms for early detection of outbreaks. **Conclusions**: In AJ and GG, updates to national policies, the transition to an electronic disease surveillance system, and human capacity building have greatly enhanced the notifiable disease systems to detect biological events.

Board 310. United States Centers for Disease Control and Prevention Domestic and International Laboratory Response to Middle East Respiratory Syndrome Coronavirus (MERS-CoV)

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Background: On Sept 20, 2012, the isolation of a novel coronavirus from a patient in Saudi Arabia who later died following a severe acute respiratory illness was reported. Subsequently named Middle East respiratory coronavirus (MERS-CoV), CDC laboratories quickly responded by developing and deploying laboratory assays and providing training and reference testing support for domestic and international public health partners. **Methods:** Real-time RT-PCR (rRT-PCR) assays were rapidly developed following release of partial MERS-CoV genome sequences in public domain. Analytical and clinical assay performance were validated and emergency use authorization by the US FDA was obtained for deployment of the assay kits to state public health and other domestic laboratories through the CDC Laboratory Response Network. Upon obtaining an isolate of MERS-CoV and limited serum specimens from MERS-CoV antibody positive patients, serological assays were developed and validated and external molecular quality assessment (EQA) panels distributed to qualify recipient laboratories. MERS-CoV rRT-PCR assays and EQA panels were further distributed to CDC Global Disease Detection and World Health Organization affiliated countries. World Health Organization sponsored training courses were conducted in countries with documented MERS-CoV circulation or at high risk of MERS-CoV importation. **Results:** To date, CDC MERS-CoV rRT-PCR assay kits have been distributed to 47 state public health laboratories in the US and 52 countries on 5 continents to support MERS-CoV surveillance, reference testing and epidemiologic studies. Five regional training initiatives have been completed, 3 in the Middle East, one in Africa and one in the South Caucasus region, with attendants from 25 countries. Serological testing capacity has been transferred to Saudi Arabia. Proficiency and confirmatory testing support are ongoing. **Conclusions:** Newly emerging pathogens will continue to challenge public health institutions to provide a rapid and effective laboratory response. Lessons learned from the CDC laboratory response to MERS-CoV can help improve future response efforts.

Board 311. Knowledge, Attitude, Practices and Training Needs for Food-handlers in Large Canteens in Southern Vietnam, 2012

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Background: Foodborne outbreaks in large canteens are often public health events of concern in Vietnam. The outbreaks have been occurring more frequently in factories than in schools. Contamination during the food preparation phase has not been addressed yet by authorities, especially in terms of the food-handlers' knowledge, attitude and practices (KAP). We conducted a study to identify and compare KAP of food-handlers in large canteens of schools and factories and propose training needs for food-handlers. **Methods:** A cross-sectional study combined with qualitative study was conducted in 2012. 909 food-handlers were randomly selected from a sampling frame of employees of large canteens in Southern Vietnam. All participants were interviewed using standardized questionnaire. Data were described and potential confounders were controlled before using logistic regression models to calculate prevalence odds ratios (POR) and 95% confidence intervals (CI) for differences in KAP between those in schools and factories. Ten focus group discussions with maximum variation sampling were used in qualitative study. **Results:** Of 909 food-handlers participating the study, 76% were females, 84% graduated from secondary school or above; median age and work experience were 38 years and 36 months, respectively. Proportions of all participants with whose KAP were considered adequate KAP were 26%, 36%, and 26%, respectively. There were associations between knowledge and attitudes, and knowledge and practices. Food-handlers in schools were about 2 times as likely to have the adequate KAP as food-handlers in factories. Among 66 investigated canteens, 9% did not separate raw food from cooked food area. 52% did not have standard rest rooms. Food-handlers suggestions included that training venue should be in work place with involvement of managers, number of trainees per course should be fewer, lectures should include more exercises, and course duration should be longer. **Conclusions:** KAP of food-handlers were generally poor, especially of food-handlers working in factories. Training courses should be prioritized for food-handlers in factories in Vietnam.

Board 312. Factors Driving Customers to Seek Health Care in Pharmacies for Acute Respiratory Illness: A Pilot Study in Dhaka City, Bangladesh

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Background: Pharmacies in Bangladesh serve as important sources of health service for all socio-economic groups. During the 2009 influenza pandemic, a survey in Dhaka reported that 48% of respondents with acute respiratory illness (ARI) identified local pharmacies as a first point of care. This study explores the factors driving urban customers to seek health care from pharmacies for ARI, their treatment adherence and outcome. **Methods:** From June_December 2012, a cross-sectional study was conducted among 100 randomly selected pharmacies within Dhaka. Study participants were patients or patient relatives aged >18 years seeking care for ARI from pharmacies without prescription. After informed consent, a structured interview was conducted with customers outside the pharmacies, after they purchased medicine. Customers were contacted by phone 5 days post-interview to ask about treatment course and outcome. **Results:** We interviewed 302 customers patronizing 76 different pharmacies. Among them 186 (62%) sought care for themselves and 116 (38%) sought care for a sick relative. Most customers (215; 71%) were male. Two hundred seventy three (90%) of 302 customers sought care from the study pharmacy as their first point of care, while 18 (6%) had previously sought care from another pharmacy, and 11 (4%) from a physician for this illness episode. The most frequently reported reasons for seeking care from pharmacies for ARI were easy accessibility to pharmacies (86%), lower cost than other health care options (46%), availability of medicine (33%), personal relationship with the drug seller (20%), and convenient opening hours (19%). After purchasing medication from the pharmacy, 270/297 (91%) of patients reported completing the full treatment course as prescribed by the drug sellers. Among them 256 (86%) were cured and 35 (12%) sought further treatment from a health care provider for the same illness episode. **Conclusions:** In Dhaka, persons with ARI preferred to first seek care at pharmacies rather than at physician or hospital clinics because they perceived treatment to be prompt, at reduced cost than other health care options and medicine could be purchased at the same time. Based on our findings, we recommend further studies to assess appropriateness of treatment by the drug sellers and targeting training to this sector.

Board 313. Implementing Automated Reporting of Outbreak Data to the National Outbreak Reporting System (NORS)

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Background: Launched in 2009, the National Outbreak Reporting System (NORS) is a web-based system used by health departments in the United States to report waterborne disease outbreaks and enteric disease outbreaks transmitted by food, person-to-person contact, animal contact, environmental contamination, and indeterminate means. To automate data reporting and validation from existing state and local outbreak databases to NORS, the Centers for Disease Control and Prevention (CDC) has developed a new application, NORSDirect. Since 2011, CDC has collaborated with six state and local health agencies as part of a pilot program to test the capabilities of NORSDirect. **Methods:** We reviewed outbreak reports uploaded through NORSDirect by primary mode of transmission and state, and evaluated barriers associated with implementing and using NORSDirect. **Results:** In January 2014, a beta version of NORSDirect was released to six health agencies participating in the pilot. From January 2014 through September 2014, 4,265 outbreak reports were uploaded by three agencies (range 8-3,720 outbreaks per agency). The most common primary mode of transmission was person-to-person in 3,309 (78%) outbreak reports, followed by foodborne (593, 14%), waterborne (45, 1%), environmental contamination (11, 0.3%), animal contact (9, 0.2%), and indeterminate/other mode of transmission (298, 7%). Six hundred and forty-six outbreaks (15%) were newly reported; the remaining were updates of previously reported outbreaks. States reported that the most common barriers to uploading reports were time constraints (reported by 2 health agencies), changes made to a state-specific outbreak surveillance system (1), and competing priorities within the health department (1). **Conclusion:** Automated electronic outbreak reporting using NORSDirect should strengthen surveillance by reducing barriers to outbreak reporting. During the pilot, many otherwise unreported outbreaks were uploaded to the system, suggesting that NORSDirect will further increase the number of outbreaks reported. Implementing NORSDirect requires time and close collaboration between CDC, state and local epidemiologists, and IT specialists to reduce barriers associated with automated outbreak reporting.

Board 314. A Pilot Program of Joint Veterinary and Human Epidemiology Training in Armenia: A One Health Approach

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Background: A One Health approach to disease prevention and control is valuable because it integrates the concepts of human, animal and ecological health to address emerging diseases. In Armenia, human and veterinary epidemiologists are traditionally trained separately and have limited interaction during disease outbreak investigations. In an effort to promote collaboration between human public healthcare workers within the Ministry of Health (HPHW) and practicing professional veterinarians within the Ministry of Agriculture (PV), a pilot program was conducted to evaluate the benefit of training professionals from these two disciplines together. **Methods:** From 2013-2014, the Government of Armenia partnered with the Defense Threat Reduction Agency to provide basic epidemiology training to two cohorts of HPHW and PVs. Course materials integrating veterinary and human disease concepts were developed by Walter Reed Army Institute of Research and Academic Engagement Partnership. Trainees participated in two one week training sessions on disease surveillance (Week 1) and outbreak investigation (Week 2), led by local Armenian trainers. Group exercises and class discussions facilitated interaction between HPHW and PVs. The program was evaluated by comparing pre- and post- test scores, course evaluations and PV focus groups. **Results:** Twenty-one HPHW and 23 PVs participated in the joint training program. Mean post-test scores for both groups demonstrated mastery of Week 1 (88% vs. 78%, respectively) and Week 2 (84% vs. 76%, respectively). Both groups improved their scores significantly between the pre and post-tests and the amount of improvement was proportionally similar. Over 90% of all participants felt that course information was relevant to their current positions. Focus group results show that PVs found the joint training beneficial because it teaches a standard approach and fosters relationships with their HPHW counterparts. **Conclusions:** The results from this pilot program clearly show that a One Health approach that trains PV and HPHW together would be valuable in Armenia. Joint training provides opportunities to improve disease surveillance by promoting collaboration across disciplines. Participants from each profession gain an appreciation for each other and for their common One Health goals.

Board 315. Underreporting of Tick-borne Disease in Residents of a High-incidence County, Minnesota, 2009

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Background: Lyme disease (LD), human anaplasmosis (HA), babesiosis, and other tick-borne diseases (TBDs) attributed to *Ixodes* ticks are thought to be widely underreported in the United States. The magnitude of TBD underreporting and, consequently, the underestimation of TBD incidence in Minnesota (MN) are unknown. To describe TBD underreporting and identify more accurate incidence estimates in an area of MN where LD, HA, and babesiosis are highly endemic, we conducted a retrospective surveillance study in Crow Wing County (CW) in north-central MN. **Methods:** To identify TBD cases diagnosed in 2009, but not reported to the Minnesota Department of Health (MDH), diagnostic and procedural billing codes suggestive of tick-borne diseases were used to select medical charts for retrospective review in medical facilities serving residents of a highly endemic county in MN. **Results:** In the review of 1,464 possible TBD events in CW residents who sought medical care during 2009, 30% had diagnostic or laboratory features that were reportable to MDH for LD, HA, or babesiosis. Of 444 illness events which should have been reported, 352 (79%) were not reported. Of these, 102 (29%) met confirmed or probable surveillance case criteria, including 91 (26%) confirmed LD cases with physician-diagnosed erythema migrans (EM) without serologic confirmation. For each confirmed and probable LD, probable HA, and confirmed babesiosis case reported to MDH in 2009, 2.8, 1.3, 1.2 and 1.0 cases likely occurred, respectively. These estimates result in upward revisions of confirmed LD, probable LD, and probable HA county-level incidences to 227.6, 78.8, and 91.8 cases per 100,000 population (up from incidences of 81.3, 60.6, and 76.5 based on originally reported cases). **Conclusions:** The estimated number of "actual" reportable confirmed LD diagnoses was been found to be nearly 3 times as many as the number reported through surveillance. Underreporting of tick-borne diseases by medical providers, especially early, localized LD with EM, can result in underestimation of disease incidence by health authorities.

Board 316. Competencies for Public Health Laboratories: Strengthening the Workforce to Improve Public Health Practice

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Background: Public health laboratories (PHLs) face challenges in workforce development that are compounded by the absence of published competencies for structured training, education, and job positions. Competencies are critical to strengthening the workforce by defining expected levels of performance and knowledge across a wide spectrum of public health laboratory practices including infectious disease surveillance, pathogen and environmental toxin diagnostics, outbreak investigation activities, safety, and other critical responsibilities. CDC and the Association of Public Health Laboratories (APHL) identified this gap and launched a collaboration to develop a comprehensive set of laboratory competencies. **Methods:** An 11-member CDC/APHL Steering Committee guided the project. A 37-member Project Planning group met in Oct. 2012 to kick off the project and establish the target audience, scope, and draft functional areas. Subject matter experts (91) from federal, state, and local public health, environmental, and agriculture laboratories, and from clinical laboratories, academia, and other entities worked in teams to develop competency and sub-competency statements across four proficiency levels for 15 domains such as: Microbiology; Surveillance; Emergency Management and Response; Informatics; Bioinformatics; Quality Management System; Safety; and Management and Leadership. **Results:** Draft competencies were vetted nationally Nov. 2013 - Jan. 2014 and 1,434 comments were adjudicated in a structured process by representatives from CDC, PHLs, and APHL. The final competency set contains 122 competencies and 522 sub-competencies and addresses APHL's 11 Core Functions of State Public Health Laboratories. Expected publication is in 2015. Stakeholders will develop tools and resources to assist PHLs in implementing the competencies. **Conclusions:** A strong, knowledgeable, and well-trained PHL workforce is needed to confront the challenges of emerging infectious diseases and to create a sustainable PHL system. The final competency set will support multiple workforce needs - such as developing job descriptions, performance objectives, competency assessments, training courses, and academic curricula - and will be critical for PHL workforce recruitment, retention, and development.

Board 317. Poliomyelitis Surveillance System and Environmental Monitoring in São Paulo State, Brazil—Tools to Prevent the Reintroduction of Wild Poliovirus

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Background: Poliomyelitis is an infectious disease caused by poliovirus transmitted through the faecal-oral route. Since 1994, Brazil and other Region of Americas were certified as polio-free areas. However, the circulation of wild poliovirus (WPV) persists in several countries in Africa, Asia and Middle East, increasing the risk of the imported WPV. We present the poliomyelitis surveillance system in São Paulo State considering the WHO alert on international spread risk of wild poliovirus, issued in May 2014. **Methods:** Description of the system, analysis of surveillance indicators and findings of the environmental monitoring. **Results:** The system is compound by: 1) Acute Flaccid Paralysis (AFP) surveillance, system to detected recent WPV or vaccine derived poliovirus (VDPV) cases, achieves annual rate of non polio AFP around 1case per 100,000 population aged < 15 years. Further passive notification, it is performed active search of cases in hospitals and systematic analysis of morbidity and mortality databases; 2) Vaccination program reaches high rates of coverage (≥ 95%) in the State; and 3) Environmental monitoring, conducted by CETESB, in routine since 1999, collects sewage and seawater samples on sentinel sites: international airport and seaports and wastewater treatment plants (WWTP). All poliovirus isolated are sent to the Enterovirus Laboratory of FIOCRUZ (WHO Reference Laboratory for Poliomyelitis in Brazil) for confirmation. From August 1999 to April 2014, a total of 1,274 samples of sewage and seawater were tested. On March 5th, 2014, a WPV serotype 1 from Equatorial Guinea was detected in a sewage sample from the WWTP influent of the Viracopos International Airport. On January 20th, at the Petrobras Pier in São Sebastião Coast, was detected a VDPV Sabin 2. **Conclusions:** These findings reinforce the importance of the environmental monitoring as preventive action for detection of imported WPV. São Paulo State is an international entrance of tourists, refugees and immigrants. Such results does not change the epidemiological condition of poliomyelitis eradicated in Sao Paulo State. No case of poliomyelitis was registered to present date. We recommend the implementing of environmental surveillance in other Brazil States as supplementary tool for the Global Polio Eradication.

Board 318. Improving Sample Management to Decrease Contamination Rates in Blood Culture Process During Population Based Surveillance, Egypt, 2010-2014

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Background: The International Emerging Infectious Program in Damanhour, Egypt has conducted Population Based Acute Respiratory Infections and Acute Febrile Illness surveillance since 2009. One of the routine tests applied in our surveillance is blood culture. Bacterial isolation is considered the gold standard for diagnosis of Brucellosis Pneumonia, Typhoid fever, and septicaemia. In 2011, we recorded high blood culture contamination and low isolation rates. Possible causes may include: misuse of antibiotics, care habits of febrile patients leading to skin flora flourish, sample collection time and handling or inadequate laboratory procedures. We implemented a strategy with the goal to improve specimen quality and improve pathogen recovery. **Methods:** After root cause analysis, corrective actions for sample management improvement with field and laboratory teams were implemented. Standard operating procedures for blood collection and transport were reviewed and staff re-trained. Changes included an extra step of cleaning the skin with soap wipes followed by disinfection with 70% alcohol and betadine prior to blood collection. To avoid early antibiotic use and to ensure that samples were immediately collected after hospitalization, we implemented afternoon and night shift collection. We changed from manual to an automated Bactec blood culture system in 2012. We implemented a weekly mentoring and supervision program for blood collection. **Results:** A total of 5013 blood cultures were processed for patients enrolled in the surveillance from 2009 to date. The highest contamination rate (21%) of blood samples with common gram-positive skin flora bacteria was observed in 2011. After the interventions started in September 2012, we decreased the contamination rate to 9% in 2014, with a relative reduction of 56%. The isolation rates remained low (~1%) with different pathogenic bacteria isolated during the period reported. **Conclusions:** Collectively, the strategies implemented decreased the blood culture contamination rates by more than half. Low pathogen recovery

was not related to contamination. Further investigations are needed to identify the possible causes of low isolation rates that may include antibiotic misuse; non-bacterial etiologies associated to cases.

Board 319. Enhanced Surveillance for Severe Pneumonia, Thailand, 2010-2014

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Introduction: The etiology of severe pneumonia is frequently not identified by routine disease surveillance in Thailand. Since 2010, the Thailand Ministry of Public Health (MOPH) and US CDC have conducted surveillance to detect known and new etiologies of severe pneumonia. **Methods:** Surveillance for severe community-acquired pneumonia was initiated in December 2010 among 30 hospitals in 17 provinces covering all regions of Thailand. Interlinked clinical, laboratory, pathological and epidemiological components of the network were created with specialized guidelines for each to aid case investigation and notification. Severe pneumonia was defined as chest-radiograph confirmed pneumonia of unknown etiology in a patient hospitalized ≤48 hours and requiring intubation with ventilatory support; patients with underlying chronic pulmonary or neurological disease were excluded. Respiratory and pathological specimens were tested by reverse transcriptase polymerase chain reaction for nine viruses, including Middle East Respiratory Syndrome Coronavirus (MERS-CoV), and 14 bacteria. Cases were reported via a secure web-based system. **Results:** Of 660 specimens sent for testing, 379 (57%) had a potential etiology identified. At least one viral agent was detected in 203 cases, with respiratory syncytial virus (RSV) identified in 52%. Bacterial pathogens were detected in 105 cases of which 71 cases had apparent mixed bacterial-viral infections. Apart from RSV, adenovirus (14%) and influenza A(H1N1)pdm09 (7%) were the most frequent pathogens identified. Since MERS-CoV testing was initiated for cases from September 2012, no cases have been identified from the 435 samples tested. Epidemiological investigations were conducted of influenza-associated deaths and cases with a history of travel outside Thailand in the 10 days prior to illness onset. **Conclusions:** Enhanced surveillance improved the understanding of the etiology of severe pneumonia cases and improved the MOPH's preparedness and response capacity for emerging respiratory pathogens in Thailand. Guidelines for investigation of severe pneumonia from this project were incorporated into surveillance and research activities within Thailand and shared for adaption by other countries.

Board 320. Characterizing Investigation Steps and Public Health Responses Taken on Emergency Department Visit and School Absenteeism Syndromic Surveillance Aberrant Events

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Background: Public health units (PHUs) in Ontario, Canada employ syndromic surveillance for early outbreak detection and situational awareness. We describe results from a prospective study characterizing aberrant events ("alerts") and corresponding investigation steps and actions for 1) emergency department (ED) visit data for respiratory and gastrointestinal syndromes, and 2) school absenteeism (SA) data. **Methods:** Of 36 Ontario PHUs, 15 participated in the ED study and 4 in the SA study. PHUs used structured "logbooks" to document alerts, investigation steps, and responses. Qualitative analysis of free-text data from the logbooks informed a coding framework (i.e. an inductive, data-driven approach). The framework was applied to the logbooks, and frequencies for each item in the framework were tabulated and analyzed descriptively. **Results:** From October 2013-August 2014, 1,109 alerts were generated from ED data for respiratory, ILI, or GI syndromes. Of these, 198 (18%) alerts were checked to determine if the aberration could be attributed to an alternative explanation (e.g. duplication or missing data rather than a true increase in cases). 775 (70%) alerts were assessed for clustering by time, place, and person factors. 450 (41%) alerts warranted a "response" taken by the epidemiologist, of which 356 (32%) were "watchful waiting". SA data from December 2013-June 2014 resulted in 523 alerts, where153 (29%) were checked for alternative explanations. 350 (67%) of the SA alerts were assessed for "person, place, and time" clustering. 170 (33%) were deemed to require public health action, where132 involved notifying schools via email. For ED data, public health units serving larger populations (i.e. > 200,000) were more likely to check for alternative explanations (23% of alerts) and clustering (81%), compared to those serving <150,000 people (0% and 55% respectively). **Conclusions:** These results indicate that the ability to check syndromic surveillance alerts varies by size of the health unit. This may be due to the increased availability of resources. The yield of public health actions from ED and SA syndromic systems is low compared to the number of alerts. For ED data, the most common action was watchful waiting while emailing schools was the most common action for SA alerts.

Board 321. The Impact of Standard Tools on the Investigation of Emergency Department Visit Syndromic Surveillance Aberrant Events in Ontario, Canada

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Background: The way syndromic surveillance aberrant events are used to inform public health varies in Ontario, Canada. We present preliminary results describing the impact of tools standardizing how local public health epidemiologists investigate emergency department aberrant events. **Methods:** 15 of the 36 public health units (PHU) were recruited, sorted by size of the population served, and using a random start were alternately assigned to intervention (n=9) or control (n=6) study arms. Intervention PHU received (1) alerts from a standard CUSUM algorithm applied to emergency department visits for respiratory and gastrointestinal syndromes; and (2) implemented a standard protocol for investigating alerts received. The control group used their usual alerting systems and investigation practices. Logbooks were used to collect open-ended data about alerts received and follow-up activities. A data-driven approach was used to generate a coding framework to characterize investigation steps and actions taken by the epidemiologist. Logbooks were coded according to the framework, and frequencies of each node were tabulated and analyzed descriptively. **Results:** Between October 2013-August 2014, 1109 alerts were received by study PHU (n = 550 by intervention PHU; n = 559 by control PHU). Intervention PHU were more likely than those in the control group to check whether an aberrant event could be attributed to an alternate explanation other

than a true increase in cases, such as checking for duplicated or missing data [190/550 alerts (35%) vs. 8/559 alerts (1.4%)]. Fewer alerts received by the intervention group control group PHU were documented as having their data characterized; for example, checking whether the cases contributing to the aberration cluster according to person, place, or time [229/550 alerts (42%) vs. 546/559 (98%)]. **Conclusion:** Provision of standardized tools appears to have influenced the manner of investigating alerts, comparing intervention and control PHU. Intervention PHU more frequently documented checking whether aberrations could be due to an error rather than a true increase in cases than control PHU. However, a smaller frequency of intervention PHU alerts that characterized alert data compared to control PHU indicates that for this component, standardized tools had less of an impact.

Board 322. Rabies Awareness in a Community of Bangladesh

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Background: Rabies is endemic in Bangladesh and represents an ongoing public health hazard resulting in at least 2000 death annually. The vast majority of these are caused by dog bites. We conducted a study to explore people's knowledge of rabies, their attitudes towards dogs and practices associated with treating dog bites. **Methods:** We surveyed 3200 households in Satkhira district of Bangladesh during April and May 2012 through face-to-face interviews using a structured questionnaire. **Results:** Out of the total 3200 respondents, 5.2% reported a history of dog bite in at least one family member, and 11.8% respondents reported a history of dog bite in domestic animals during the previous year. Among dog bite victims, 3.6% human and 15.8% animals died. Community dogs (39.2%) and stray dogs (44.5%) were responsible for attacking humans and animals. Seventy-three percent of subjects have heard about rabies and there was a high level of awareness (86%) that dog bite is the main cause of rabies and that rabies can be prevented by vaccination (85%). Thirty seven percent of the respondents obtained information about rabies from physicians, 27% from television and 20% from the municipality. Among dog bite victims, 59% went for traditional to native healers, 29% were treated with rabies vaccine, 4% washed the wound with only water, 2% washed the wound with soap, and 4.8% did not take any measure after being bitten by a dog. As a measure for dog population management, 56% preferred sterilization, whereas the rest felt that the number of dogs will increase if some are not killed. **Conclusions:** Dog bite is not uncommon in humans and animals in this region. The subjects interviewed had a fair level of knowledge and awareness regarding rabies and its prevention. It is their current health care seeking behavior that should be improved through additional education and awareness.

Board 323. Leveraging Partnerships for Improved National Public Health Institutes

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Practitioners in the field of Health Systems Strengthening (HSS) aim to build and fortify the organizational, financial, legal and policy frameworks of health systems to improve service delivery.The U.S. Centers for Disease Control and Prevention (CDC) National Public Health Institute (NPHI) program partners with numerous internal and external partners when helping create or strengthen a country's public health focal point or NPHI. In collaboration with partners, CDC's NPHI program aims to: 1) Strengthen capacity and infrastructure for a better functioning public health system 2) Implement activities to improve efficacy/effectiveness of the NPHI 3) Engage in sustainable activities so time limited partnerships have long term impact The NPHI program engages directly with a country's Ministry of Health and their NPHI (CDC-like institution) if it exists. CDC NPHI program staff also engage bilateral and multilateral stakeholders (e.g., World Health Organization), private foundations, non-governmental organizations, other high income NPHIs, CDC's technical experts in the U.S. and abroad, and organizations like the International Association of National Public Health Institutes. The NPHI team works with countries to assess their public health needs and determine what system specific improvements will address those needs. Concurrently, technical advisors from CDC give advice on best practices in implementation. The process is monitored and evaluated using a maturity model/staged development tool, which focuses on a country's improvement in priority public health areas. CDC's investments and partnership relies on good leadership and governance in order to successfully make organizational/workforce/financial improvements. These improvements will in turn will lead to they key improvements in public health training and service delivery to respond to global health threats. This presentation informs the field of HSS practice. Partnerships are critical to the success of an NPHI, but require commitment and perseverance to maintain. The lessons learned will be presented through case studies from partner countries.

Board 324. Teaching Modern Disease Surveillance and Investigation Skills in Low-income Nations: DTRA Cooperative Biological Engagement Program (CBEP) in Kenya and Uganda

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Background: As signatories to the International Health Regulations 2005 (IHR), Kenya and Uganda are committed to improving their national capability to detect, diagnose, report and respond to disease epidemics and potential pandemic threats. The governments of these nations noted a need for enhanced skills of local public health officials, and partnered with the Defense Threat Reduction Agency's CBEP to address this gap. **Methods:** Between 2012 and 2014, trainings were provided to core outbreak response teams, consisting of clinical, surveillance, veterinary and laboratory officers, from 5-6 districts at a time. Training was delivered in two one-week modules, the first on Basic Surveillance and the second on Outbreak Investigation. Concepts were taught through classroom lectures and reinforced with practical exercises and hands-on training in Microsoft Excel and EpiInfo. Trainings were conducted by a local cadre of trainers developed by epidemiologists from the Walter Reed Army Institute of Research through a Training of Trainers approach. District teams also completed surveillance projects involving collection, analysis and interpretation of surveillance data on diseases impacting their districts. **Results:** From 2012 to 2014, over 250 public health officials in approximately 50 districts were trained in Kenya and Uganda. Ministry of Health officials in both countries cited improved surveillance reports and analyses from trained districts. The program identified several successful strategies including training across disciplines with a One Health approach, teaching foundational computer skills, reinforcing skills through mentored surveillance projects, developing trainer teams of national and district-level experts to improve coordination across levels of the public health system and enhance program sustainability. **Conclusions:** The earliest opportunity to identify and contain infectious disease lies at the local level. There is a vital need for training in low-income countries, where severe outbreaks are most common and local officials are

least equipped to handle them. Disease surveillance training programs such as these provide lower resourced countries with the capability to minimize the spread of potential outbreaks.

Board 325. Phylogenetic Analysis of Avian Influenza AH5N1 from a Recent Outbreak in Egypt (2014/2015)

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Background: Highly pathogenic avian influenza Avirus subtype H5N1 was first reported in Egypt in 2006 in both poultry and human. Between 2006 and October 2014, 177 human infections have been confirmed in Egypt with a Case Fatality Rate (CFR) of 37%.From November 2014, a surge in A/H5N1 has occurred in poultry and in human throughout Egypt with 127 human infections till 10 March 2015 (CFR34%). We report the HA sequences of representing samples from human and poultry from the ongoing outbreak. **Methods:** HA gene was sequenced from RNA extracts from oropharyngeal swabs collected from 17 H5N1 human cases and nine A/H5N1 isolates recovered from infected chicken. Four overlapping DNA fragments covering the entire HA gene were amplified using specific primer sets for the hemagglutinin (HA) gene. Sanger sequencing was performed and the generated sequences (1700 nucleotides) were aligned to all previously publishedsequences for phylogenetic analysis. **Results:** Phylogenetic analysis of HA sequence from 15 human cases demonstrated a distinct monophyletic group with a bootstrap support value of 98 within subclade 2.2.1-C viruses and showed high nucleotide similarity to each other (98.6 to 99.7%) and less nucleotide similarity (97.2 to 97.9%) to cases from March 2014. Mutations previously known to increase the binding of H5N1 to human receptors were detected in all specimens; unique point mutations at E251I, Q322K, and N425K were seen in three samples. HA sequence from poultry isolates showed that they were within subclade 2.2.1-C and that sequences were99.3 to 100% similar. Sequenced HA genes from 2014/15 outbreak samples were more similar to each other (98.9 to 99.6%) than to sequences from 2012/13 samples (96.9 to 98.7%). **Conclusion:** Phylogenetic analysis of influenza A H5N1 virus from human and poultry in Egypt during the November epizoonotic fall within subclade 2.2.1-C viruses forming a distinct group. Minor variation in sequences when compared to viruses from previous years, is within the normal virus drift. Homogeneity among viruses from poultry and humans, points to common ancestry. The significance of the novel mutations warrants further investigation. Monitoring of emerging A/H5N1 viruses in Egypt will continue with the goal to inform on possible genetic changes that would drive transmission, virulence in humans and poultry.

Board 326. Adult Immunization Programs and Chronic Disease Partnerships

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Background: The Advisory Committee on Immunization Practices recommends vaccines for adults and publishes an adult immunization schedule each year. Many adult vaccination recommendations are based on the presence of certain chronic health conditions, such as diabetes, heart disease, and asthma, which increases the risk of certain vaccine preventable diseases and their complications. Despite these recommendations, adult immunization rates in the United States are low among individuals with chronic conditions, leaving many individuals at risk. We assess resources for adult immunization program implementation and coordination with chronic disease programs. **Methods:** We analyzed data from the 2013 Program Annual Progress Assessment Survey (PAPAS), which was completed by CDC immunization program awardees in spring of 2014 to assess immunization program activities during the 2013 calendar year. Data from 56 immunization programs in the U.S. (50 states, the District of Columbia and 5 cities) was included in the analyses of adult immunization program activities, resources, and collaborations with chronic disease prevention programs. **Results:** Of the 56 immunization programs, 73% (41) reported having an adult immunization coordinator. Of these programs, 43% of adult coordinators spent 1-25% of their time on adult immunization activities; 32% (13) spent 26-50%, 15% (6) spent 51-75%, and 10% (4) spent 76-100%. A minority of programs collaborated with state chronic disease programs: 31% (17) collaborated with diabetes prevention programs, 16% (9) with heart disease prevention programs and 21% (12) with asthma treatment and prevention programs. **Conclusions:** Few immunization programs have full time staff members devoted to adult immunization activities which likely limits their abilities to promote the ACIP recommendation and establish preventive health service programs to immunize adults with chronic conditions. Improved coordination and collaboration among immunizations and chronic disease prevention programs may help to reduce missed opportunities to increase awareness and immunization rates among adults with chronic health conditions. Further evaluation of these types of collaborations is necessary to completely understand their impact on adult immunization rates.

Board 327. Need for Effective Public Health Strategies: Evidence From Hospital-based Mortality Records in Federal Medical Centre, Owo, Ondo State, Nigeria, 2006-2014

O. S. Ilesanmi[1,2], O. Fawole[3,2], P. Nguku[2], A. Oyemakinde[2], P. Adewuyi[2]; [1]Federal Med. Ctr., Owo, Ondo State, Nigeria, [2]Nigeria Field Epidemiology and Lab. Training Programme, Abuja, Nigeria, [3]Dept. of Epidemiology and Med. Statistics, Univ. of Ibadan, Oyo State, Nigeria

Background: Vital events registration is not accurately done in Nigeria, hence no data is available on mortality. Hospital based data can yield useful information to characterize mortality which has occurred in the absence of community based data. Cause-specific mortality data are important to monitor trends in mortality over time. This study describe all causes of mortality in Federal Medical Centre, Owo, a tertiary health care facility in South West Nigeria. **Methods:** A retrospective review of the records of all patients that died in the hospital from 2006 to 2014 was conducted. Data was exported from excel and analysed with SPSS version 21 to generate proportions. Extracted from the records included age, sex, underlying cause of death and date of admission and death. **Results:** From 2006 to 2014 a total of 1326 death occurred in the Hospital. The median age at death was 46 years (range: 0-110); 277 (20.9%) of deaths were among those less than one year of age. Males were 703(53%). The median Length of stay in hospital was 4 days (range: 0-277). Highest number of death 217(16.4%) was recorded in 2009 and on Wednesdays 210(15.9%). More deaths occurred in January and February 153(11.5%) and 135(10.3%) respectively. Communicable disease caused death in 243(18.3%) with HIV 164(67.5%) and TB 25(10.3%) leading. Birth Asphyxia 63(22.7%) and Low Birth weight 75(27.5%) were the commonest cause of death in under one. **Conclusion:** The leading causes of mortality identified in this study are preventable. Infant mortality remains a large public health problem in

Nigeria. This data may be used to quantify mortality in Nigeria. More Public health strategies and interventions are need to reduce death from communicable diseases and infants.

Global Health Initiatives

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Board 328. From Idea to Activation: The Vietnam Ministry of Health EOC and the US CDC Global Health Security Agenda

J. C. Kile[1,2], L. N. Vu[3], P. J. Giannone[2], T. T. Do[1], J. B. Crockett[2], P. D. Tran[3], M. McConnell[1], L. T. Nguyen[3]; [1]CDC, Hanoi, Vietnam, [2]CDC, Atlanta, GA, USA, [3]Ministry of Hlth., Hanoi, Vietnam

Background: The Global Health Security Agenda (GHSA) is a United States Government program to promote a world safe and secure from global health threats from infectious diseases. In support of GHSA, the U.S. Centers for Disease Control and Prevention (CDC) introduced a Global Health Security Demonstration Project in March 2013 to the Vietnam Ministry of Health (MOH). With MOH participating in the project with CDC, we sought to establish an emergency operations center (EOC) and systems for disease outbreak surveillance and preparedness, early detection, and coordination and response. **Methods:** Using emergency operations and management information and guidelines from existing international sources, MOH and CDC identified a number of steps toward developing an emergency management facility and system for the EOC. MOH and CDC developed an EOC management plan with standard operating procedures and forms, consistent with international standards for EOC development and operations. EOC training manuals were developed, core EOC staffs were trained, and an exercise was designed and conducted to learn and practice EOC operations and emergency management principles. **Results:** From March through September 2013, CDC introduced GHSA to the MOH, of which an EOC was one important part. MOH and CDC identified a location for a public health emergency operations center in Vietnam, enhanced the facility and resources, developed an EOC management and operations plan, conducted EOC and emergency management training, and designed and conducted a capabilities-based exercise. On 11 August 2014, MOH activated the EOC in preparedness response to the WHO determination of a public health emergency of international concern regarding the Ebola epidemic in West Africa. **Conclusions:** Development of a functioning international-type EOC and emergency management system is possible within the existing framework of a countries disease response systems and organizational structures. The decision to develop and manage a public health EOC system assists in consolidating resources, systems, and partners for infectious disease preparedness and response, further enhancing national, regional and global public health security.

Board 329. Teaching Modern Disease Surveillance and Investigation Skills in Low-income Nations: DTRA Cooperative Biological Engagement Program (CBEP) in Kenya and Uganda

Withdrawn at Author's Request (See Board 324)

Board 330. Global Health Capacity Building Through the Global Health Security Agenda

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Background: In February, the United States launched the Global Health Security Agenda (GHSA), in partnership with 28 nations, WHO, OIE and FAO. It is intended to accelerate progress on implementation of the International Health Regulations (2005) enhancing countries' abilities to prevent, detect, and respond to infectious diseases. To translate political attention into global health action, the US developed the "Action Package" concept, and 11 such packages, as a path forward to achieve the 9 objectives set out within GHSA. The packages represent activities led or taken on by countries together, which will address specific gaps in global health security in a measurable and time-limited way. A White House Ministerial Meeting in September, highlighted commitments made by countries in taking on the Action Packages, emphasizing the need for action in their implementation. Our intent is to highlight the activities that have been taken on by partner countries, as examples of how the GHSA is contributing to public health capacity building on a global scale. **Methods:** Following the introduction of the Action Package concept at a GHSA meeting in Helsinki last May, countries identified specific packages where they would like to lead/contribute. Action package leaders are responsible for ensuring ongoing development, refinement, and implementation of the Action Package, while contributing countries support implementation of the package either domestically, regionally, or internationally. **Results:** As a result of the GHSA political process, over 100 multisectoral commitments were made to either lead or contribute to action packages. **Conclusions:** Enhancing the capacities necessary towards achieving global health security requires multisectoral global investment. The vision is that countries participating in the Agenda will continue to organize around these Action Packages and begin to take on activities leading towards full realization of specific GHSA targets with/in partner countries. The Action Packages process is a unique multilateral forum for technical level-engagement, providing an opportunity to bring additional partners, sectors and resources into work that supports public health capacity building necessary to enhance countries abilities to prevent, detect and respond to infectious disease threats.

Immigrant and Refugee Health

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Grand Hall

Board 331. Tuberculosis and Diabetes Among United States-bound Adult Refugees, 2008-2012

S. R. Benoit, E. W. Gregg, S. Jonnalagadda, W. Zhou, J. A. Painter; CDC, Atlanta, GA, USA

Background: Type 2 diabetes is one of the most rapidly increasing chronic diseases and is the leading cause of renal failure, non-traumatic lower-limb amputations, and blindness among US adults. Diabetes increases the risk for active tuberculosis (TB). Our objective was to study the association between diabetes and TB among US-bound adult refugees. **Methods:** We reviewed overseas medical evaluations completed by panel physicians of 220,687 adult US-bound refugees from January 1, 2008, through December 31, 2012, by using CDC's Electronic Disease Notification System. Screening for diabetes is not required for admission to the United States, but it should be documented in the examination forms when known. We found diabetes in the forms by searching for related keywords (e.g., NIDDM, diabet) and medications (e.g., metformin,

insulin) with text parsing techniques. All refugees are screened for TB and the results are recorded on the forms. We calculated the proportion of TB cases with diabetes and used logistic regression to determine the association between TB and diabetes. **Results:** Among four countries with >100 refugee cases of TB, the percentage of TB cases with diabetes varied: Burma 1.1% (8/740), Somalia 1.2% (2/170), Bhutan 2.5% (13/510), and Vietnam 5.0% (6/120). The odds of TB among persons coming from those four countries was 1.6 (95% CI, 1.1-2.3) as high among refugees with diabetes as those without diabetes, controlling for age group, sex, body mass index, and birth country. **Conclusions:** The likelihood of TB was higher among refugees with diabetes than those without diabetes, a finding consistent with other studies. The International Union Against Tuberculosis and Lung Disease and the World Health Organization established a framework to prevent and control both diseases. Diabetes status among adult refugees should be considered for TB-risk stratification.

Board 332. Evaluation of Annual Selective Supplementary Immunization Activities Among Pre-school Migrant Children in Beijing, 2006-2013

R. Ma, P. M. Sun, L. Lu, J. Wu, H. X. Pang; Beijing Ctr. for Disease Control and Prevention, Beijing, China

Background: Unselective supplementary immunization activities (SIAs) targeting the whole population within an age range have been widely used to strengthen routine immunization programs. However, migrant children (children not having local Hukou) were more likely to miss routine immunizations and suffered higher incidence of vaccine-preventable diseases, especially measles, than registered children (children having local Hukou), which posed a big challenge. **Methods:** Annual selective SIAs among pre-school migrant children were conducted in Beijing within one month after Chinese New Year during 2006-2013. Nine doses of 6 vaccines were involved: Three doses of oral poliomyelitis vaccine (OPV), 2 doses of measles-containing vaccine (MCV), and the 1st dose of hepatitis B vaccine (HepB), diphtheria, tetanus and pertussis combined vaccine (DTP), meningococcal polysaccharide vaccine (MPV) and Japanese encephalitis vaccine (JEV). House-to-house searches were performed by village/community committees to obtain the list of the target children. By checking immunization cards in local clinics, immunization providers identified the children who missed target vaccine doses. All those dose absentees were tracked by committees until they received their missed doses. **Results:** The reported number of the target children in annual SIAs was 15.2%-40.2% higher than in official statistics and had kept rising from 189,904 in 2006 to 513,729 in 2013, with the average annual growth rate of 15.3%. For each target dose, ≥98% dose absentees got their missed shot during each SIA. The pre-SIA coverage of each target dose among migrant children had increased since 2006 and eventually reached above 98% in 2013, which were very close to the routinely reported coverage level among registered children. For children targeted by MCV, measles incidence ratio of migrant to registered children decreased from 54:1 in 2006 to 1:1 in 2013. **Conclusions:** Annual selective SIAs among pre-school migrant children in Beijing were well performed and helped to improve health equity and routine immunization programs despite increasing target population. It set a good example to other developing areas challenged by the same problem.

Social Determinants of Health and Infectious Diseases

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Board 333. Profile of Viral Hepatitis in Saudi Arabia

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Background: The epidemiology of viral hepatitis in Saudi Arabia has undergone major changes, concurrent with major socio economic developments over the last two to three decades.This disease represents a major public health problem in Saudi Arabia resulting in the need for considerable healthcare resources. **Method:** A retrospective analysis of the reported cases of viral hepatitis was conducted based on the reports of The Ministry of Health in Saudi Arabia about Hepatitis A, B and C cases in all the regions of Saudi Arabia from 2006 to 2010. **Results:** Our study demonstrated that the incidence of viral hepatitis showed a decreasing pattern over the study period, except for the incidence of hepatitis B in Saudis that showed a small increase. Of hepatitis A, B, and C, HBV was the most predominant type of hepatitis, accounting for (53%) of the cases, followed by HCV (30%) and HAV (17%). HAV infection predominates in children (5-14 years) with 60% of HAV cases, HBV in young adults (15-44 years) with 69% of HBV cases, and HCV in older adults (>45 years) with 59% of cases ($p < 0.01$). **Conclusion:** Despite significant changes in the incidence of viral hepatitis A, B and C, it remains a major public health problem in Saudi Arabia; however, it showed a significant decline in the last two decades that could be attributed to the nationwide vaccination programs and the improved health facilities, but further investigations and better health controls are needed to control the increase in HBV incidence.

Board 334. Predictors of Condom Use Among Sexually Active Young Women—National HIV Communication Survey, South Africa, 2012

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Background: In South Africa, young women aged 16-24 years are three to six times more likely to become HIV infected compared with young men in the same age group. Condom use is one of the most effective strategies to combat HIV infection. In this study, we determined predictors of condom use among young women in South Africa. **Methodology:** We analyzed nationally representative data from the 2012 National HIV Communication Survey that included sexually active young women aged 16 to 24 years. We performed logistic regression to determine predictors for condom use using STATA version 13. **Results:** Of the 1,029 women, (median age of 21 years), 595 (58%) reported condom use at last sex act. On multivariate analysis, delayed sexual debut (AOR 2.4, 95%CI: 1.4-4.2), living separately from a regular partner (AOR 2.6, 95%CI: 1.3-5.6, p=0.009), being a student compared to being unemployed (AOR 3.2, 95%CI: 1.7-6.3, p<0.001), and having sex with a recent acquaintance versus with a married partner (AOR 10.0, 95%CI: 2.6-33.3, p=0.009) were more likely to use condom at last sex. **Conclusion:** Condom use is associated with delayed sexual debut, living separately from a regular partner, being a student compared to being unemployed, and having sex with a recent acquaintance. Behavioral interventions discouraging early sexual debut can increase condom usage among young women in South Africa.

Board 335. Multidrug Resistant Tuberculosis and Treatment in KwaZulu-Natal, South Africa: A Long Distance Relationship

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Background and Objectives: Almost half of all MDR TB cases in South Africa occur in the KwaZulu-Natal (KZN) province, which also has the highest HIV prevalence in South Africa at 17%. Long distance to MDR TB treatment facilities has been noted to be one of the major risk factors for defaulting treatment, but has not been quantified to date. **Methods:** We conducted a retrospective cohort study of KZN residents diagnosed in 2011 with MDR TB to assess factors associated with treatment success. Treatment success was defined as cured or completed treatment while failure was defined as treatment default, treatment failure, or death. Final clinical outcome was assessed two years after treatment initiation. The key risk factor of interest, distance to the treatment facility, was calculated in kilometers from residential address. Multivariable logistic regression was used to determine factors associated with treatment success. **Results:** Data from 635 eligible patients were analysed, from which a final treatment outcome was available for 582 (92%). Treatment success was observed for 284 (49%) patients, while treatment failure was observed for 298 (51%). Among patients with a treatment outcome, 75% (434/582) were HIV positive. The median distance travelled was 49km (range 0.1km to 509km). HIV status, sex and previous TB drug history (i.e. new or previously treated) were not associated with treatment success. Travelling less than 100km was associated with treatment success (OR 2.2, 95% Confidence Interval [CI] 1.6-3.1; adjusted OR [aOR] 2.6, CI 1.7-4.1) as was age <19 years (OR 1.6, CI 0.9-2.8; aOR 3.2, CI 1.4-7.1). Treatment at the centralised King DinuZulu MDR TB treatment facility was significantly associated with treatment success in univariate analyses (OR 1.6, CI 1.1-2.3) but after adjustment for distance, age, HIV status, sex and drug history this factor was no longer significant. **Conclusion:** This analysis demonstrates that proximity to MDR TB treatment facility is a significant factor in MDR TB treatment success. Therefore, establishing high quality MDR TB services should be made available within geographically accessible distances in KZN to reduce the burden of disease.

Gender and Infectious Diseases

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Board 336. HIV/AIDS and Disclosure to Partners: A Situation Analysis of HIV Positive Women in Oyo State, Nigeria

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Background: Partner consent and support can substantially enhance adherence to Prevention of Mothers-to-Child Transmission (PMTCT) interventions. This study explores the issues concerning disclosure of HIV status to partners of HIV sero-positive mothers in PMTCT facilities in Oyo State, Nigeria. **Methodology:** We conducted a cross sectional study on 560 HIV positive mothers attending PMTCT facilities in Oyo State using a two stage sampling technique. Semi-structured questionnaire was used to collect data on socio-demographics, disclosure to partners and HIV status of their partners. Data was analyzed using Epi-info software version 7. **Result:** The mean age of respondents was 29±5 years while that of their partners was 37±3 years. Five hundred and fifty-five (99.1%) of respondents were married. Seventy four percent (414/560) of the mothers were aware of their husband's HIV sero-status. Of these, 65.4% (271/414) of the partners were HIV positive. Eighty nine percent (498) of the women have disclosed their HIV status to their partners. Of these, 197(39.6%) required the assistance of health workers while 301(59.4%) did it by themselves. Following disclosure of HIV status, 86.9% of the partners were supportive, 5.7% were indifferent, and 6.7% were quarrelsome and abusive while 1.0% was violent. Women who believed disclosure caused physical abuse (OR=1.81, 95% CI: 1.17-2.90), caused divorce (OR=2.01, 95% CI: 1.25-3.22) and was unimportant (OR= 2.26, 95% CI: 1.33-3.87) were two times less likely to disclose their status. **Conclusion:** The reactions of partners of HIV positive mothers to disclosure of their wives' HIV status are predominantly supportive. This should strengthen strategies to promote partner disclosure. **Keywords:** Partners, Disclosure, HIV, Mothers, Nigeria

Vulnerable Populations

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Board 337. Neighborhood Poverty and Influenza-related Hospitalizations, FluSurv-NET 2010-2012

K. Yousey-Hindes[1], **J. L. Hadler**[1], A. Pérez[2], E. Anderson[3,4], M. Bargsten[5], S. Bohm[6], M. Hill[7], B. Hogan[8], M. Laidler[9], M. L. Lindegren[10], K. L. Lung[11], E. Mermel[12], L. Miller[13], C. Morin[14], E. Parker[15], S. M. Zansky[16], S. S. Chaves[2]; [1]Yale Sch. of Publ. Hlth., New Haven, CT, USA, [2]CDC, Atlanta, GA, USA, [3]Emory Univ. Sch. of Med., Atlanta, GA, USA, [4]Atlanta VA Med. Ctr., Atlanta, GA, USA, [5]New Mexico Dept. of Hlth., Santa Fe, NM, USA, [6]Michigan Dept. of Community Hlth., Lansing, MI, USA, [7]Salt Lake County Hlth. Dept., Salt Lake City, UT, USA, [8]Maryland Dept. of Hlth. and Mental Hygiene, Baltimore, MD, USA, [9]Oregon Hlth. Authority, Portland, OR, USA, [10]Vanderbilt Univ. Sch. of Med., Nashville, TN, USA, [11]Ohio Dept. of Hlth., Columbus, OH, USA, [12]Rhode Island Dept. of Hlth., Providence, RI, USA, [13]Colorado Dept. of Publ. Hlth. & Environment, Denver, CO, USA, [14]Minnesota Dept. of Hlth., St. Paul, MN, USA, [15]California Emerging Infections Program, Oakland, CA, USA, [16]New York State Dept. of Hlth., Albany, NY, USA

Background: Previous studies have shown that measures of lower neighborhood socioeconomic status are correlated with higher influenza-related hospitalizations in New Haven County, CT. It is unknown whether this disparity also exists in other parts of the United States. FluSurv-NET (FSN) conducts population-based surveillance for laboratory confirmed influenza-related hospitalizations among residents of over 70 counties in the 10 Emerging Infections Program states (CA, CO, CT, GA, MD, MN, NM, NY, OR, TN) and four additional states (OH, MI, RI, UT). We examined the distribution of FSN cases across neighborhood poverty strata. **Methods:** From October 2010-April 2011 and October 2011-April 2012, FSN identified 8716 hospitalized influenza cases. Of these, 7932 (91%) were successfully geocoded and linked to US Census data. We used census tract as the neighborhood unit. Poverty was measured according to the 2008-2012 American Community Survey as household income below the federally defined poverty level (for the preceding 12 months). We categorized neighborhoods by

their percent of households in poverty (<5%, 5-<10%, 10-<19%, ≥20%) and calculated age adjusted (2000 US Standard Population) influenza-related hospitalization incidence overall and for each FSN site stratified by neighborhood poverty status. **Results:** For both seasons combined, the age adjusted cumulative incidence of influenza-related hospitalizations in high poverty (≥20%) neighborhoods was 43.4 per 100,000 population (95%CI: 42.3, 44.6), nearly twice the incidence in low poverty (<5%) neighborhoods (21.9 per 100,000, 95%CI: 20.8, 23.1). This relationship was observed in all 14 surveillance sites with the greatest disparities observed in northern and northeastern states lead by Minnesota (Standardized Rate Ratio (SRR) 3.4; 95%CI: 2.7, 4.3) and the smallest in Georgia (SRR 1.3; 95%CI: 1.1, 1.7). **Conclusions:** High poverty neighborhoods consistently experienced greater influenza hospitalization rates than low poverty neighborhoods although the extent of this disparity varied by site. Studies have shown that neighborhood disadvantage and crowding correlate with lower resident health status. Ongoing monitoring of area-based socioeconomic correlates of health may help target interventions where they are needed most.

Board 338. Epidemiology of Skin and Soft-tissue Infections in US Army Trainees at Fort Benning

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Background: Soldiers in training are at high risk for skin and soft-tissue infection (SSTI), especially those caused by methicillin-resistant *Staphylococcus aureus* (MRSA). Robust epidemiological, microbiological, and molecular data are vital to developing prevention strategies. The objective of this investigation was to describe the epidemiology and clinical characteristics of SSTI in a high MRSA setting. **Methods:** In July 2012, we initiated a prospective observational cohort study among US Army Infantry trainees at Fort Benning, GA to determine overall and MRSA SSTI incidence and to describe the clinical characteristics of disease. Clinical *S. aureus* isolates underwent molecular characterization, including pulsed-field gel electrophoresis (PFGE). **Results:** From July 2012 through September 2013, 29,621 trainees completed 14-week Infantry training. Of those trainees, 1,096 developed SSTI for an overall rate of 0.04 per 100 person-days. The MRSA SSTI rate was 0.01 per 100 person-days. Rates of SSTI were highest during the summer months. The median interval from training start to clinical presentation for SSTI was 41 (range 0-108) days. The most frequent clinical manifestations were cellulitis (49.6%) and abscess (30.1%) with the majority (62.4%) of infections on the lower extremities. Of the 1,096 SSTI subjects, 558 clinical specimens were collected, of which 469 (84.1%) were culture-positive for *S. aureus*, with MRSA accounting for 59.7%. Of the 180 MRSA isolates available for analysis, 165 (91.7%) were pulsed-field type USA300. **Conclusions:** Skin and soft-tissue infections continue to impose a substantial burden in the trainee population. The epidemiology is dynamic, but USA300 MRSA continues as the predominant SSTI genotype. Effective strategies for SSTI prevention in this and other high-risk settings are critically needed.

Board 339. Infectious Causes of Mortality in an Urban Slum in Nairobi, Kenya, 2009-2013

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Background: Mortality data are important indicators of public health and are crucial for setting priorities for public health interventions and research. An increasing proportion of the world's population lives in urban informal settlements; there are limited data on the causes of deaths in these marginalized populations. **Methods:** Kenya Medical Research Institute in collaboration with Centers for Disease Control and Prevention conducts population-based surveillance of infectious diseases in Kibera urban slum since 2006. Verbal autopsies (VA) have been routinely performed for reported deaths since January 2009 using World Health Organization standardized VA questionnaires administered to caregivers or close relatives of the deceased. InterVA-4 software is used to determine probable causes of death. We examined primary causes of deaths between 2009 and 2013 with a focus on infectious diseases. **Results:** Out of 757 reported deaths, verbal autopsy interviews were done for 513 (67.8%). Overall, infectious diseases were found to be the primary cause of 326 (63.5%) deaths; among these the leading causes included acute respiratory infection (ARI)/pneumonia (n=111, 34.0%), human immunodeficiency virus/acquired immunodeficiency syndrome (HIV/AIDS) (n=61, 18.7%), malaria (n=41, 12.6%) and pulmonary tuberculosis (n=40, 12.3%). In children <5 years old (n=245), infectious diseases were found to cause 191 (77.9%) deaths; these deaths were primarily due to ARI/pneumonia (n=105, 54.9%) and malaria (n=27, 14.1%). In persons ≥5 (n=268), 135 (50.3%) deaths were attributed to infectious causes, including HIV/AIDS (n=49, 36.3%) and pulmonary tuberculosis (n=40, 29.6%). The proportion of deaths with an infectious cause was 71.2% (156/219) in 2009-2010 and 58.7% (101/172) in 2012-2013. **Conclusion:** Infectious diseases contribute to the majority of deaths in this urban slum setting. Despite the availability of free HIV care in Kibera, adults are still dying from HIV and HIV-related illnesses; there is need to ensure the quality and accessibility HIV services. Reducing child deaths will require strengthened prevention and case management for pneumonia and malaria. While infectious causes of death may be declining, much work remains to reduce infectious mortality.

Board 340. Description of Dengue in Children Aged Less Than 18 Months—Puerto Rico, 1999–2011

Withdrawn at Author's Request

Board 341. Silent Risk of Tick-borne Diseases in Georgia, USA

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Background: Vector-borne diseases, including tick-borne diseases (TBD) are on the rise in the USA and worldwide, possibly due in part to changes in climate and meteorological conditions. There have been few studies in the state of Georgia addressing the prevalence of TBD. The purpose of this study was to assess the contemporary risk of TBD exposure in a rural population in South-Eastern Georgia. **Methods:** A self-assessment survey of symptoms of recent exposure and knowledge of TBD was administered to 258 healthy individuals visiting a university health center. Blood was drawn and serological testing was performed using the indirect microimmunofluorescence (IFA) test and *Rickettsia rickettsii* antigen (RR-AG). **Results:** Of the 258 responders, 244 reported their participation in regular recreational activities potentially associated with tick exposure; however, only 11 individuals (4%) experienced a self-reported tick bite during the previous summer or fall. Most participants acknowledged their ability to recognize ticks, but only 48% (n=169) were able to correctly identify them when provided with pictures of a variety of arthropods. Similarly, only 38% and 18% of

participants (n=257) were knowledgeable about proper practices of tick avoidance and prevention of tick bites, respectively. Fifty-six percent of the participants tested positive for IgG antibody reacting with RR-AG (titer of ≥128, 64 as the positive cutoff). **Conclusions:** The assessment survey identified a significant knowledge gap regarding TBD among adults in Georgia. The significant level of TBD exposure we detected may affect the serological diagnosis of clinical rickettsial diseases in Georgia, USA because preexisting antibody may be interpreted as false positives. Continuous education about TBD is needed to improve awareness of the risks of exposure to ticks, to promote proper methods of tick protection and removal, and to disseminate current knowledge about these commonplace arthropods.

Board 342. A Mysterious Case of Spontaneous *Streptococcus dysgalactiae* subsp. *equisimilis* (SDSE) Bacteremia and Epidural Abscess: A Case Report

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Background: *Streptococcus dysgalactiae* subsp. *equisimilis* (SDSE) was identified as a novel human B hemolytic isolate in 1996. This group bears Lancefield antigens C and G and shares close resemblance with Group A streptococci. Increasing numbers of SDSE infections have been identified recently especially in elderly patients with underlying immune compromise. **Summary:** A 92 year old male with history of hypertension and diabetes mellitus presented with a week of lower backache and progressive paraparesis. Exam was positive for fever, mild tachycardia and lower extremity weakness of bilateral iliopsoas and quadriceps, reduced sensations and absent ankle reflxes. Labs were remarkable for leukocytosis and elevated ESR, CRP. Contrast enhanced MRI of the lumbar spine confirmed a 3 cm epidural abscess at L3-4 level. The patient underwent urgent decompression with abscess drainage and there was no evidence of vertebral involvement also confirmed on histopathology. Four sets of blood cultures resulted positive for SDSE. The same was isolated from the epidural abscess and synovium however spinal tap was sterile. Antibiotics were appropriately de-escalated to parenteral ceftriaxone. Prompt neurologic recovery was seen after drainage of the abscess. A rigorous effort was made to search for the source of bacteremia and epidural abscess but repeated thorough history, physical examination, transesophageal echo failed to reveal any focus of infection. CT of the abdomen revealed an incidental 9x8 cm heterogenous mass in the pancreatic tail suggestive of a neoplasm. Treatment was completed with 6 weeks of antibiotics. **Conclusion:** This is an intriguing case as no underlying source of bacteremia or abscess could be isolated. SDSE is a rare cause of spinal epidural abscess. Till date, only three cases of SDSE spinal infections been reported where work up revealed an underlying cellulitis in 2 and infective endocarditis in the other. Pancreatic neoplasms can lead to translocation of gut flora leading to bacteremia and consequent epidural abscess in our patient. With changing demographics towards greater geriatric patients with significant age related co-morbidities like DM and malignancies, we can expect not only an increasing incidence of SDSE infections, but also atypical presentations.

Board 343. Bacterial Etiology of Postpartum Endometritis in Peri-urban Karachi, Pakistan—Data from a Prospective Evaluation Study

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Background: Puerperal sepsis remains the principal cause of maternal morbidity and mortality in South Asia. A multicenter study in Pakistan and Bangladesh was undertaken to develop and validate clinical algorithms and determine bacterial etiology of puerperal sepsis. We describe the bacterial etiology of endometritis in women with physician-confirmed sepsis in peri-urban areas of Karachi, from August 2013 to July 2014. **Methods:** Recently delivered women, from an 8000-strong birth cohort under newborn and maternal health surveillance, underwent ten visits by lady health visitors at specific postpartum days in four peri-urban settlements (Ibrahim Hyderi, Bhains, Bilal, and Ali Akbar Shah colonies) of Karachi. Febrile women were evaluated for puerperal sepsis and referred to a primary-health physician. Those with physician-confirmed sepsis were sampled for urine and blood culture, and if consenting, an endometrial brush for culture and PCR, collected by a gynaecologist at the Jinnah Postgraduate Medical Centre (JPMC), Karachi. The study was approved by Institutional Review boards of the Aga Khan University, and JPMC, Karachi, Pakistan, and the Johns Hopkins University, Baltimore, USA. Data was entered and analysed in SPSS v 16.0. **Results:** Of 347 enrolments for puerperal sepsis, 221 women consented for endometrial sampling. Sixty percent of endometrial cultures were positive for bacteria by culture, while 66% were positive for any of *C.trachomatis*, *Mycoplasma* spp, or *Ureaplasma* spp, by PCR. The most common isolates by culture were *E.coli* (31.3%, n=42), *G.vaginalis* (22.4%, n=30), anaerobes (22.4%, n=30), *S.aureus* (12.7%; n=17), and *S.pyogenes* (7.5%; n=10). *C.trachomatis* was detected in 0.9% (n=2) of samples. Blood cultures obtained on 316 patients were negative in 98.7% (n=312), with 2 blood cultures positive for *E.coli*, while 2 samples grew contaminants. Urine cultures also revealed a predominance of *E.coli* (14.4%, n=49 of 341), however, there was only 7.7% agreement between endometrial and urine culture results. **Conclusions:** *E.coli* and other facultative aerobic bacteria are the predominant causative agents of puerperal endometritis in peri-urban Karachi. *C.trachomatis* was seen infrequently. Endometrial cultures are of greatest value in establishing bacterial etiology of puerperal sepsis, as blood cultures are frequently negative, and urine cultures show poor concordance with endometrial cultures.

Board 344. Influenza-like Illness and Influenza Vaccination During Pregnancy in Quetzaltenango, Guatemala

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Background: Influenza-like illness (ILI) during pregnancy may be associated with severe complications and has been hypothesized to impact birth outcomes, such as preterm and intrauterine growth restriction. The Pan-American Health Organization recommends vaccination of all pregnant women against influenza, but coverage in this high risk group remains low or unknown in many countries. More information on the burden and etiology of ILI during pregnancy could help strengthen vaccination programs. **Methods:** To estimate incidence and identify potential etiologies of ILI (fever and cough or sore throat) during pregnancy in rural Quetzaltenango, Guatemala, we conducted active surveillance (May 2013 - September 2014) for ILI among pregnant women 18-40 years of age from <20 weeks gestation until birth, which consisted of weekly screening by phone calls or home visits and case confirmation by a nurse visit to the home. We collected nasopharyngeal swab specimens from participants with ILI and tested these by polymerase chain reaction for

respiratory syncytial virus (RSV), human metapneumovirus (HMPV), influenza A/B, parainfluenza virus (PIV) 1/2/3, and adenovirus (ADV). Influenza vaccination status was assessed by questionnaire. **Results:** We evaluated 185 pregnant women during 3099 person-weeks and detected a total of 47 ILI cases (15 per 1000 person-weeks), 13 of which were second and 3 of which were third repeated cases within participant. We detected a viral infection in 14 (30%) of the ILI cases: 7 (15%) influenza, 3 (6%) ADV, 3 (6%) PIV 3, 3 (6%) RSV, 1 (2%) HMPV, and 1 (2%) PIV 2. Only 14% (95% CI: 8-19%) of women reported influenza vaccination during pregnancy, on average during week 13 of gestation (range 1 to 29 weeks). We detected 7 influenza-positive ILI during 2679 unvaccinated person-weeks (3 per 1000 person-weeks) and no influenza-positive ILI case during 342 vaccinated person-weeks. **Conclusions:** These pilot data provide an initial estimate of ILI incidence during pregnancy in rural Guatemala. Influenza virus infection was a frequent cause of ILI during pregnancy. Further research is required to better understand the public health benefit achievable by increased influenza vaccination coverage during pregnancy.

Board 345. Increase of Invasive *Haemophilus influenzae* Cases and *Haemophilus influenzae* Serotype A Cases in Minnesota, 2005-2014

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Background: Evaluate an increase in invasive *Haemophilus influenzae* (Hi) cases and determine if there is an association with specific serotypes. **Methods:** Minnesota Department of Health (MDH) conducts statewide active surveillance for invasive Hi cases. Hi isolates are submitted as part of CDC Active Bacterial Core Surveillance. We analyzed trends in Hi case incidence and serotypes, and compared Hi serotype a (Hia) case characteristics to non-Hia cases from 2005 through 2014. Non-Hia cases were defined as Hi with a serotype other than Hia or untypeable. **Results:** 835 Hi cases were reported and 92% of cases had an isolate submitted. Hi incidence increased from 1.1/100,000 population in 2005 to 2.3/100,000 population in 2014 (X2 trend= 13.1, p<0.001). The proportion of cases with an isolate submitted increased from 87% to 95% (X2 trend = 11.1, p<0.001). The proportion of Hia isolates increased (4% in 2005 vs 14% in 2014, X2 for trend=8.7, p 4 isolates) or non-typeables were observed. The most dramatic increase in the proportion of Hia isolates occurred in 2013 and 2014 (10% and 14% of isolates respectively). From 2005 to 2011 the proportion of Hia isolates ranged from 0 to 8%. Hia cases were more likely to be young children (<2 years or 2-5 years; p<0.001 and p=0.008 respectively), American Indian (p<0.001), live outside of the Minneapolis-St. Paul Metropolitan area (p=0.011), have meningitis (p80 years old (p=0.011) or have an underlying medical condition (p=0.002) compared to non-Hia cases. 3 Hia cases (6%) and 84 non-Hia cases (12%) died; however, the difference was not statistically significant. There were no differences in other case or clinical characteristics. **Conclusions:** We observed an increase in Hi incidence and the proportion of Hia isolates in Minnesota from 2005-2014. Hia cases were likely to be children <5 years of age, American Indian, and present as meningitis or pneumonia. Continued surveillance is necessary to monitor Hia trends and future analysis should include comparison of Hia molecular characteristics.

Board 346. Methicillin Sensitive *Staphylococcus aureus* Bacteremia from Soft Tissue Infection Presenting as Septic Pulmonary Embolism: A Case Report and Review of Literature

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Background: Septic pulmonary embolism (SPE) is a rare disorder mostly seen among immunocompromised patients, and often presents with nonspecific clinical features. It is commonly associated with IV drug use, right sided endocarditis and indwelling catheters or devices, but should also be considered in other extrapulmonary suppurative processes. **Objective:** We report a rare case of SPE from Methicillin-sensitive *Staphylococcus aureus* (MSSA) soft tissue infection and highlight the learning points related to its presentation, risk factors, diagnostic approach, clinical course and treatment. **Results:** A 46 year old female with past medical history of uncontrolled type II diabetes and alcoholic cirrhosis status post transjugular intrahepatic portosystemic shunt (TIPS) presented with a 2 week history of fever, night sweats, cough and back pain. Three weeks prior to presentation, she had developed a soft tissue abscess at the fifth digit on the right hand, requiring drainage. On admission, the patient displayed signs of severe sepsis. Initial blood cultures revealed gram positive cocci, and she was started on vancomycin. A chest Xray was obtained which did not reveal any abnormalities. Later, the patient developed hypoxemia, which prompted a chest CT scan that showed multiple bilateral pulmonary nodules with central distribution. Transthoracic and transesophageal echocardiograms did not show any vegetations. No signs of osteomyelitis were detected on a complete spinal MRI. Infection of the TIPS catheter was ruled out by Indium WBC scan. Clinical exam and imaging did not reveal any evidence of thrombophlebitis. The only possible identified source of infection was the recently drained soft tissue abscess. Final blood cultures grew MSSA, the patient was switched to nafcillin and completed 6 weeks of treatment with no pulmonary complications. **Conclusions:** SPE should be considered in immunocompromised patients presenting with sepsis and non-specific respiratory complaints and as seen in our case, infections other than the ones more commonly mentioned in literature should be considered as a source of SPE. A high index of suspicion is necessary, as initial imaging studies can be normal. Patients should be monitored for respiratory complications. Length of treatment when source is unclear should still be 6 weeks.

Board 347. Intestinal Parasitic Infection and Associated Symptoms Among Children in Tea Plantation Sector, Sri Lanka

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Background: Intestinal parasitic infections (IPI) are endemic worldwide. More than 3 billion people particularly in developing countries are affected and about 10.5 million new cases are reported annually because of these infections. Objective of this study was to examine the presence of IPIs and their association with clinical signs and symptoms among children in tea plantation sector, Sri Lanka. **Method:** 489 children age between 1 to 12 years from a tea plantation area in Kandy, Sri Lanka were enrolled to this study from January to April 2013 using an interviewer administered structured questionnaire and stool samples were subjected to wet preparation and formaldehyde-ether sedimentation techniques for identification of parasites. The data was analyzed using SPSS version 17.0. **Results:** 61% of the children had intestinal symptoms (stomach pain, diarrhoea, vomiting, flatulence, loss of appetite,), 32% had respiratory symptoms (wheezing, cough, sore throat) and 36% had cutaneous symptoms (itching, rash,). The overall prevalence rate of IPI was 53.2% and *Ascaris lumbricoides* was the commonest. Reported symptoms were analyzed for association with the presence of parasites.

Stomach pain (p = 0.001), loss of appetite (p = 0.009), vomiting (p = 0.01), diarrhea (p = 0.01), cough (p = 0.012) and itching (p = 0.002) were significant with presence of one or more of intestinal parasitic organisms in stool samples. **Conclusions:** IPIs were more common in this community and many symptoms were significantly associated. Longer-term studies will help to determine whether the parasite burden of these children causes more subtle health effects.

Board 348. Incidence of Influenza-associated Respiratory Infection Among Pregnant Women in Bangladesh, 2013-2015

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Background: Influenza vaccine is recommended for pregnant women who are at increased risk for severe influenza illness leading to hospitalization, mortality and loss of pregnancy, yet it is not part of routine immunization in many low-income countries including Bangladesh. We estimated the incidence of influenza-associated infections in pregnant women in Bangladesh to inform policy decisions regarding influenza vaccine. **Methods:** We enrolled pregnant women of any gestational age from 8 sub-districts in Bangladesh over two consecutive influenza seasons (2013 and 2014). Field research assistants (FRA) contacted participants weekly until delivery by phone or home visit to identify new onset of influenza-like-illness (ILI), defined as onset of fever and cough within last 7 days. FRAs went to participants home to collect nasopharyngeal swabs if the onset was within last 72 hours (2013) and within last 7 days (2014). Swabs were stored and transported in dry shippers to the laboratory for influenza testing by rRT-PCR. Person-days contributed by participants from enrollment to delivery were recorded and incidence of influenza-associated infection/100,000 person-weeks (pws) was estimated. **Results:** We followed 1,819 pregnant women for 20,844 pws in 2013 and identified 254 ILI episodes; 133 (45%) were identified within 72 hours of onset and 121 (91%) swabs were collected. Eight (7%) of 121 were positive for influenza virus. In 2014, we followed 1,932 pregnant women for 23,992 pws, identified 304 ILI episodes and 290 (95%) swabs were collected. Of 290, 113 (39%) were positive for influenza virus. The incidence of influenza-associated infection in pregnant women was estimated at 85 cases/100,000 pws (95% CI: 51-136) in 2013 and at 494 cases/100,000 pws (95% CI: 407-589) in 2014. No severe outcomes such as loss of pregnancy or hospitalization for respiratory infections were identified among women with confirmed influenza. **Conclusion:** The incidence of influenza-associated infections in pregnant women varied over two influenza seasons; the 2013 incidence could be an underestimate because the follow-up period began after the influenza season started in Bangladesh. Data from multiple influenza seasons among pregnant and non-pregnant women would be useful to assess if pregnant women are at increased risk and should be targeted for influenza vaccination in Bangladesh.

Board 349. Coxsackievirus B3: An Ethiologic Agent of Acute Febrile Illness in Bandung, Indonesia

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Background: Coxsackievirus B3 (CVB3) virus has been implicated as the causative agent of various outbreaks, associated with hand foot and mouth diseases, aseptic meningitis, acute myocarditis, and inflammatory cardiomyopathy. The identification of CVB3 in Indonesia has never been reported. **Methods:** Undiagnosed cryopreserved specimens were obtained from factory workers in Bandung who displayed symptoms of acute febrile illness (n=209). RNA was isolated from serum, followed by cDNA synthesis using random primers. Specimens were tested by conventional PCR using enterovirus genus-level primers, followed by specific primers and sequencing to confirm the strain. Concurrently, the virus was isolated in Rhesus Monkey Kidney Epithelial Cells (LLC-MK2). **Results:** We identified CVB3 virus in an archived specimen from a patient that presented with symptoms of fever, headache, myalgia, and nausea. Sequencing results of VP1 region from both the clinical sample and tissue culture supernatant showed 97% homology to CVB3 virus isolated in Taiwan. Virus propagation in LLC-MK2 cell culture exhibited severe cytophathic effects two days post infection. **Conclusion:** We report the finding of CVB3 as the viral causative agent of an acute febrile case in Bandung, Indonesia which is the first detection in the country.

Board 350. *Salmonella*-related Hospitalizations in Seniors in Canada: Current Status to Inform Potential Future Burden

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Background: *Salmonella* is one of the most prevalent bacteria associated with acute enteric illness in Canada and seniors are considered a vulnerable population more likely to develop severe illness. According to Statistic Canada's population projections from 2015 to 2035, while the adult (20-59) population will increase by only 5%, the population of people aged 60 and over could increase by more than 56% and more than 112% for people aged 80 and over. This shift is likely to modify hospitalization rates for infectious diseases, including Salmonellosis. Therefore, it is important to know the characteristics associated with *Salmonella*-related hospitalizations in seniors in order to anticipate how this demographic shift may affect the future Canadian burden of hospitalizations. **Methods:** Data from a period of ten years (2001 to 2010) were extracted from the Canadian Institute for Health Information's Hospital Morbidity Discharge Database. Data were used to calculate hospitalization rates and to describe characteristics of *Salmonella*-related hospitalizations in seniors (60+) and adults (20-59). **Results:** From 2001 to 2010, 6148 *Salmonella*-related hospital admissions were recorded in adults of 20 years and over. Of them, 50% were recorded for people 60 years of age and over for an annual hospitalization rate of 5.1 cases/100 000, in comparison of 1.7 case/100 000 in other adults (20 to 59). The length of hospitalization stay was longer in senior with a median length of stay of 7 days, compared to 4 days in other adults and when *Salmonella* was the most responsible diagnosis for hospitalisation, death occurs in 3% of patients in seniors and 0.5% in other adults. Data on chronic diseases affecting seniors hospitalized with Salmonellosis and temporal trends will also be presented. **Conclusions:** Although seniors represent 23% of reported *Salmonella* cases in adults in Canada during this time period, 50% of *Salmonella*-related hospitalizations occurred in this age group and this proportion is expected to increase. This proportion is of particular

concern because the data shows that hospitalizations in this age group are associated with a greater burden than hospitalizations in other adults. Targeted prevention actions for seniors are essential and research on risk factors for *Salmonella* specific to elderly people should also be pursued.

Board 351. High Prevalence of Intestinal Parasitic Infections Among School-age Children in Thailand: A Comparative Study

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Background: Parasitic infections are one of risk factors for malnutrition in school-age children. Malnutrition is known to affect child growth and education abilities. Over the last decade, there is no national data on prevalence of intestinal parasitic infections in Thailand. In this study, we studied the prevalence of intestinal parasitic infections among school-age children and compared sensitivity of methods for detection of intestinal parasitic infections. Methods: Preliminary cross-sectional surveys were performed in 16 schools in all regions of Thailand. Fecal samples were collected from 1,909 students in 7 provinces from each region. The samples were examined for intestinal parasites by simple smear, formalin-ether concentration, and Locke-Egg-Serum (LES) medium culture. Results: Out of 1,909 students, 713 (37.3%) were infected with at least one intestinal parasite. The highest prevalence (83.8%) was found in Kanchanaburi province located in western region of Thailand. Blastocystis sp. was the most common parasite (32.8%), followed by Giardia lamblia (4.2%), Ascaris lumbricoides (3.6%), hookworms (1.6%), Entamoeba histolytica (0.7%), Trichuris trichiura (0.5%), *Enterobius* bermicularis (0.5%), Strongyloides stercoralis (0.4%), minute intestinal flukes (0.2%), and Taenia sp. (0.1%). Mixed parasitic infections were found in 121 (17.0%) students (86.8% infected 2 species, 11.5% infected 3 species, 1.7% infected 4 species of the intestinal parasites). In the comparative study, we found that the concentration method (74.0%) was more sensitive than simple smear (55.0%) for helminth detection. However, these methods were not different for protozoa detection (31.2% by simple smear and 33.5% by concentration). LES culture was the most sensitive method (69.2%) for protozoa detection. Conclusions: Our results indicate the high prevalence of intestinal parasite among Thai students. Improvements in sanitation, personal hygiene, water quality, and basic health education are needed. Moreover, high sensitive methods should be developed for large-scale screening of the diseases. Further studies of environmental factors, economic factors, as well as personal and community hygiene on the prevalence of intestinal parasitic infections are under investigation.

Board 352. Exposure to Zoonotic Disease Among Oncology Patients: A Pilot Study in Romania

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Background: Patients receiving immunosuppressive cancer treatments in developing country settings, where there is often a high degree of interaction between humans and animals, may be at increased risk for opportunistic zoonotic infection or reactivation of a latent infection. This pilot study was performed to characterize the seroprevalence of zoonotic pathogen exposure among hematologic cancer patients undergoing chemotherapeutic treatments in Romania, where a large percentage of the general population lives and/or works in close contact with livestock animals. **Methods:** A convenience sample of 58 hematologic cancer patients undergoing chemotherapy was recruited from the Ion Chiricuta Oncology Institute Hematology Clinic in Cluj-Napoca, Romania. Participants were administered a cross-sectional risk factor survey to establish animal exposure history. A serological survey using IgG and IgM ELISA was performed in-country to determine seroprevalence of the common zoonotic pathogens *Toxoplasmosis gondii* and *Coxiella burnetti*, both of which can be transmitted to humans from a range of livestock and pet animals. **Results:** Overall, 49% of the participants tested positive for IgG antibodies to *T. gondii* and 12% tested positive for IgG antibodies to *C. burnetti*, indicating either past infection or asymptomatic chronic infection. IgM antibodies to *C. burnetti* were detected in 8% of participants, indicating possible recent or acute infection, including 2 individuals who tested positive for both IgG and IgM antibodies. Although 59% of participants reported living or working on or near a farm with livestock animals, the relationship between farm-dwelling/working status and positive serology was not statistically significant. **Conclusions:** *T. gondii* and chronic *C. burnetti* infection have previously been shown to be important opportunistic zoonotic infections in severely immunocompromised individuals. The present study indicates that a substantial proportion of hematologic cancer patients patients in Romania may be at risk for zoonotic infection or for reactivation of latent zoonotic *T. gondii* or *C. burnetti* infection. These results suggest that special attention should be paid to cancer patient's exposure to livestock animals in areas where much of the population lives in rural settings.

Poverty and Infectious Diseases

Tuesday, August 25, 5:00 PM - 6:15 PM

Grand Hall

Board 353. Costs of Hospitalization for Respiratory Syncytial Virus Illness Among Children Aged <5 Years and Associated Economic Impact on Households in Bangladesh, 2010

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Background: In Bangladesh, acute respiratory infection (ARI) is a major cause of hospitalizations and deaths among children < 5 years, and hospitalization for ARI was found to be a catastrophic cost to affected families. Studies found respiratory syncytial virus (RSV) as the most common viral pathogen for hospitalization with ARI. We estimated the costs of hospitalization for RSV illness in children <5 years and the associated economic impact on the families. **Methods**: From May through October 2010, all children <5 years hospitalized with acute respiratory illness and laboratory-confirmed RSV infection

through rRT-PCR were identified from sentinel influenza surveillance program at four tertiary hospitals. After hospital discharge of children, research assistants (RA) interviewed parents using a structured questionnaire to record direct medical (e.g. physician fee, hospital bed, medicines, diagnostic tests) and non-medical costs (e.g. food, lodging and transportation during hospitalization). We followed WHO-Choice estimates to calculate healthcare service costs. Research assistants collected data on caregivers' lost work days (indirect costs) for the illness episode. We added direct (i.e. sum of medical, non-medical and healthcare service costs) and indirect costs to calculate cost/episode of hospitalization for RSV illness. Additionally, RA collected data on strategies used by families to meet treatment costs. **Results**: We interviewed parents of 39 children with RSV illness; median age was 4 months (IQR= 2-7). The median direct cost was US$62 (IQR=43-101), indirect cost was US$19 (IQR=11-29) and total cost was US$94 (IQR=67-127). The median out-of-pocket cost represented 24% of monthly household income of affected families. Twenty (51%) of 39 families borrowed money to pay for treatment and of 20, seven borrowed from community lenders at monthly interest rates of 50-120%. Twenty (51%) families spent less on food in that month to balance costs incurred during hospitalization. **Conclusions**: Costs for hospitalization with RSV illness in children <5 years result in considerable out-of pocket and indirect costs that could force the affected families to debts and impoverishment. This study data suggests the importance of non-pharmaceutical interventions, and RSV treatment and vaccines.

Board 354. Does Socioeconomic Disadvantage Account for Unfavorable Treatment Outcome of Tuberculosis? A Taiwanese Cohort Study

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Background: Socioeconomically disadvantaged groups have been long associated with higher tuberculosis (TB) disease burden. In Taiwan, strategies such as free access to TB service, Directly Observed Therapy Strategies (DOTS) program, and active case finding including low-income households have been systematically implemented. We used a nationwide TB cohort to assess the association between socioeconomic status and treatment outcomes. **Methods:** All newly confirmed TB reports between January and December 2013 were extracted from the national registry. The data was linked to information of 2013 low-income and lower-middle income households (i.e. average of monthly income less than 1.5 times of the absolutely standard of living), obtained from the Department of Social Assistance and Social Work, Ministry of Health and Welfare. TB cases were classified into two groups: from low-income or lower-middle income households (LMI) or others (non-LMI). We analyzed demographics, clinical features at diagnosis, and treatment outcomes (success, died or other outcomes). Patients who transferred out or had not completed treatment till October 1, 2014 were excluded from the analysis. **Results:** In total, 11,171 cases were enrolled: 437 in LMI group and 10,734 in non-LMI group. LMI group was younger at diagnosis (median age 51 vs. 68 years, P<0.001) and had greater proportion of male (78% vs. 70%, P<0.001). The proportions of sputum smear positive or culture positive were not statistically different between two groups (37% vs. 40%, P=0.47 and 74% vs. 77%, P=0.50, respectively), but advanced chest x-ray lesions were observed more in LMI group (20% vs. 14%, P=0.012). More patients in LMI group were detected by active case finding (8% vs. 2%, P<0.001) and received DOT care (97% vs. 92%, P=0.004) than non-LMI group. LMI group had higher success treatment rate compared with non-LMI group (age-adjusted OR 2.03, 95% CI 1.46-2.83), particularly in patients aged ≥65 years (85% vs. 65%, P<0.001). **Conclusions:** TB cases with lower socioeconomic status have not yet suffered unfavorable treatment outcomes in Taiwan. Pro-poor measures could ensure health benefits among socially disadvantaged groups. Sustained TB control activities and government commitment are required to prevent catastrophic outcomes of TB in this vulnerable population.

Board 355. *Salmonella* Incidence and Census Tract Poverty Level, California FoodNet, 2008-2013

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Background: *Salmonella* infections cause considerable morbidity. However, little is known about salmonellosis and socioeconomic inequality. We explored the potential association between poverty and *Salmonella* incidence in the California FoodNet three-county catchment area. **Methods:** Using 2008-2013 California FoodNet data, we geocoded addresses of laboratory-confirmed *Salmonella* case-patients who reported no international travel in the 7 days prior to illness onset and linked them to census tract poverty level data from the 2008-2012 American Community Survey. Cases were categorized into four socioeconomic strata based on the percent of persons in the census tract living below the federal poverty line (<5%, 5-9.9%, 10-19.9%, ≥20%). For each stratum, we calculated average annual age-adjusted incidence rates overall and for major *Salmonella* serotypes, race/ethnicity categories and age groups. We obtained overall and group-specific denominators from the 2010 Census. We used the Cochran-Armitage test for trend and calculated relative risks and 95% confidence intervals comparing the highest poverty stratum to the lowest poverty stratum. **Results:** Over 98% (2,378/2,414) of *Salmonella* cases were successfully geocoded. Case-patients living in the highest poverty census tracts had 1.35 (95% CI 1.19-1.53) times the risk of *Salmonella* infection compared to residents of the lowest poverty census tracts. By age group, this trend was significant for children <1 and 5-17 years old and for adults 60 years and older (P<0.001, P<0.004 and P<0.03, respectively). By race/ethnicity, the association was more pronounced among Asians where the relative risk was 2.34 (95% CI 1.85-2.98). By serotype, a similar association was seen for *Salmonella* Heidelberg (RR=2.05, 95% CI 1.32-3.17) and Typhimurium (RR=1.75, 95% CI 1.16-2.62) incidences, but an inverse association was seen for *S.* Enteriditis (RR=0.70, 95% CI 0.53-0.92). **Conclusions:** In California FoodNet, domestically-acquired *Salmonella* incidence increases with increasing poverty level. This association varies by age group, by race/ethnicity, and by *Salmonella* serotype. Analyses with *Salmonella* incidences in other jurisdictions will be interesting to see if similar associations between poverty level and salmonellosis are found.

Board 356. Survey of Rotavirus Infection in Iraqi Pediatric Patients at Three Hospitals

A. A. Al-Obaidi; Iraq Ministry of Hlth., Baghdad, Iraq

Background: Rotavirus, a major infection effecting Iraqi children, has only been studied at the hospital level in Iraq. This study analyzes Rotavirus infection across three different hospitals in Baghdad in order to take into consideration socio-economic factors. It was found that Rotavirus equally effects children living across the socio-economic spectrum in Iraq. **Methods:** Data was collected and analyzed from three hospitals in Al-Kark district of Baghdad; each hospital serves a different socio-economic level. The study included 300 pediatric patients' age 2-4 years old with acute gastroenteritis from November 3, 2011 to May 31, 2012. Two types of questionnaires were used to identify participants: The first was administered to all patients admitted with acute gastroenteritis and included basic information of name, diagnosis and Rotavirus

status. All confirmed cases of Rotavirus were asked to complete the second questionnaire which requested vaccination history. Latex agglutination test was used for diagnosis and patients' socio-economic status was identified based on address and area of residency. **Results:** Out of 300 pediatric patients included, Rotavirus was detected in 225 cases (75%).146 (65%) of Rotavirus patients were hospitalized and treated while 21 patients did not receive treatment and died outside of the hospital. 6 patients had received vaccination against Rotavirus and were experiencing re-infection. No significant differences were detected among the socio-economic level of patients with regard to rate of infection. There was no significant (P≥ 0.05) difference between the infected groups of the three hospitals. This study utilized methods outlined in Snedecor G. W & W. G Cochren's Statistical Methods. **Conclusions:** There was no significant difference in the rate of infection between the three hospitals demonstrating that Rotavirus is a democratic virus, not eradicated easily. The study also shows that children age 2-4 years old are susceptible to high rates of infection, likely due to orofecal routes of transmission in daycare facilities. Vaccination may reduce the rate of Rotavirus infection significantly but does not eliminate chance of re-infection. A wider study including several hospitals in Iraq would help determine a more accurate rate of infection among Iraqi children and bring attention to this serious public health concern.

Outbreak Investigation: Lab-Epi Response

Tuesday, August 25, 5:00 PM - 6:15 PM

Grand Hall

Board 357. Investigation of a Group A *Streptococcus* Outbreak in a Long-term Care Facility — Georgia, 2014

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Background: Group A *Streptococcus* (GAS) pharyngitis is common among children and can quickly spread once introduced into a long-term care facility (LTCF), causing severe disease among vulnerable residents. Stringent infection control is the best approach for prevention and control of GAS outbreaks in LTCFs. In July 2014, the Georgia Department of Public Health (DPH) was notified of 2 invasive GAS cases among residents of a LTCF-A. DPH investigated to determine the extent of the outbreak and make recommendations for its control. **Methods:** We defined a case as illness in a LTCF-A resident from whom GAS was isolated from a normally sterile site (invasive) or non-sterile site (noninvasive) during January-July 2014. We performed case finding by reviewing LTCF-A and area hospital GAS-positive cultures during the preceding 4 months. We collected and cultured oropharyngeal and wound swabs from all LTCF-A residents and staff; positive cultures without illness indicate GAS carriage. The Georgia Public Health Laboratory performed culture, isolation, and identification of GAS. All recovered isolates were sent for further analysis and emm typing at CDC. We assessed infection control and prevention (ICP) practices at LTCF-A. **Results:** We identified a total of 6 GAS cases (2 invasive and 4 non-invasive) diagnosed during April-July 2014. Swabs collected from 6/150 (4%) staff and 12/212 (6%) residents grew GAS. GAS recovered from four cases, 10 resident carriers, and 4 staff carriers were the same GAS type, emm 89.0; all worked or resided in the same wing of LTCF-A. All cases and carriers were treated with appropriate antibiotics and were GAS negative upon follow-up testing one month after treatment. Multiple deficiencies were identified during the ICP evaluation including deficiencies in hand hygiene, wound care technique, disinfection of equipment, and ICP policies. **Conclusion:** Transmission of GAS occurred among residents and staff in one wing of LTCF-A; deficiencies in ICP policies and hand hygiene could have allowed for transmission. DPH made recommendations to improve hand hygiene, wound care protocols, equipment disinfection, awareness of infection among residents, staff ICP education, and to conduct enhanced surveillance for GAS infections for 4 months.

Board 358. Linking Listeriosis to Recalled Foods: Use of Whole-genome Sequencing to Enhance Public Health Investigations

B. R. Jackson[1], E. Strain[2], C. Tarr[1], W. Klimke[3], L. Katz[1], J. Beal[2], K. Jackson[1], Y. Chen[2], S. Stroika[1], M. Parish[2], A. R. Datta[2], H. Carleton[1], A. Conrad[1], L. Burall[2], C. Grim[2], Z. Kucerova[1], M. Salter[2], A. Reimer[4], B. Major[5], E. Harvey[6], L. Steinbock[7], A. Saupe[8], A. Sorenson[9], H. Waechter[10], E. Boothe[11], I. Vilcins[12], P. Gerner-Smidt[1], R. Mody[1]; [1]CDC, Atlanta, GA, USA, [2]Food and Drug Admin., College Park, MD, USA, [3]NIH, Natl. Ctr. for Biotechnology Information, Bethesda, MD, USA, [4]Publ. Hlth. Agency of Canada, Winnipeg, MB, Canada, [5]Canadian Food Inspection Agency, Toronto, ON, Canada, [6]Massachusetts Dept. of Publ. Hlth., Boston, MA, USA, [7]City of Northampton Hlth. Dept., Northampton, MA, USA, [8]Minnesota Dept. of Hlth., Saint Paul, MN, USA, [9]Minnesota Dept. of Agriculture, Saint Paul, MN, USA, [10]New York City Dept. of Hlth. and Mental Hygiene, Queens, NY, USA, [11]Tennessee Dept. of Hlth., Nashville, TN, USA, [12]Texas Dept. of State Hlth. Services, Austin, TX, USA

Background: *Listeria monocytogenes* (*Lm*) infection is estimated to be the third leading cause of death from foodborne illness in the United States. Linking listeriosis outbreaks and cases to specific foods identifies food safety gaps. However, listeriosis outbreaks are often unsolved because of the small number of cases involved, and determining the source of sporadic (*ie*, not associated with an outbreak) infections has rarely been possible. Many food recalls for possible *Lm* contamination are reported annually. We used real-time whole-genome sequencing (WGS) of *Lm* isolates to enhance listeriosis investigations. **Methods:** Beginning September 1, 2013, CDC, state and local public health laboratories, FDA, and USDA performed WGS on all clinical *Lm* isolates received through public health surveillance and on food and environmental isolates of *Lm*, including isolates associated with regulatory testing. Sequences were deposited in public domain in the Sequence Read Archive at NCBI/NIH to allow isolates from all sources to be analyzed together. State and local health departments interviewed patients using standardized *Listeria* Initiative questionnaires and targeted supplemental forms. We used combined epidemiological and WGS data to establish links between illnesses and recalled foods. **Results:** From September 2013-September 2014, 2 listeriosis outbreaks and 1 sporadic case were linked to foods recalled for *Lm* contamination. In each event, patients reported eating the recalled food and all patient isolates were highly related by WGS to isolates from recalled products. The recalled products were peaches and nectarines (2 cases in 2 states), Hispanic-style soft cheese (5 cases from 4 states), and prepackaged lettuce (1 case). The level of traceback information about the brand and source of product consumed by patients varied. **Discussion:** WGS greatly enhanced *Lm* surveillance, allowing linkage of 2 listeriosis outbreaks and 1 sporadic case of listeriosis to foods recalled for *Lm* contamination. WGS provided far greater resolution of relationships between isolates than the current subtyping method, pulsed-field gel electrophoresis. Contaminated peaches, nectarines, and prepackaged lettuce had not previously been

associated with human listeriosis. WGS-enhanced surveillance will improve food safety.

Board 359. Increase in *Salmonella* Serotype IIIa 18:z4,z23: Isolated from Retail Meats and Humans—United States, 2003-2012

H. Tate[1], A. Brown[2], Y. Chen[1], J. Folster[2], C. Li[1], J. Abbott[1], B. Tolar[2], S. Ayers[1], P. Fields[2], E. Crarey[1], C. Kabera[1], S. Zhao[1], P. McDermott[1]; [1]FDA, CVM, Office of Res., Laurel, MD, USA, [2]CDC, NCEZID, Div. of Foodborne Waterborne and Environmental Diseases, Atlanta, GA, USA

Background: The National Antimicrobial Resistance Monitoring System (NARMS) is a collaboration among CDC, FDA, USDA, and state health departments to track antibiotic resistance in foodborne bacteria from humans, retail meats, and food animals. During 2002- 2012, NARMS observed an increase in *Salmonella enterica* subsp. *arizonae* serotype IIIa 18:z4,z23:- isolated from ground turkey. We report findings from an investigation into potential links to human infections. **Methods:** Antimicrobial susceptibility data from NARMS and pulsed-field gel electrophoresis (PFGE) data from PulseNet, CDC's molecular subtyping network for foodborne disease surveillance, were examined to identify possible links between retail meats and human cases of *Salmonella* serotype IIIa 18:z4,z23:-. Select retail and human isolates also underwent whole genome sequencing (WGS). **Results:** Serotype IIIa 18:z4,z23:- first appeared in NARMS in 2003. By 2012, 114 of 117 *Salmonella* serotype IIIa 18:z4,z23:- isolates were collected from ground turkey, 97% of which were from samples collected in western states: CA(47), OR(33), NM(16), and CO(15). Of the 76 turkey isolates with accompanying slaughter plant information, 73 (96%) were from plants associated with a single brand. The majority (95%) of the retail isolates were *Xba*I PFGE pattern RXKX01.0002. During this same period of time, there were 117 human isolates of this serotype, most exhibiting the same RXKX01.0002 pattern. Ninety-four percent of human isolates were from western states, including CA, AZ, WA, NV, CO, ID, OR, and UT. Thirty-eight percent of the human isolates came from blood. PulseNet identified one outbreak cluster attributed to ground turkey. WGS analysis of 18 retail and 5 human isolates revealed that these isolates were highly clonal, with an average single nucleotide polymorphism difference of 42 nucleotides. All of the isolates harbored major virulence factors, including *spv* genes which may be associated with extra-intestinal infection. Resistance genotypes were shared among 1 human and 7 retail isolates. **Conclusions:** This study supports published evidence that ground turkey can be a source of *Salmonella* IIIa 18:z4,z23:- human infections, although other possible sources should be explored. Insights from WGS data can enhance traditional surveillance techniques.

Board 360. Finding Outbreaks Faster: Measuring the Time to Detection

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Background: To reduce the impact of infectious disease outbreaks, diminish the threat of pandemics, and move towards increased global compliance with the International Health Regulations the world must leverage emerging technologies and new networks to find disease outbreaks faster. Systems such as ProMED-mail, the Global Public Health Intelligence Network (GPHIN), and HealthMap, have enabled faster disease detection in many areas of the world by complementing traditional surveillance systems. However, existing metrics are inadequate for measuring progress towards more timely outbreak detection. **Methods:** In 2010 Chan et al. examined the timelines for 281 WHO-verified outbreaks reported in Disease Outbreak News (DON) from 1996 to 2009. The study found that the median time from 'outbreak start' to 'outbreak discovery' dropped from 40 to 19 days during that time. To obtain more granular national data, a working group was convened in 2014 to adapt the methods from Chan et al. for use at the national level. **Results:** Field epidemiology training programs (FETPs) in Kenya, Pakistan, Taiwan, and Zimbabwe, working with their associated Ministries of Health, are currently implementing this methodology to examine the detection, verification, and response timeliness to infectious disease outbreaks in their countries. Preliminary results from these studies and best practices for engaging countries in this type of analysis will be shared. **Conclusions:** Lessons learned and best practices from FETPs' experiences will be used to implement additional studies at the national level through the Training Programs in Epidemiology and Public Health Interventions Network (TEPHINET), the umbrella organization for field epidemiology training programs around the world. Measuring time to outbreak detection is but one new method for tracking progress towards improved global health security.

Board 361. Dengue Virus Infection Among Members of the Uganda People's Defense Force Deployed to Somalia

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Background: Outbreaks of dengue have occurred in East Africa over the last several years. In May 2011, a dengue outbreak was recognized among African Union Mission in Somalia (AMISOM) peacekeepers when several Ugandans were diagnosed with an acute hemorrhagic febrile illness. In response to the outbreak, we conducted a seroincidence study to determine the risk of dengue virus (DENV) infection following Uganda Peoples Defense Force (UPDF) deployment to Somalia. **Methods:** Serum specimens were obtained from 337 participating UPDF soldiers to determine DENV exposure and infection rate pre- and post-deployment. Testing included anti-DENV IgG antibodies by immunoassay and neutralizing IgG antibodies by microneutralization test (MNT). A dengue case was defined as positive for IgG seroconversion and confirmed by MNT. IgG seroconversion was defined as a negative anti-DENV IgG result in the pre-deployment specimen and a positive result in the post-deployment specimen or a 4-fold titer increase. MNT positive titer to only one serotype was classified as a primary DENV infection. Reactivity to multiple DENV serotypes by MNT was classified as a secondary DENV infection. **Results:** Of the UPDF soldiers that deployed to Somalia 60% seroconverted. The MNT results showed that 81% of the IgG positive specimens had neutralizing antibodies specific to DENV. Only 13.3% of the IgG positive specimens had a primary infection to either DENV1, 2 or 3. Twenty one percent of the specimens had DENV3 as the predominant serotype amongst UPDF soldiers. **Conclusions:** DENV exposure determined by the seroincidence study following UPDF deployment to Somalia matched the identified circulating serotypes in Somalia during the dengue outbreak in 2011 indicating that the source of infection was Somalia. With many of the UPDF soldiers having previous immunity against DENV, assessment of the location of the acquired infection should be determined by laboratory testing of any suspected acute febrile illness consistent with dengue for appropriate treatment and patient management. Further analysis of questionnaire performed on soldiers will determine if mosquito avoidance

during deployment to Somalia was an effective prevention method.

Board 362. Investigation of an Outbreak of Cholera in Diepsloot, Gauteng Province of South Africa, September 2014

E. D. Mathatha; Natl. Inst. for Communicable Diseases, Johannesburg, South Africa

Background: Cholera is a potentially epidemic secretory diarrhea caused by certain members of the species Vibrio cholerae. On 01 September 2014 a laboratory confirmed cholera case was reported. The case was a 37 years old male from Diepslot, Johannesburg, South Africa. We investigated the outbreak to institute appropriate management of cases, prevent further spread and institute control interventions. **Methods:** An outbreak response team was activated at the district level. Field investigations included a detailed interview with affected case, contact tracing, environmental assessments in affected area/households, microbiological investigations, and review of water and sanitation facilities. Close contacts to the case were interviewed using a structured questionnaire regarding the presence of clinical symptoms, possible exposures and travel history. Water and stool samples were collected. **Results:** Cholera was confirmed in a 37 year old male patient admitted to Helen Joseph Hospital, with watery acute diarrhea, vomiting and severe dehydration. Vibrio cholera 01 serotype Ogawa was isolated by conventional culture and sero-typing. A total of 22 contacts were identified and interviewed. Among the 22 contacts, five more people reported a history of diarrhea, vomiting and abdominal pains, one child and four adults. None of the 17 stool samples that were collected from the contacts tested positive for cholera, however 13 (76%) were positive for either one or a combination of Shigella sonnei, Salmonella species and Diarhogenic ecoli. The water tested negative for cholera. The cholera case had travelled to Zimbabwe on the 24 September 2014 and returned the next day. He then started presenting with vomiting and diarrheal symptoms on the 26 September 2014. **Conclusion:** The source of the outbreak was not identified. Our findings suggest that the environment was free of cholera. It is possible that the patient contracted the infection during his travel to Zimbabwe. The outbreak was well contained and no further cases were reported. A comprehensive health education on cholera and health and hygiene was given to the residents. This outbreak confirms that the surveillance system is able to detect a case of cholera within the health system, and is closely linked to public health response.

Board 363. Measles Outbreak Investigation in an Urban Slum—Ghazipur Village, Delhi, India

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Background: An unexpected occurrence of suspected measles cases was reported in April, 2014 from Ghazipur village, urban slum in Delhi. We conducted case-interviews, community-based household survey and case-control study to identify associated risk factors, and proposing recommendations to prevent future outbreaks. **Methods:** Case defined as anyone with fever and maculo-papular rash, and at least 1 of cough/coryza/conjunctivitis during 1st February-30th April 2014 resident of Ghazipur. Six blood samples collected randomly for testing by IgM Elisa at NCDC Laboratory. Cases interviewed for information on household characteristics, vaccination status and reasons for non-vaccination. A household survey in B-block of Ghazipur was performed to identify cases, estimate vaccine-coverage, vaccine-effectiveness (V.E.), and age-specific attack rate. Migratory behaviour was defined as living in Ghazipur for <3 years. Two controls selected for each case, one from same house and other from neighbourhood. Risk factors were identified by 1:2 age-matched analyses by logistic regression using Epi Info-7. **Results:** Total 69 measles cases were identified in Ghazipur village. Two of six samples tested positive for measles, the median age was 3 years (range: 0.5-21 years), one-dose measles vaccination coverage in 1-5 years of age was 61.6% & V.E of 89.6%. The highest AR was among children aged 0-5 years (25.1/1000). Risk factors for measles were migratory behaviour (odds ratio [OR] 6.3; 95% confidence interval [CI] 1.4-29.1), >2 children sharing one room (OR 2.6; 95% CI 1.1-6.4) and >3 families sharing one toilet (OR 12.3; 95% CI 1.6-95.5). **Conclusions:** Low vaccination coverage caused measles outbreak in Ghazipur. Significant risk factors included migratory behaviour and overcrowded living. We recommended strengthening routine immunization, including outreach services for targeting migratory populations, and periodic campaigns to ensure ≥95% two-dose measles vaccination coverage.

Board 364. An Outbreak of Foodborne Salmonellosis Linked to a Bread Takeaway Shop in Ben Tre City, Vietnam

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Background: On 23 May 2013, clinicians in a provincial hospital of Ben Tre City reported an unusual increase in the number of patients with gastroenteritis to Ben Tre Food Safety Agency (FSA). The clinicians noted that some cases had consumed stuffed bread from a food stand a few hours before onset of illness. The number of cases admitted to the hospital increased sharply to more than 150 cases on 24 May 2013. We conducted an investigation to identify the vehicle, source, causative agents of a community-wide foodborne outbreak. **Methods:** we conducted a case-control study in which cases were city residents diagnosed with gastroenteritis and hospitalized in Ben Tre City from 22 to 25 May 2013; forty-one cases were randomly selected from a list of hospitalized patients. Controls were age- and gender-matched healthy neighbors of cases. Participants were interviewed by using a standard questionnaire. Samples from patients and food were tested at reference laboratories. We used conditional logistic regression to calculate matched odds ratios (mORs) for the association of gastroenteritis with food items consumed. **Results:** Of the 41 cases enrolled in the study, 61% were males with median age of 33 years; they were hospitalized in 12 wards of the City. Of 13 food items consumed by the cases, only stuffed bread was significantly associated with gastroenteritis (mOR=21.3; 95% CI=6.3-71.8). Among the 29 cases who ate stuffed bread, median time to illness onset was 9 hours. Patient stool samples and bread samples were positive for *Salmonella species*. **Conclusions:** Stuffed bread was the likely vehicle of the outbreak. Laboratory testing capacity for serotypes of Salmonella should be strengthened in Vietnam. Food-handler training in basic food safety measures should be improved.

Board 365. Improving Foodborne Disease Outbreak Response Capacity in State and Local Health Departments Through the Foodborne Diseases Centers for Outbreak Response Enhancement (FoodCORE)

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Background: Each year foodborne diseases (FBD) cause illness in approximately 1 in 6 Americans, resulting in 128,000 hospitalizations and 3,000 deaths. Decreasing resources impact the ability of public

health officials to identify, respond to, and control FBD outbreaks. Geographically dispersed outbreaks present the added challenge of multijurisdictional coordination across all levels of the public health system. FoodCORE provides targeted resources to state and local health departments to improve the completeness and timeliness of laboratory, epidemiology, and environmental health activities for FBD surveillance and outbreak response. **Methods:** FoodCORE centers, selected through competitive award, implemented work plans designed to make outbreak response activities faster and more complete in their jurisdiction. During 2014, FoodCORE expanded to ten centers. Centers work collaboratively to implement metrics and develop model practices for FBD response so they can be shared with other local and state FBD programs across the United States. **Results:** Since the program began in October 2010, centers increased the proportion of *Salmonella,* Shiga toxin-producing *E. coli*, and *Listeria* (SSL) isolates with molecular subtyping (from 86% to 98%) and reduced the time to conduct this subtyping; for *Salmonella* this was reduced by over 60%, from 13 days to 5 days. Epidemiologic interviews were attempted for more SSL case-patients (99% vs 93%) and the average time to attempt interviews was reduced from a median of 4 to 2 days. The centers document practices that result in improvements. Model practices for streamlining and standardizing case-patient interviewing, isolate receipt and testing, and cross-cutting response activities are available on the FoodCORE website (http://www.cdc.gov/foodcore). **Conclusions:** FoodCORE centers conduct better, faster, more complete laboratory surveillance and outbreak response investigations. By conducting fast, thorough investigations, FoodCORE centers contribute critical information to help solve outbreaks quickly and ultimately help stop the spread of foodborne disease. FoodCORE strategies and model practices could be replicated in state and local health departments or international public health settings with similar infrastructures to improve FBD response.

Board 366. Household Cluster Investigations During the Early Stages of the Chikungunya Epidemic in Puerto Rico, 2014

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Background: Chikungunya is a mosquito-borne viral illness characterized by fever and intense joint pain. The first locally-acquired, laboratory-confirmed chikungunya case in Puerto Rico occurred in May 2014. To determine the extent of unreported chikungunya cases and describe the clinical spectrum of disease and health care-seeking behaviors of individuals with chikungunya, cluster investigations around the residences of laboratory-confirmed chikungunya cases were conducted during the early stages of the outbreak. **Methods:** All households within a 50 meter radius of a laboratory-confirmed case residence were offered participation in the investigation. Participants completed a questionnaire about household characteristics, demographics, recent illnesses, and mosquito avoidance behaviors. Participants provided a serum specimen, which was tested by RT-PCR and IgM capture ELISA to detect evidence of current or recent infection, respectively, with chikungunya virus (CHIKV) or dengue virus (DENV). **Results:** During June 20–August 19, 21 investigations were conducted, including 137 households and 250 participants. Of all participants, 70 (28%) had evidence of current (n = 12) or recent (n = 58) CHIKV infection. No participants had evidence of current DENV infection, and 13 (5%) had evidence of recent DENV infection. One participant had evidence of recent infection with CHIKV and DENV. Of all participants with evidence of CHIKV infection, 59 (84%) reported an acute illness in the past three months. Of these, the most commonly reported symptoms were fever (93%) and joint pain (94%); most (90%) participants reported both. Of all symptomatic participants with evidence of CHIKV infection, 43 (74%) sought medical care. Of these, 18 (42%) were diagnosed as chikungunya, 10 (24%) were hospitalized, and 1 (2%) was reported as a suspected chikungunya case. Median duration of illness was 6 days (range: 2–21), and median duration of hospital stay was 7 days (range: 3–15). **Conclusions:** These findings demonstrate a high degree of health care seeking behavior for persons with chikungunya; however, few cases were reported. Due in part to these findings, in July chikungunya was made a reportable condition in Puerto Rico and multiple media campaigns were initiated to improve public and clinical awareness of chikungunya.

Board 367. Dengue Outbreak in South Texas, 2013

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Background: Fewer than 60 locally-acquired dengue cases were reported in south Texas during 1980-2012. During July-October 2013, concurrent with an ongoing epidemic in northern Mexico, 17 dengue cases were reported, 6 of which reported no recent travel history. To better determine the incidence of dengue in south Texas, enhanced dengue case surveillance was implemented. **Methods:** Dengue cases were detected by: 1) compiling data from reported cases and specimens tested at private diagnostic laboratories; 2) reviewing medical records at eight hospitals for dengue-like illness; 3) performing RT-PCR and sequencing at CDC on available serum specimens from suspected cases previously tested by anti-dengue virus (DENV) IgM ELISA at private laboratories; and 4) interviewing and offering dengue diagnostic testing to case-patients' household members. **Results:** During 2013, South Texas clinicians requested dengue diagnostic testing for 264 patients, of which 39 (15%) were positive by IgM ELISA. Of 83 IgM-negative specimens that were further tested by RT-PCR, 14 (17%) were positive. In total, 53 (20%) laboratory-positive dengue cases were identified. Of 22 specimens that tested positive by RT-PCR, DENV-1 was detected in 19 (86%) and DENV-3 was detected in 3 (14%). Of all 53 laboratory-positive dengue cases, 26 (49%) were locally acquired and 20 (38%) reported recent travel to Mexico. Most (55%) cases were hospitalized. Dengue diagnostic testing was performed on 51 additional household members from 22 case-patient homes, of which 6 (12%) had serologic evidence of recent DENV infection; 5 reported no recent travel, and 1 reported recent dengue-like illness. Circulation of two genetically distinct strains of DENV-1 derived from Central America was detected. **Conclusions:**

Enhanced surveillance enabled detection of the most locally acquired dengue cases ever identified during an outbreak in south Texas. Due to the frequency of false negative anti-DENV IgM ELISA results, dengue diagnostic testing for acute cases of dengue-like illness should follow an algorithm which includes both IgM ELISA and RT-PCR. Because the burden of dengue is expected to continue in south Texas, dengue clinical awareness, laboratory capacity, and surveillance should continue to be improved.

Board 368. Emergence of Rabies Clusters Among Owned Dogs in Thai-Laos Border Area, Wiangkan District, Chiang Rai Province, Thailand, November 2013 - February 2014

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Background: On 26th November 2013, Thailand Bureau of Epidemiology was notified about 6 first confirmed rabid dogs during 14th to 26th November 2013 in Thai-Laos border area, Wiangkan district. The investigation objectives were to describe epidemiological characteristics of the epidemic, assess sources and risk of the outbreak and provide control measures. **Methods:** Rabies situation in Wiangkan district during 2011-2014 was reviewed. Case finding for rabies dog in the communities was done using dog survey and owner interview. To confirm rabies, dog heads were sent for Rabies antigen test by Fluorescent Antibody Technique. The rabies vaccination guideline for both human and animals was studied. **Results:** Twenty-one (47%) from 45 suspected dogs were confirmed rabies cases. Among those, 16(76.2%) were owned dog, but only one got vaccination during past one year. One backyard pig received rabies from a rabid dog biting. Ten people were bitten by those rabid dogs, all of them got fully immunized and nobody developed illness. Factors possibly contributing the incidence included no law enforcement for dog registration, dog population could be moved into the area freely which resulted in increasing unimmunized and rabid dog immigrants during years. With multi-sectoral approach, rabies vaccine 11,401 doses were provided to local dogs and cats in November 2013 and January 2014. Some suspected dog and stray dog were terminated. Animal registration system was enhanced. **Conclusion:** There was the first presence of rabies in Wiangkan district, Thai-Lao border area, during November 2013 to February 2014. Low rabies vaccine coverage among dogs due to large amount of unregistered dogs without proper population control may cause the outbreak. The strong immunization system in human could prevent the incidence in human. **Keywords:** rabies, animal, border, Thailand.

Board 369. An Outbreak of Cholera in the Context of Scarce and Intermittent Water Supply in Netrokona Municipality, Bangladesh, 2013

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Background: *Vibrio cholerae* is endemic in Bangladesh. A collaborative rapid response team investigated a severe diarrhoea outbreak in Netrokona municipality to determine the etiology, attack rate and transmission pathways. **Methods:** A probable cholera case was defined as ≥3 loose stools in 24 hours that led to hospitalization, receipt of intravenous fluids, or death in a municipal resident with onset during 15 August–15 October 2013. The district hospital's registry was reviewed to identify probable cases. We interviewed and collected rectal swabs from probable cases admitted on 7–9 and 20–24 September 2013. We conducted a stratified cluster survey in November 2013 to determine probable case load in the municipality. We reviewed municipal records and interviewed water engineers to explore water supply and sanitation. A convenience sample of water was collected from municipal-supplied taps of probable case households, streets, source pumps, and tube wells to test for common enteric pathogens. **Results:** Among 1,568 hospitalized probable cases identified. 5 (0.3%) died. Of 4,870 municipal residents surveyed, 85 (2%) were probable cases, 42% reported drinking exclusively tap water, 19 (13%) drank pond or river water due to deficient municipal supply or drying up of tube wells, and 87% lacked sanitary latrines. *V. cholerae* was cultured from rectal swabs collected from 33 (80%) of 41 sampled patients. Untreated ground water was supplied intermittently for 1–2 hours thrice daily to 1,288/11,415 (11%) households and 41 street taps. According to engineers, the majority of the residents used tap water for drinking despite the municipal's poor pipeline coverage. Thermotolerant coliforms were detected in all and *V. cholerae* in one (11%) of nine tap water samples collected. **Conclusions:** This outbreak affecting a town with water scarcity and suboptimal sanitation infrastructure likely resulted from ingress of contaminants into pipeline water during interruptions in supply. It is critically important to improve infrastructure for safe water delivery in Bangladesh, but this will take time and resources. Meanwhile, vaccination may be a cost-effective strategy to mitigate cholera in municipalities and should be explored, and future studies should aim to identify sustainable water purification strategies for households.

Board 370. Investigation of Diarrhoeal Disease Outbreak in Swaziland in July 2014

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Background: Media reports in July 2014 alerted the Swaziland Ministry of Health that there were increased numbers of diarrhoea cases and deaths. The Ministry instituted a preliminary enquiry and requested support from the World Health Organization Regional Office for Africa (WHO AFRO). The WHO AFRO response team in collaboration with the Swaziland Emergency Preparedness and Response Unit investigated the diarrhoeal outbreak in August 2014. **Methods:** The response teams visited health facilities, interviewed key stakeholders and completed field questionnaires. The team also collected data on diarrhoea cases and deaths, interviewed caregivers and assessed diarrhoea case management. Stool specimens, collected as part of the rotavirus sentinel surveillance program in July 2014, were analysed by the Swaziland National Reference Laboratory and a sub-set sent to the Centre for Enteric Diseases (CED), National Institute for Communicable Diseases (NICD) for additional screening. **Results:** Swaziland health facilities reported roughly 15,000 cases of diarrhoea in children under-thirteen years with most infections in children under-five in July and the beginning of August 2014. The crude incidence was 88 cases per 1000 children under-five. The number of diarrhoea cases began increasing on the 14th July 2014 and

peaked on the 28th July 2014. Fifty-three deaths, primarily due to late presentation and co-morbidity, were associated with the outbreak. The quality of case management according to the Integrated Management of Childhood Illnesses (IMCI) standards was generally poor. Screening of stool specimens revealed that rotavirus (G1P[8]) was responsible for 74% (138/186) cases requiring hospitalization. **Conclusions:** Swaziland experienced a substantial diarrhoea season in 2014 with partial laboratory screening suggesting that rotavirus was responsible. The case fatality rate (0.35%) was well below the 1% target for diarrhoeal disease. The IMCI case management was inadequate due to lack of training. The study highlights the need to accelerated introduction of the rotavirus vaccine in Swaziland to February or March 2015 for maximum impact. In addition, the expansion of enteric pathogen testing protocols, IMCI training and strengthening of Integrated Disease Surveillance and Response was recommended.

Board 371. A Tale of Two Receptions: Two Norovirus Outbreaks at a Banquet Facility — Connecticut, 2013

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Background: In October 2013, the Connecticut Department of Public Health (DPH) was notified of gastrointestinal illnesses following two receptions held two weeks apart at the same facility. To determine the cause and extent of illnesses, we conducted epidemiologic and environmental investigations for each event. **Methods:** Two case-control studies were conducted, one for each reported event. Case-patients were defined as reception attendees with diarrhea (≥2 stools/day) or vomiting within 72 hours after the reception. No guest lists were available for either event; attendees were identified through initial complaints to DPH and subsequent interviews. Stool specimens were collected from all food workers and some ill event attendees and tested at DPH State Laboratory. Norovirus (NoV) positive samples were submitted to Wadsworth for sequencing. **Results:** Of 150 reception A attendees, 60 were interviewed; 34 case-patients and 23 control subjects were identified. On univariate analysis, several food items had elevated odds ratios (OR) including six hors d'oeuvres, wine, water and ice. Five case-patients tested positive for NoV genotype I (GI). Five of 26 food workers tested positive for NoV; two for both GI and GII, two for GI, and one for GII. The food worker positive for GII reported working while symptomatic. All GI specimens were GI.3C with identical gene sequences; the single GII specimen was genotype GII.7. Of 125 reception B attendees, 55 were interviewed; 32 case-patients and 18 control subjects were identified. No food items were identified with elevated ORs on univariate analysis. Five case-patients tested positive for NoV GII. Eight of 28 food workers tested positive for NoV; two tested positive for GI and six for GII. One GI specimen was GI.3C, identical to that found in reception A and two GII specimens were GII.7 that differed by six base pairs from reception A. **Conclusions:** Epidemiologic and laboratory data suggest two outbreaks of NoV occurred at two different events held two weeks apart at the same facility; one attributed to NoV GI.3 and the second to NoV GII.7. Illness at the first reception was likely due to contaminated food items while the source for second reception remains undetermined. Laboratory findings helped determine that these were in fact, two distinct outbreaks at the same facility.

Board 372. Outbreaks of Listeriosis in England Linked to Crabmeat: A Novel Food Vehicle

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Background: Listeriosis is a rare but severe food-borne disease that predominantly affects pregnant women and their unborn and new-born babies, the elderly and the immuno-compromised. Seafood is known to support the growth of *Listeria* spp. including *Listeria monocytogenes,* the most common causative agent of human listeriosis. Two outbreaks of listeriosis linked to the consumption of crabmeat were investigated in England during 2013 following routine monitoring of an enhanced surveillance database. To date, crab meat remains a novel vehicle for listeriosis in UK with only one known documented outbreak of listeriosis implicating synthetic crab meat as a vehicle in Canada. **Methods:** Isolates of cases of *L.monocytogenes* are submitted to the Gastrointestinal Bacteria Reference Unit for confirmation and molecular typing. Reported cases are followed up to ascertain clinical history, food history, and any relevant epidemiological information using standardised questionnaires. Cases were identified using the enhanced surveillance system managed by Public Health England (PHE) with linked epidemiological and microbiological data. **Results:** The first outbreak involved three cases linked to a single producer and occurred between 2011 and 2013. Isolates from cases, food and environmental samples procured from the crab meat processor were indistinguishable and had the same rare fAFLP type (*L .monocytogenes* serotype 4, fAFLP type 1.72). Notable characteristics of this outbreak were the extended period between onsets of illness and that the geographical distribution of cases did not reflect the distribution of the product. The second outbreak involved 12 cases of *L. monocytogenes* serotype 4, fAFLP type V.3 and five of *L. monocytogenes* serotype 4, fAFLP type V.6 with identical profiles to food and environmental isolates from another crabmeat producer. Notable characteristics of this outbreak were the outcome of the whole genome sequencing and the frequent reporting of buying crabmeat or seafood from mobile vendors. **Conclusions:** These are the first known outbreaks of listeriosis in England linked to consumption of crab meat. The importance of routine food sampling, multi-disciplinary investigations, temperature control during distribution and international harmonisation of surveillance systems are discussed.

Board 373. Acute Gastroenteritis Cases at a Home for Abandoned Children, Johannesburg, South Africa, May 2014

Withdrawn at Author's Request

Board 374. Use of an Information Technology Platform to Facilitate Data Sharing in Multistate Enteric Disease Outbreak Investigations

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Background: Enteric (foodborne and animal-related) illness affects 1 in 6 Americans annually, resulting in 128,000 hospitalizations and 3,000 deaths. Multistate enteric disease outbreaks are complex and require federal and state public health partners to quickly evaluate epidemiologic, laboratory, and traceback data to enable an effective public health response. To address this challenge, the DFWED Outbreak Response and Prevention Branch (ORPB) sought to develop an information technology solution. **Methods:** The System for Enteric Disease Response, Investigation, and Coordination (SEDRIC) is customized commercial off-the-shelf software from Palantir Technologies. It facilitates collaborative multistate enteric

disease outbreak investigations by integrating surveillance data in real time, visualizing outbreak data rapidly, and providing a secure platform for collaboration. Users have access to outbreak dashboards, time trend maps, customizable traceback diagrams, and patient line list management capabilities. **Results:** ORPB has enrolled over 225 SEDRIC users across CDC, all 50 states, the U.S. Food and Drug Administration, and the U.S. Department of Agriculture's Food Safety and Inspection Service. The line list editor has been successfully piloted in 18 multistate outbreak investigations. States have obtained cluster-specific outbreak information 24-48 hours faster using SEDRIC compared to typical laboratory communications. Twenty-eight SEDRIC trainings have been conducted in the last two years, including two trainings at national conferences and five on-site trainings at state health departments. **Conclusions:** SEDRIC has improved the speed and ability to respond to, investigate, and coordinate multistate enteric disease outbreaks. SEDRIC has facilitated rapid sharing of critical information to solve outbreaks, remove contaminated foods from commerce, and protect additional people from getting sick.

Board 375. Emerging Zika Fever Outbreaks in Thailand, 2012-2013

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Background: In May 2013, Zika fever was confirmed in a Canadian traveler returning from Thailand. A retrospective investigation of patients with rash in Thailand was immediately initiated to assess for possible Zika virus infections. **Methods:** We reviewed reported outbreaks of fever with rash in Thailand that etiologies was unknown but negative PCR for Chikungunya and Dengue viruses in acute sera and negative measles and rubella IgM in convalescent sera. Acute sera from archived samples of the undetermined outbreaks were sent to the Arbovirus Diseases Branch, CDC-US and Department of Virology, AFRIMS-Bangkok to test for Zika virus genome by PCR. Convalescent sera were also tested for antibodies to Zika by ELISA at CDC-US and to dengue by ELISA at Thai NIH. A confirmed Zika virus infection was defined as a patient who had positive Zika virus PCR. **Results:** Four suspected outbreaks in Thailand from February 2012 to September 2013 met our criteria. Seven out of 46 (15.21%) cases were positive Zika virus by PCR. The locations of events were in a province borders with Myanmar (1 case), Cambodia (1 case) and Laos (4 cases) and one case was in a northern province. Female (6/7) was predominant. Age ranged from 1 to 69 years (median 51 years). The most common clinical presentation in all outbreaks was rash, followed by fever, joint pain and non-purulent conjunctivitis, respectively. Fifteen cases had convalescent sera (blood collected ≥ 7 days after onset) and Zika virus IgM was positive in 12 cases (80%), negative in 2 cases and equivocal in one case. Among 9 cases tested positive Zika IgM, 6 (66.67%) also revealed positive Dengue IgM. **Conclusions:** A lab-confirmed Zika fever outbreaks in Thailand was first observed in 2012, based on evidence detected from available samples. The high cross-reactivity of antibodies between Zika and Dengue was observed. The diagnosis of Zika infection by IgM alone must be cautious and a definite diagnosis needs antigen detection (e.g., PCR), especially in Dengue endemic countries. Strengthening laboratory capacity began in August 2014 with the assistance of the US CDC. Currently, 5 laboratory centers in Thailand are able to run Zika PCR. Enhanced surveillance and outbreak investigations for Zika infections were implemented to determine the disease burden and molecular characteristics of the virus in Thailand.

Board 376. Outbreak of Dengue Fever in Ouagadougou, Burkina Faso, 2013

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Background: From October 18 to November 8, 2013, two medical centers in the central region of Burkina Faso, received 43 patients with atypical symptoms evoking Dengue Fever (DF). **Methods:** A total of 43 available sera were screened for IgM and IgG antibodies against dengue virus (DENV), using rapid tests SD BIOLINE Dengue IgG/IgM (SD Standard Diagnostics, Korea) at the bacteriology and virology laboratory of the teaching hospital, Centre Hospitalier Universitaire Yalgado Ouédraogo (CHU-YO) in Ouagadougou. The molecular detection of DENV was performed at the Influenza National Reference Laboratory of Burkina Faso, using CDC DENV-1-4 Real-Time RT-PCR (rRT-PCR) reagents, primers and protocols. **Results:** Seven of 43 sera (16.3%) were positive for IgM/IgG while 21/43 (48.8%) sera were positive by rRT-PCR. DENV 3 subtype was identified in all positive specimens. The rapid test had a good specificity (100%) but a very low sensitivity (28.5%) in comparison to rRT-PCR testing. Except a missing age for one patient and one 17-years old patient, the other 19/21 (90.4%) dengue confirmed cases were from adult patients over 20 years. **Conclusions:** Our results identified DENV 3 subtype as the etiologic agent of occurred outbreak in Ouagadougou in 2013 and indicated the essential contribution of rRT-PCR for DF detection.

Board 377. Investigation of a Diarrhea Outbreak in a Public Hospital Refectory in São Paulo City, São Paulo State, June 2014

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Background: Occurrence of Foodborne Diseases is increasing significantly worldwide related to the failures in the chain of production of food or water. We summarize the findings of the diarrheal outbreak investigation notified to the Center for Epidemiologic Surveillance of São Paulo State, in June 2014, associated to the ingestion of food prepared by industrial cuisine in the public hospital in São Paulo city and the sanitary measures to control and prevent new outbreaks. **Methods:** Descriptive and case-control studies were conducted in the public hospital and in six departments from the State Secretary of Health of São Paulo. Case was defined as the person with diarrhea with or without other gastrointestinal symptoms who had lunch in the Public Hospital refectory during June 2-3, 2014. Control was the person without diarrhea or other gastrointestinal symptoms who had lunch in this refectory in the same period. A questionnaire was applied to obtain epidemiological data in order to identify the common infection source. Stool samples were tested by the Adolfo Lutz Institute, our reference laboratory, and by other public laboratory, reference of this hospital. **Results:** A total of 158 persons were interviewed, 66.5% in the public hospital and 33.5% from the State Secretary of Health of São Paulo: 78 (49.3%) cases (patients) and 80 (50.6%) controls (non-patients). The median age was 46 years (range= 22-69 years); 65.3% were male. The median incubation period was 13 hours (range=1.5-24 hours). Univariate analysis of risk foods showed association and statistical significance for the "roasted meat" [OR=4.9; 95% CI=1.7-13.7; p<0.005] and for the

"green soup" [OR=3.1; 95% CI=1.4-6.8; p<0.01] served in June 3, 2014. Despite our recommendations only four persons collected stool samples: two performed by Adolfo Lutz Institute were positives for *C. perfringens* toxin. It was not possible to analyze leftovers of the foods consumed due to this refectory discarded the food samples in disagreement with the sanitary regulation. **Conclusions:** The investigation confirmed the diarrhea outbreak in the hospital refectory associated to "roasted meat" and "green soup" caused by toxins of *C. perfringens*. The irregularities in the cuisine were corrected. We recommended enhancement of several measures to prevent future outbreaks.

Board 378. Re-emergence of Urinary Schistosomiasis in Europe? Investigation of a Cluster of *Schistosoma haematobium* Infections Acquired in Southern Corsica

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Background: *Schistosoma haematobium* is a tropical parasite causing silent infections in millions worldwide with potential evolution toward severe urinary and reproductive diseases. Evidence of re-emergence in Europe has been detected. A cluster of cases of urinary schistosomiasis was reported in April 2014 among French and German tourists linked to exposure in the Cavu River, Southern Corsica, between 2011 and 2013. The early response consisted in prohibiting bathing in the river, nationwide screening of all people exposed to the river and treating confirmed cases. **Methods:** We set up a surveillance of autochthonous urinary schistosomiasis to describe the extent of the outbreak and identify potential sites of transmission in France and Corsica. Cases were defined as a French resident with serology positive for schistosomiasis or demonstration of schistosome eggs in urine and no history of contacts with fresh water in known endemic areas. We documented symptoms, place and time of exposure to fresh water of cases. We searched 13 streams for intermediate snails host in Corsica. Collected specimens were tested for infestation by natural emission of parasite larvae. **Results:** Since June 2014, over 20,000 French residents have been screened for schistosomiasis. 65 autochthonous cases have been reported, including 18 with a symptomatic infection. All bathed in the Cavu in 2013. Among patients residing in France (n=49), 73% reported bathing in the river in August 2013. Over 500 specimens of *Bullinus truncatus* were retrieved from 3 streams including Cavu. None tested positive. **Conclusions:** This cluster shows that environmental conditions are suitable for local transmission of *S. haematobium* in Corsica. Surveillance should be continued in France and considered in Mediterranean countries to detect new foci and guide necessary control measures.

Board 379. Outbreak of *Vibrio parahaemolyticus* Associated with Raw Shellfish, Connecticut, 2013

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Background: The incidence of *Vibrio* infection has been increasing in CT and nationally in the past decade. In 2013, CT observed an increase of 115% in reported cases of *V. parahaemolyticus* compared to the previous two years. The CT Departments of Public Health (DPH) and Agriculture Bureau of Aquaculture (DA/BA), working with local health departments, investigated these cases to determine the source of illness and to implement control measures. **Methods:** In CT, infection with *Vibrio* spp. is a provider and laboratory-reportable condition. Clinical laboratories are also required to submit isolates to the DPH State Laboratory. *V. parahaemolyticus* isolates were subtyped by pulsed-field gel electrophoresis (PFGE) and forwarded to the Centers for Disease Control and Prevention (CDC) for serotyping. Cases were interviewed using the CDC Cholera and Other Vibrio Illness Surveillance Report (COVIS) form. Seafood investigations and shellfish trace backs were conducted. **Results:** During June - October 2013, 28 *V. parahaemolyticus* infections were reported. Cases ranged in age from 9 to 79 years (median 52 years); 17 (61%) were male. Three (11%) cases were hospitalized; no deaths occurred. Among the 24 (86%) gastrointestinal cases, 21 (88%) reported consuming raw shellfish including raw oysters (18, 86%), and/or raw clams (7, 33%). Among 27 isolates tested, 16 (59%) yielded the predominant outbreak PFGE strain and 18 (67%) were serotype O4:K12. Shellfish trace backs identified two specific harvest areas in CT as the source of this outbreak. **Conclusions:** In 2013, an outbreak of *V. parahaemolyticus* occurred in CT. The CT outbreak was part of a larger multistate outbreak with over 100 cases identified from 13 states. The outbreak was associated with serotype O4:K12 (the Pacific Northwest strain), which prior to 2012, had not been associated with shellfish outside of the Pacific Northwest. Illnesses were associated with eating raw shellfish from Atlantic Coast harvest areas, including CT. Prompt case investigations and shellfish trace back efforts in CT led to closure of implicated harvest areas and recall of shellfish. In 2014, the CT DA/BA implemented more stringent *V. parahaemolyticus* Control Plan in harvest areas linked to the 2013 outbreak. Record low number of *V. parahaemolyticus* infections have been reported in CT in 2014.

Board 380. Estimating Remaining Risk for Use in Targeted Follow-up in an Outbreak of Fungal Infections Due to Contaminated Methylprednisolone Injections, Tennessee, 2012

M. A. Kainer, M. Kanago, A. Wiese, B. Berger, J. Ward, J-Y. Min; Tennessee Dept. of Hlth., Nashville, TN, USA

Background: By October 26, 2012, 70 cases of fungal infections associated with contaminated methylprednisolone (MPA) injections had been reported to the Tennessee Department of Health (TDH); nine patients died. Eight patients presented with posterior circulation stroke, and four had symptoms less than 48 hours before presenting with stroke. We sought to determine if there was opportunity for intervention among asymptomatic non-cases to prevent stroke and death. **Methods:** We estimated cumulative individual patient risk of fungal infection using a logistic regression model built with data from Clinic A. One component of a CDC decision analysis fit a Weibull distribution to data on time between most recent MPA injection and symptom onset for the 145 cases reported to CDC at the time. Using this curve, proportion of cumulative individual infection risk remaining was calculated and applied to each exposed non-case patient's cumulative risk prediction from the logistic model to assign each a "remaining risk" score. **Results:** A total of 598 MPA-exposed patients were included in the logistic model. Multivariate risk factors for infection were: age >60 years (adjusted odds ratio(aOR): 2.2; 95% CI: 1.13, 4.29), at least one injection with translaminar approach (aOR: 2.09; 95% CI: 1.00, 4.38), and increasing cumulative dose of lot

06292012@26 in 40mg increments injected 46-60 days and > 60 days after production(aOR: 1.32; 95% CI: 1.05, 1.65 and aOR: 1.64; 95% CI: 1.29-2.09, respectively). Cumulative risk estimates ranged from 0.11% (95% CI 0.01%-1.30%) to 63.67% (95% CI 24.93%-90.24%). By October 26, 2012, no patient's remaining risk was greater than 0.82% (95% CI 0.23%-1.50%). Six patients with outlying risk scores (95% CI of remaining risk >1.0% on 10/26) were identified, and their names were provided to the clinics for more intensive follow-up. **Conclusions:** Using logistic regression in conjunction with a decision analysis model, we assessed risk of infection remaining among exposed asymptomatic patients. By October 26, most patients had an estimated remaining risk of <1%, and those with outlying risk estimates were targeted for additional follow-up. In this evolving situation, accounting for time since exposure proved critical for accurately estimating patient risk.

Board 381. Review of Antifungal Treatment Regimens and Clinical Outcomes in an Outbreak of Fungal Infections Due to Contaminated Methylprednisolone Acetate Injections in Tennessee

M. A. Kainer, J. Ward, A. Wiese, B. Berger, M. Kanago, J-Y. Min; Tennessee Dept. of Hlth., Nashville, TN, USA

Background: In September 2012, the Tennessee Department of Health investigated an outbreak of fungal infections among patients who received epidural injections of contaminated methylprednisolone acetate. Most initial cases presented with meningitis and received antifungal treatment. However, many of these cases and subsequent cases also developed localized infections near the injection site. Our objective was to review antifungal treatment regimens and describe characteristics of disease progression. **Methods:** For confirmed and probable cases of fungal infection following an epidural steroid injection in Tennessee, clinical data including physician notes, medication administration records, and laboratory results were abstracted from hospital medical records. Cases were classified as having disease progression if they developed new complications or worsening of initial syndrome. Statistical analyses were performed to examine the characteristics of treatment and disease progression. **Results:** Of 152 total cases, 68% had at least one hospitalization. Fifty-six cases (37%) had evidence of disease progression, and 15 (10%) died. Eighty-eight cases (58%) were treated with voriconazole, 56 (37%) also received amphotericin B, and 64 (42%) did not receive either drug or treatment was unknown due to outpatient status. Serum voriconazole level results were available for 73 cases, 70 of whom reached a therapeutic level (≥ 2µg/ml). Forty-nine cases reached a therapeutic level prior to disease progression. The median time from initial syndrome to disease progression was 25 days (range 4-165). Fifty-seven cases (38%) had multiple healthcare encounters. Reasons for repeat encounters included new findings due to disease progression, worsening of initial syndrome, side effects from antifungal treatment, and other unrelated illness. **Conclusion:** A large proportion of cases experienced a prolonged course of illness and disease progression. Treatment regimens varied widely among cases. Long-term clinical data with outpatient treatment information, in addition to multivariate analyses controlling for confounders, are warranted to examine whether there is an association between treatment regimen and disease progression.

Board 382. Risk Factors for Fungal Infection Following Injection with Contaminated Methylprednisolone Acetate in Tennessee

M. A. Kainer, A. Wiese, M. Kanago, J. Ward, J-Y. Min, B. Berger; Tennessee Dept. of Hlth., Nashville, TN, USA

Background: In September 2012, the Tennessee Department of Health investigated an outbreak of fungal infections among recipients of epidural glucocorticoid injections at three outpatient clinics. Contaminated methylprednisolone acetate (MPA) from one compounding pharmacy was implicated as the source of fungal exposure. We identified risk factors for infection among recipients of MPA injections. **Methods:** Glucocorticoid injection procedure records from June 26 to October 2, 2012, were abstracted; cases were classified according to CDC definitions. A cohort analysis was performed to identify risk factors for infection among MPA recipients. The Mantel-Haenszel chi-square statistic or Fisher's exact test was used for univariate analysis of categorical variables; multivariate analysis was conducted using logistic regression. In analyses by MPA lot, patients with uncertain lot designation were excluded. **Results:** In Tennessee, 1021 patients received MPA injections. 153 patients (15%) met the case definition; 126 had localized infection, 79 had meningitis, 3 had stroke (with no lumbar puncture), and 2 had joint infection. Univariate risk factors for fungal infection included: age >60 years, female sex, injection received at Clinic B, exposure to multiple procedures, exposure to MPA lot 06292012@26, and exposure only to vials >50 days old (compared to exposure to newer vials only). In multivariate analysis, risk factors for infection included age >60 years (adjusted odds ratio (aOR): 3.15; 95% CI: 1.99, 4.99); undergoing ≥1 translaminar procedure (aOR: 1.81; 95% CI: 1.15, 2.83); and cumulative dose of lot 06292012@26 injected 46-60 days and >60 days after production, in 40-mg increments (aOR: 1.40; 95% CI: 1.18, 1.65; aOR: 1.85; 95% CI: 1.55, 2.21, respectively). Risk factors for meningitis or localized infection were similar to the results for all cases, though receiving an injection at Clinic A was a risk factor for meningitis (aOR: 3.02; 95% CI: 1.29, 7.04). **Conclusions:** We identified risk factors for fungal infection following MPA injection. Of note, infection risk increased with every 40-mg exposure to MPA lot 06292012@26 with shelf life >45 days, indicating that these vials may have been more heavily contaminated than vials from lot 05212012@68 and newer vials of lot 06292012@26.

Board 383. Investigation of a Cluster of Methicillin-sensitive *Staphylococcus aureus* Infections Among Patients who Received Joint Injections in a Tennessee Outpatient Clinic

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Background: On 9/9/2013, the Tennessee Department of Health (TDH) was notified of 3 joint infections among patients who received injections of triamcinolone and lidocaine on 9/5 at a single primary care clinic. TDH advised the clinic to sequester the medications and stop performing injections.Triamcinolone was supplied from an out-of-state compounding pharmacy; lidocaine from a manufacturer. **Methods:** All 5 patients who received a joint injection on 9/5 were followed up; data were abstracted. One open triamcinolone vial was used on 8/30; patients who received joint injections on that day were notified to monitor for symptoms. On 9/13, TDH staff obtained the sequestered medications and observed infection control and injection practices. The opened vials of medication were sent to the TN Public Health Laboratory, in addition to clinical isolates from the cases. CDC, FDA, and an out-of-state board of pharmacy were notified. **Results:** Of the 5 patients with knee or shoulder injections on 9/5, 4 had evidence of a joint infection. There was a 5 hour window between first and last injections. No other patients who received injections from the clinic

had symptoms/signs of infection. During the clinic visit, suboptimal medication preparation and hand hygiene practices were observed, and there was no area dedicated to medication preparation. Recommendations were provided and implemented, including avoiding use of multi-dose vials. Methicillin-sensitive *Staphylococcus aureus* (MSSA) was isolated in all 3 cases where a clinical isolate was available, and pulsed-field gel electrophoresis confirmed that all strains were indistinguishable. Cultures of opened preservative-containing vials of triamcinolone and lidocaine were negative. **Conclusion:** TDH interventions helped the clinic address unsafe medication preparation and injection practices. The investigation highlighted the need for ongoing training, oversight, and outbreak detection in the outpatient setting. Further experiments are planned to test survival of MSSA in a vial with preservative for at least 5 hours, to address the possibility of extrinsic contamination of one of the vials as the source of the cluster.

Board 384. An Investigation of a Fatal Hand, Foot, and Mouth Disease (HFMD) Prompts Health Alert with a Survey of Knowledge, Attitude, and Practice (KAP) in Prevention and Control in Child Care Centers (CCCs) in Surin Province, Thailand 2014

N. Boonthanapat; FETP Thailand, Nonthaburi, Thailand

Background: In 2014, several HFMD outbreaks among young children were in Surin province in the northeast of Thailand. Unfortunately, a 10-month old boy with HFMD visited a community hospital and died on 10th July 2014. An investigation was conducted to confirm diagnosis, identify cause of death, and implement prevention and control measures. To determine proportion of CCCs had knowledge regarding the daily screening and prevention and their practice during HFMD outbreaks, the KAP from CCCs in the province was surveyed. **Method:** Review the death's medical record, interview his parents about symptoms and travel history, and case finding of HFMD in his village was conducted. Suspect case defined as a ≤5 year child who had either criteria of vesicles at oral cavity, or maculopapular rash at palm or foot or buttock during 1-19 July 2014. Among those, proper throat swabs and fresh stools were tested for enterovirus (EV) isolation. Self-response questionnaire of the KAP survey was developed with a reliability of Cronbach's alpha = 0.75 in the pilot study and distributed to all CCCs in this province. **Result:** On 7th July 2014, he had maculopapular rash at both legs, vesicles at head and neck. 9th July, he visited a private clinic with vomiting and loss of appetite. Next 12 hours, he developed generalized seizure and visited the hospital with unconsciousness, and died with diagnosed severe HFMD. His serum and stool specimen were negative for EV71 IgM and isolation. Of 4 family members and 28 neighbor contacts, only 2 neighbors had positive to Coxsackie-A6 and A16 by isolation. 4th July, his mother brought him to the village CCC that 4 of 26 children detected enterovirus non EV71 from stools. 71% of all 497 CCCs in the province responded, 86% of those notified health authorities when found a suspect, 82% had daily screening with 49% using flashlight for mouth exam, 64% had seen rashes of HFMD and provided isolation, 50% did not know severe symptoms of EV71without rash, and 35% agreed to close CCC 1 week after a cluster detection. All misunderstood using alcohol hand rub for viral killing. **Conclusion:** Various EV causes of this HFMD outbreak with a fatal child occurred in the province. Better practice & knowledge were educated for CCCs to improve sanitation, personal hygiene, correct daily screening and isolation with effective collaboration.

Board 385. An Outbreak of Ocular Bacterial Conjunctivitis Due to Unencapsulated *Streptococcus pneumoniae*

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Background: From August to September 2014, Marine Corps Base Camp Pendleton experienced an outbreak of ocular conjunctivitis among military recruits. This study examines an outbreak among recruits infected by a novel strain of untypable S. pneumoniae, despite receiving the 21-valent Pneumococcal vaccine. This recent emergence of ocular bacterial conjunctivitis shows remarkable resemblance to a 2003 outbreak among military trainees, attributed to a novel unencapsulated strain of S. pneumoniae. The 2003 outbreak was preceded by two other similar outbreaks—MCRD, San Diego, CA (1980) and the Recruit Training Command, Great Lakes, IL, (1996). This study prompts further investigation and surveillance of pathogenic S. pneumoniae. **Methods:** Conjunctival swabs were obtained from infected recruits and sent to the Naval Health Research Center. Samples underwent routine testing, including Gram stain and catalase biochemical reactions. Suspicious isolates were tested using the Becton Dickinson Phoenix Automated Microbiology System, as well as optochin disk and the bile solubility tests. Positive isolates were serotyped using the Pneumotest-Latex Rapid Agglutination Test and Quellung reaction. **Results:** A total of 23 conjunctivitis samples were tested. Fifteen samples tested positive for S. pneumoniae. All 15 of the positively identified S. pneumoniae samples were tested using automated and manual methods. Seven of the samples tested did not grow, and one sample identified as S. haemolyticus. Each positive isolate tested negative for Latex Agglutination and Quellung groups. All S. pneumoniae isolates are suspected to be from the same novel serotype. **Conclusion:** Additional research, focused on the development of a manual method for antibiotic susceptibility testing, as well as sample identification validation through molecular laboratory sequencing, should be performed. Our data suggest that the causative agent for ocular conjunctivitis among military recruits is an unencapsulated, untypable novel strain of S. pneumoniae.

Board 386. Investigation of an Outbreak of Infections with Rare *Salmonella* Serotypes Linked to Pet Bearded Dragon Lizards, 2012–2014

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Background: Reptiles are the fastest growing sector in the U.S. pet industry, with bearded dragons one of the most popular species. Risk of reptile-associated salmonellosis is an ongoing public health problem, especially among children, senior citizens, and immunocompromised persons. In 2014 we investigated an outbreak of infections with rare *Salmonella* serotypes, Cotham and Kisarawe, linked to pet bearded dragon lizard exposure. **Methods:** A case was defined as illness in a person infected with *Salmonella* Cotham or Kisarawe between 01/01/2012–06/21/2014. A binomial probability distribution was used to compare exposure and focused questionnaire data reported by ill persons to a U.S. reptile ownership survey. Traceback of reptiles purchased by ill persons was

conducted in collaboration with the pet industry, resulting in onsite sampling at three reptile breeders in two countries and several U.S. pet stores. **Results:** *Salmonella* Cotham and Kisarawe account for ≤0.01% of all serotypes in CDC's *Salmonella* database. A total of 166 cases in 36 states were identified with onset dates between 02/2012_07/2014. The median patient age was three years (range <1 - 79) and 56% were ≤5 years. Thirty-seven percent (37%) were hospitalized. Patients reported significantly higher exposure to any reptile (83%, p<0.001) than reported on the reptile ownership survey; 96% of 74 patients with lizard contact specifically reported bearded dragons. Sampling of bearded dragons and their environments resulted in isolation of outbreak serotypes at each sampled facility; isolation proportions ranged from 9 - 24%. *Salmonella* was more commonly recovered from eggs and younger lizards compared to older lizards. **Conclusions:** Epidemiologic, microbiologic, and traceback evidence linked an outbreak of rare *Salmonella* serotypes disproportionately affecting young children, to contact with pet bearded dragons and their environments. To reduce the risk of reptile-associate salmonellosis, owners should be made aware of the potential for household contamination by pet reptiles and strategies should be developed to improve breeder practices, facility biosecurity, and monitoring protocols. This outbreak highlights the need for a comprehensive One Health approach to zoonoses prevention involving human, animal, and environmental health.

Board 387. Utilization of CDC Serologic Assays to Detect Antibodies to Middle East Respiratory Syndrome Coronavirus (MERS-CoV) in Two US Imported Cases

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Background: In 2012, a new coronavirus emerged in the Middle East which was named Middle East Respiratory Syndrome Coronavirus (MERS-CoV). CDC rapidly developed four serologic assays to aid in the detection of antibodies to this new CoV. In 2014, two US imported cases infected with MERS-CoV were identified with the help of the CDC serologic assays. The timely collection of sera from the two infected patients allowed the kinetics of the MERS-CoV antibody response to be determined. **Methods:** The sera from the two US patients were tested using the MERS-CoV whole cell antigen and the recombinant MERS-CoV nucleocapsid (MERS-CoV_N) protein-based ELISA. To confirm the presence of MERS-CoV antibodies in patient's sera, an immunofluorescent assay (IFA), which uses Vero cell monolayers infected with MERS-CoV, was performed. The patient sera were also tested with a second confirmatory assay, MERS-CoV microneutralization (MNt) assay, to detect the presence of neutralizing antibodies. Sera collected within the first two weeks to approximately 31 days post-symptom onset were analyzed using these serologic assays to ascertain the kinetics of the MERS-CoV specific antibody response. **Results:** Within the two weeks post-symptom onset, antibodies to MERS-CoV were detected in sera from both patients by ELISA and IFA. The second patient had a four-fold increase in antibody titer while the first US patient had approximately a thirty-fold increase in titer by ELISA. The presence of neutralizing antibodies was detected in both cases two to three days after the initial detection of MERS-CoV antibodies by ELISA and IFA. Both anti-nucleocapsid antibody and neutralizing antibody titers were detectable up to 31 days post-onset of illness. **Conclusions:** These results highlight the importance of serological follow-up on all confirmed cases of MERS-CoV in order to increase our understanding of the antibody response kinetics following infection and underscore the significance of having well characterized detection as well as confirmatory assays.

Board 388. Measles Outbreak in Urban Slums of Lagos State, Southwestern Nigeria, April 2013

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Background: Measles is a leading cause of childhood morbidity and mortality in Nigeria. In April, 2013, a suspected measles outbreak was reported in 20 of the 57 Local Government Areas in Lagos State, Nigeria. We investigated the outbreak to identify the risk factors for the infection and to institute control measures. **Methodology:** We conducted an unmatched case control study. We defined a case as any person with fever and maculo-papular rash with any one of cough, coryza or conjunctivitis living in the affected communities from the 8th to 22th of April, 2013. A control was any person without the symptoms above in the same community. We recruited 200 hospital-based cases and 200 neighborhood controls. We used a semi-structured questionnaire to collect data on demographic characteristics and potential risk factors. We collected 5 blood specimens to identify measles IgM using ELISA technique. Data were analyzed with Epi-info version 7software. **Result:** A total of 218 cases and 1 death were recorded (attack rate 1.7%, case fatality rate 0.5%). Most of the cases (75%) were under five years of age. Males constituted 55 % (120) of cases. Most (78%) of the measles cases had not been immunized against Measles. All the 5 (100%) samples tested positive for Measles IgM. Cases were more likely than controls to be unvaccinated against Measles (AOR=9.4, 95% CI2.9-29.9), had contact with a suspected measles case (AOR= 4.3, 95%CI 1.5-12.8) and their caregiver was a farmer or laborer by profession (AOR=1.5, 95%CI 1.0-8.3). **Conclusion:** An outbreak of Measles occurred in Lagos State. Low Measles vaccination coverage contributed to the occurrence. There is need to strengthening routine and supplemental Immunizations in Lagos State. Selective vaccination of children from 9 months was done. **Keywords:** Measles, Disease Outbreaks, Case-control Studies, Lagos State, Immunization, Nigeria

Board 389. Hospital-based Quarantine for Ebola Virus Disease Contact Tracing at Fousseyni Daou Hospital — Kayes, Mali, 2014

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Background: On October 23, 2014, Mali announced its first case of Ebola virus disease (EVD) in a female, aged 2 years, who had traveled with 3 family members from Guinea to Kayes, Mali. CDC assisted the Malian government with rapid implementation of contact tracing, an integral part of EVD containment and active surveillance. **Methods:** Regional authorities identified the patient's contacts, including family members, friends and other pediatric patients and their caregivers, and health care workers. Because of concern for the contacts' safety and to ensure rapid detection and isolation of secondary cases, the government quarantined 52 (66%) of 79 Kayes contacts at Fousseyni Daou Hospital for 21 days; the remaining 27 contacts were monitored in their communities. The contacts' temperatures and health status were assessed twice daily by hospital and district health office staff. Epi Info™ VHF was used to track contacts. The hospital and other EVD-responding partners provided quarantined contacts with food and other basic necessities. **Results:** Among the 52 quarantined contacts, 29 (56%) were female; median age was 26 (range: 0.3-69) years. All 52 contacts complied with twice-daily assessments throughout the quarantine period. No secondary

EVD cases occurred. Challenges included provision of resources to support quarantined contacts, concerns among contacts related to their quarantine status, and coordination of contact tracing activities between hospital, district, and national authorities. In addition, concern existed that new contacts in Mali might hide or deny contact status because of fear of being quarantined. **Conclusions:** In situations with small case and contact numbers, quarantining contacts in 1 location can be an alternative to community-based contact tracing. However, quarantine creates substantial challenges that should be considered before implementation.

Board 390. Outbreak of Odyssean Malaria, Gauteng Province, South Africa, January 2015

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Background: In South Africa, malaria is a notifiable disease. KwaZulu-Natal, Mpumalanga and Limpopo are the malaria endemic provinces. Since 1996, Gauteng, a non-malaria endemic province, has had an increase in reported odyssean patients, defined as any person with laboratory-confirmed malaria antigen and no relevant travel history, recent blood transfusion or recent receipt of an injection. We describe an investigation of a reported patient of odyssean malaria in Gauteng Province in January 2015. **Methods:** The patient and family were interviewed. Environmental, entomological and laboratory investigations were conducted. **Results:** On 8 January 2015, an 11 year old female from Protea Glen, Johannesburg, presented to a general practitioner with fever, night sweats, weakness and loss of appetite. At hospital admission, she had no reported history of injections, transfusions, travel to or interactions with persons from a malaria endemic area. Blood cell and platelets counts, kidney and liver function tests were all normal. Malaria smear was positive for parasites (9%) and P. falciparum antigen was identified. The patient improved after receiving antimalarial medication and was discharged after five days of treatment on 13 January 2015. A visual residential inspection on 14 January 2015 revealed no mosquitoes. No vector breeding sites were identified in the surrounding area. The residence is 500 meters from a major highway and location of a busy filling station frequented by trucks and taxis. No additional patients were reported in the vicinity. **Conclusion:** This patient likely acquired malaria from an infective mosquito inadvertently translocated from a malaria endemic area. No specific vector control interventions were recommended after the investigation. Health-care providers in Gauteng Province should remain vigilant for odyssean malaria and provide early treatment for laboratory-confirmed malaria.

Board 391. Mobile IT Supporting Contact Tracing in the Ebola Outbreak Surveillance and Outbreak Response Management and Analysis System (SORMAS) to Support the Control of Epidemic-prone Diseases

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Background: The control of infectious disease outbreaks such as Ebola Virus Disease (EVD) requires timely and efficient implementation of various measures, such as validation of suspect cases and follow-up of exposed contact persons. This can be supported by immediate bidirectional information exchange and enhanced coordination of control measures between the health authorities at all levels. In order to address these objectives, we developed a comprehensive surveillance and outbreak response management and analysis system (SORMAS) that includes mobile applications and is designed after the need of field officers involved in EVD outbreak response in Nigeria 2014. **Methods:** We applied the Design Thinking approach to analyze processes and user-specific needs based on the experiences of the Nigerian Ebola Emergency Operation Center (EOC). The SORMAS system architecture follows a cloud-based approach applying In-Memory Database (IMDB) technology. All data exchange is encrypted using latest web standards, e.g. HTTPS protocol. The user interface consists of specific front-ends for smartphones and tablet devices, which are independent from physical configurations. **Results:** We identified and defined seven user types. The overall EVD-process model comprises 59 elements (data artifacts, process activities, etc.) connected by 58 edges representing process, data, and information flows. This main process model encapsulates another 6 sub-processes. Of these, the largest one describes the contact tracing process and comprises 94 elements connected by 110 edges, and again encapsulates another sub-process of smaller size. First prototype tests took place in Nigeria in March 2015. A field pilot will take place in April and May 2015 in two Nigerian states, with an exercise simulating the EVD outbreak generated by an agent based model. In addition, SORMAS will be piloted for avian influenza (e.g. H5N1), measles and cholera with real cases occurring during the pilot phase. Results of the systematic evaluation of the pilot will be presented. **Conclusions:** SORMAS allows real-time, bidirectional information exchange between health care workers and an EOC, assures quality management and coordination of control measures, generates automated status reports, and geo-references cases and contacts. It has the potential for becoming a generic systematic tool for surveillance and outbreak management for any epidemic-prone diseases.

Board 392. Diarrheal Illness Outbreak in Siyanda District, Northern Cape Province, South Africa, 2013

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Background: An increase in diarrhoea affecting mostly children <5-years was reported at Siyanda District public hospital in April 2013, including four deaths. An investigation was requested to identify the causative agents and possible sources, and to implement prevention and control interventions. **Methods:** A descriptive cross-sectional study was conducted. Patients presenting at healthcare facilities in Siyanda District with diarrhoea with/without vomiting during 26 April -7 July 2013 were line-listed. Stools and water samples were collected. Enteric pathogens diagnosis was carried-out using reverse-transcription polymerase chain reaction (RT-PCR); real-time RT-PCR; genotyping; electron microscopy (EM); microscopy, culture and sensitivity. **Results:** 953 cases of diarrehoal illness were recorded, with 58% (553/953) being children <5-years. There

were 0.71% (6/847) diarrhoea-associated deaths in children <2-years. Of the 88 stool samples tested, rotavirus was detected in 43% (38/88). Other viruses were detected in 21.5% (19/38); of these 63.1% (12/19) had rotavirus co-infections. The predominant rotavirus-strains detected were G3P[8] 44.7% (17/38), G9P[8] 42.1% (16/38), G2P[6] 10.5% (4/38), and G1P[8] 2.6% (1/38). Rotavirus was detected on EM. Bacteria were detected in 26.2% (16/61); 37.5% (6/16) had rotavirus co-infection. Non-Typhi Salmonella was detected in 11.5% (7/61) and diarrhoeagenic E. coli species in 8.2% (5/61). Parasites were detected in 15% (3/20) of the samples. No pathogens were found in water samples. **Conclusion:** Rotavirus was the predominant pathogen found in this investigation however, other diarrhoeagenic organisms were also identified. Although rotavirus vaccination status of the cases were unknown, the rotavirus vaccine introduced in South Africa in August 2009, reportedly provides cross-protection against the strains detected in this outbreak from hospitalization and adverse outcomes. In future diarrhoeal outbreaks, risk factor analyses for severe diarrhoea outcomes and rotavirus vaccination data collection should be performed.

Board 393. Crimean Congo Hemorrhagic Fever, Sudan, 2013 and 2014

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Background: The German Partnership Program for Excellence in Biological and Health Security was launched in 2013 and is funded by the German Federal Foreign Office. Currently, the program funds projects in 18 countries in the fields of infectious disease surveillance, detection & diagnostics, biosafety & biosecurity, capacity building and networking. In Sudan one focus of the partnership is the detection of highly pathogenic viruses and identification of known and yet unknown etiological agents in outbreak situations. In 2014 an outbreak of hemorrhagic fever in humans was reported from different states of Sudan (South Darfur, West Kordofan, South Kordofan). The NPHL investigated the cases and forwarded 29 sera samples from patients suffering from hemorrhagic fever to the RKI. **Methods:** The sample-set included a panel of 10 sera collected during former hemorrhagic fever outbreaks in the same region in 2013. All sera were tested with qPCR assays for Marburg virus, Ebola virus and CCHFV. Additionally all samples were subjected to metagenomic deep sequencing on an Illumina MiSeq sequencer. **Results:** CCHF was identified by two independent qPCR assays in a sample from November 2013 and November 2014, respectively. Deep sequencing confirmed these results. Based on the available sequences the novel CCHFV strain 'Sudan 2014' shares 96% identity (na) with its closest relative CCHFV SPU 187/90 from South Africa. **Conclusions:** CCHFV is reported to be transmitted by ticks in Europe, Asia and Africa and known as etiological agent of severe hemorrhagic fever in humans and livestock. Beside insect-repellent no preventive measures are available. The pathogenicity and characteristics of this novel strain have yet to be determined. We started with cell-culture isolation attempts and CCHF serology for IgG and IgM in the remaining sera. Further molecular analysis and phylogeny will contribute to clarify divergence of the CCHFV strains detected in 2013 and 2014. First results will be presented.

Board 394. Cluster of Ebola Viral Disease Linked to a Single Funeral Event—Sierra Leone, 2014

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Background: As of 15 March 2015, 11,751 cases (72% confirmed) of Ebola and 3,691 related deaths have been reported in Sierra Leone. During September 2014, a sudden increase of Ebola cases occurred in Moyamba, a rural and previously low-incidence district. We investigated to determine the source and risk factors, and recommend prevention and control measures. **Methods:** We conducted a retrospective case-series analysis of laboratory-confirmed Ebola cases in Moyamba. Interviewers completed standardized forms with patients or proxies regarding potential exposures during one month before illness onset, including contact with suspected cases, corpses, or ill persons, funeral attendance, and hospital or traditional healer visits. **Results:** Among 281 suspected case-patients investigated during July 11-October 31, 2014, 109 (39%) were confirmed positive; 37% (40/109) of whom died. Median age was 30 (range: 11 months-84) years; 59% were male. Seventy-eight (72%) of the confirmed case-patients reported contact with an ill person, 42 (39%) attended a funeral, 36 (33%) touched a corpse, and 8 (7%) visited a hospital or traditional healer. Incidence peaked the week of September 13-19 (32 confirmed cases). Twenty-eight confirmed case-patients attended the same pharmacist's traditional funeral September 5-7 and developed symptoms a median of 9 (interquartile range: 7-12) days afterwards; 8 died. Case fatality was significantly higher among men attending his funeral (44% vs 0%, p=0.02). Of pharmacist funeral attendees, 57% had contact while he was ill; 75% touched his corpse. Contact with pharmacist funeral attendees led to 8 known additional confirmed cases. Alerted to this funeral, the District Health Management Team implemented rapid, localized response measures, including door-to-door active surveillance, neighborhood watch, quarantine, prompt isolation and treatment of case-patients, and safe burials by trained teams. **Conclusions:** A traditional funeral led to a sharp increase in Ebola cases, highlighting the potential for high levels of transmission from a single event. A higher case fatality rate among men may be explained by more intense contact with the corpse. Response measures likely reduced ongoing transmission. To achieve zero new infections, enhanced community-based surveillance strategies are critical to quickly identify high-risk events and prevent transmission.

Board 395. Evaluation of the Timeliness of Enteric Disease Surveillance: Is Achieving the Benchmark Good Enough?

E. Galanis[1], M. Taylor[1], K. Romanowski[1], J. Stone[2], J. Jeyes[3], O. Bitzikos[4], G. Tone[5], C. Nowakowski[6], A. Paccagnella[7], S. Forsting[4], S. Li[1], M. Murti[2], L. Hoang[1,7]; [1]British Columbia Ctr. for Disease Control, Vancouver, BC, Canada, [2]Fraser Hlth. Authority, Surrey, BC, Canada, [3]Interior Hlth. Authority, Vernon, BC, Canada, [4]Vancouver Coastal Hlth., Vancouver, BC, Canada, [5]Northern Hlth. Authority, Prince Georges, BC, Canada, [6]Island Hlth., Victoria, BC, Canada, [7]British Columbia Publ. Hlth. Microbiol. and Reference Lab., Vancouver, BC, Canada

Background: Timely surveillance of enteric diseases is necessary to identify and control outbreaks to prevent further transmission. Measuring the time from onset of illness to reporting of cases to public health (PH) authorities in a consistent way can improve understanding of the process and identify steps requiring improvement. This study aimed to evaluate the timeliness of enteric disease surveillance in British Columbia (BC), Canada. **Methods:** Date information on 1808 cases of Salmonella (N=1303), Shiga-toxin producing E. coli (STEC) (N=227), Shigella (N=213) and Listeria (N=15) infections in 2012-13 in BC were collected from PH and laboratory forms and databases. The time

period between each step in the investigation of a case was calculated from onset to PH interview and from onset to final lab diagnosis reported to PH authorities (pulsed field gel electrophoresis or PFGE). Median and ranges were derived. Results were compared to international benchmarks. **Results:** There was a median of 11-14d (range 2-168d) from onset to PH interview. The longest interval for Salmonella, Shigella and Listeria was from onset to sample collection (median 3-7d); the longest interval for STEC was from sample collection to PH receipt of first lab report (median 5d). There was a median of 0-1d (range 0-62d) from PH receipt of lab report to interview which is comparable with US Foodcore metrics (median 0.6-1d). There was a median of 27-36d (range 13-179d) from onset to PFGE report to PH. The longest interval for all pathogens was from PFGE run to PFGE report to PH (median 8-10d). The median time from specimen receipt by the provincial lab to PFGE run is 8-10d which is comparable with US Foodcore metrics (median 6-11d from specimen receipt to PFGE upload). **Conclusions:** It takes approximately 2 weeks from onset of illness to obtain epidemiological information from a case with a reportable enteric disease and approximately 1 month to obtain complete isolate subtyping. Our findings are similar to US benchmarks but may be too long to allow timely detection of outbreaks. Improving modifiable intervals should improve our ability to identify and solve outbreaks.

Board 396. Data Management in the West Africa Ebola Outbreak—Lessons Learned from Piloting a New Software Tool

I. J. Schafer, L. A. McNamara, E. Knudsen, P. E. Rollin, A. Islam; CDC, Atlanta, GA, USA

Background: The Epi Info Viral Hemorrhagic Fever (VHF) Application was developed in 2013 as a solution to challenges experienced managing outbreak data during four 2012 filovirus outbreaks. The main goals of development included joining case and contact data in a single database; automating the determination of which contacts need tracing each day; and improving the consistency and effective use of outbreak case and contact data. **Methods:** The Epi Info VHF application was first deployed to the field in Guinea in March, 2014 in response to the ongoing West Africa Ebola outbreak. The application has since been used in Liberia, Sierra Leone, Nigeria, Mali, Senegal, Uganda, and two U.S. states. Development to improve and adapt the application to West Africa's needs has been ongoing; key improvements include adding capabilities for multi-user data entry and for merging databases from different locations at a central level. **Results:** Within two days of deployment in Guinea, the application was being used to direct and report contact tracing activities in Conakry; within one week, a centralized case database had been established and was used to generate daily country situation reports. Other countries have used the application in varying ways: centralized versus decentralized, and for case data with or without contact data. **Conclusions:** Overall, the Epi Info VHF application has enabled compatible case data from multiple West African countries to be reported at the international level and has improved the accuracy and organization of contact tracing in several locations where the contact tracing features were utilized. However, challenges have been encountered accommodating country-specific needs within a single software product, coordinating data management efforts among international response agencies, and using the application in low-resource settings with limited internet access and IT support. The use of the Epi Info VHF application in the ongoing outbreak highlights the fundamental importance of good data management in ensuring high quality, actionable data, regardless of the software in use. Consistent data collection and flow between different outbreak response components, clear communication and collaboration among response partners, and training of skilled data managers are essential to maintaining high quality data that can guide a successful outbreak response.

Board 397. Explosive Post-disaster Diarrhea Outbreak in the Solomon Islands, April–June 2014

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Background: Extreme weather events can precipitate epidemic transmission of diarrhea. We describe a nationwide diarrhea outbreak following a flash flood disaster in the Solomon Islands in the Western Pacific. **Methods:** The Early Warning and Response Network surveillance system (EWARN) detected an outbreak of diarrhea on April 20th 2014 in the capital city of Honiara and Guadalcanal province. We conducted retrospective review of outpatient registrars in health facilities nationwide to identify cases prior to and during the outbreak. A public adverse event system was utilized to identify diarrhea-related deaths. Hospital laboratory testing results for diarrheal pathogens were collected. **Results:** During the outbreak period from April 5 to June 29, 2014, we identified 6,361 cases of diarrhea in the Solomon Islands (pop., 578,740). The majority of cases (62%) were reported from Honiara where the mean weekly incidence rate increased from 1.75 to 4.81 cases per 1,000 population before (June 2013 to March 2014) and during the outbreak, respectively. The highest attack rates (288 cases per 1,000 population) occurred among children <5 years of age. Although flooding was limited to Honiara and Guadalcanal, multiple other areas and islands had significant increases in case numbers of diarrhea starting four weeks after the start of the outbreak in Honiara. Rotavirus was identified as the causative agent in 27/54 (50%) cases tested. In total, 27 children died due to diarrhea related causes, which exceeded the 23 deaths directly attributed to the flash flood emergency. **Conclusions:** Our findings indicate that a disaster caused a large nationwide epidemic of diarrhea and included islands unaffected by the initial flash flood event. Although laboratory testing was limited, rotavirus appears to be an important pathogen in this outbreak. Childhood immunization with rotavirus vaccine may be an important intervention to mitigate the potential health impact of extreme weather events, events that are predicted to increase in severity due to climate change.

Infectious Diseases and Policy Implications

Wednesday, August 26, 12:30 PM - 1:45 PM
Grand Hall

Board 398. Effectiveness of the Influenza Vaccine Against Laboratory-confirmed Influenza in Young Children Using a Test-negative Design in Bangkok, Thailand, 2013-2014

W. Kittikraisak[1], P. Suntarattiwong[2], D. Ditsungnoen[1], S. Fernandez[3], I-K. Yoon[3], K. Lindblade[1,4], F. S. Dawood[4], S. J. Olsen[4], T. Chotpitayasunondh[2]; [1]Thailand Ministry of Publ. Hlth.–US CDC Collaboration, Nonthaburi, Thailand, [2]Queen Sirikit Natl. Inst. of Child Hlth., Bangkok, Thailand, [3]Armed Forces Res. Inst. of Med. Sci., Bangkok, Thailand, [4]CDC, Atlanta, GA, USA

Background: The Thai Advisory Committee on Immunization Practices recommends annual influenza vaccination for children aged 6 to <36 months. We evaluated effectiveness of the 2013 Southern Hemisphere inactivated influenza vaccine in children aged 7-60 months in Bangkok using a test-negative design. **Methods:** From September 2013-May 2014, children with influenza-like illness (ILI) seeking care at Queen Sirikit National Institute of Child Health were screened with a rapid influenza test. Each child with a positive test and the next two children with ILI in the same age group (7-24 and >24-60 months) with negative results were enrolled and had a combined nasal and throat swab tested for influenza using real-time reverse transcription polymerase chain reaction (rRT-PCR). Cases were subjects testing positive for influenza by rRT-PCR. Using the vaccination card as the data source, vaccination was defined as receiving two vaccine doses (≥28 days apart) in the 2013-2014 season or two doses (≥28 days apart) in any previous season and one dose in the 2013-2014 season. Vaccine effectiveness (VE) was estimated as (1- odds ratio)*100% derived from logistic regression controlling for confounders. **Results:** Of 541 children enrolled (200 cases and 341 controls), 235 (43%) were 7-24 months old, 306 (57%) were >24-60 months old, 301 (56%) were male and 77 (14%) had ≥1 underlying medical condition. Among cases, 78 (39%) were positive for A(H1N1)pdm09, 66 (33%) for A(H3N2) and 56 (28%) for influenza B. Overall vaccine coverage was 8%, with 4% of cases and 10% of controls vaccinated. Vaccine coverage was higher in children with medical conditions than in healthy children (17% vs. 6%; p<0.01). After adjusting for medical condition and age, VE against: all circulating viruses, 63% (95% CI 18%, 83%); A(H1N1) pdm, 77% (95% CI 1%, 95%); A(H3N2), 58% (95% CI -28%, 93%); and influenza B, 35% (95% CI -94%, 78%). Virologic surveillance data showed >80% of circulating influenza B strains matched the lineage in the vaccine. **Conclusions:** Although vaccination among children aged 7-60 months was moderately effective against medically-attended, laboratory-confirmed influenza, vaccination coverage in this population is low. Strategies to increase vaccination coverage should be implemented among young children in Thailand.

Board 399. Anatomy of a Shigellosis Outbreak: Treatment Policies and Implications for Antibiotic Resistance—Central Indiana, 2014

S. J. Feinman[1,2], T. Gorden[3], M. Hoyt[4], S. Richards[3], J. Brown[3]; [1]Council of State and Territorial Epidemiologists, Atlanta, GA, USA, [2]Indiana State Dept. of Hlth., Indianapolis, IN, USA, [3]Indiana State Dept. of Hlth., Surveillance and Investigation Div., Indianapolis, IN, USA, [4]Indiana Univ. Fairbanks Sch. of Publ. Hlth., Indiana Univ.-Purdue Univ., Indianapolis, IN, USA

Background: Shigellosis is an acute gastrointestinal illness caused by the bacteria *Shigella*. Due to the self-limiting nature of mild illness and emergence of antibiotic resistance among *Shigella* spp., antibiotic therapy is only recommended for severe cases. In March 2014, a large outbreak of shigellosis among daycare and school attendees began in central Indiana. The current state Communicable Disease Rule (CDR) excludes shigellosis patients from attending daycare or school until they meet antibiotic treatment requirements or provide two successive negative stool tests. This policy encourages the use of antibiotic therapy for mild cases and is inconsistent with current treatment recommendations. **Methods:** Demographic and clinical data were obtained from 1,051 outbreak-associated shigellosis cases meeting the confirmed or probable criteria in the national surveillance case definition. Cases with a self-reported onset date between March 1, 2014 and December 31, 2014 were included in the analysis. Characteristics, including antibiotic prescribed, of severe cases (defined as symptoms of bloody stool and/or fever) were compared to those of mild cases. **Results:** The majority of individuals in the outbreak were aged ≤ 9 years (71%) and 88% of all cases were treated with antibiotics. Treatment status did not vary based on severity of symptoms; 368 of 427 (86%) mild cases and 555 of 624 (89%) severe cases were treated with antibiotics. The majority of cases (57%) were prescribed azithromycin. Amoxicillin, which is not recommended for treating shigellosis, was prescribed for 7% of cases. Length of antibiotic treatment for all antibiotics averaged 4.6 days (maximum: 13 days). Early susceptibility patterns showed resistance to sulfa drugs; later resistance patterns show a combined resistance to sulfa drugs and azithromycin. **Conclusion:** Most mild cases in this outbreak were treated with antibiotics in order to comply with current state daycare and school exclusion policies. Policies which encourage antibiotic treatment may increase emergence of antibiotic resistance. The state of Indiana is currently revising the CDR exclusion policy to correspond with national treatment recommendations and minimize selection pressure for antibiotic resistance.

Board 400. Risk Factors for *Vibrio parahaemolyticus* Infection in Southern Coastal Region of China

S. Wu[1], Y. Liao[2], Y. Li[2], J. Mou[2], Z. Xu[3], R. Cui[3], J. Klena[1], X. Shi[2], Y. Lu[2], Y. Qiu[2], Y. Lin[2], X. Xie[2], H. Ma[2], J. Cheng[2], J. Varma[1], L. Ran[4], Q. Hu[2]; [1]CDC, Beijing, China, [2]Shenzhen Ctr. for Disease Control and Prevention, Shenzhen, China, [3]Xixiang people's Hosp., Shenzhen, China, [4]Chinese Ctr. for Disease Control and Prevention, Beijing, China

Background: *Vibrio parahaemolyticus* (VP) is one of the most common causes of foodborne infection in China, especially in coastal regions. Even though VP infection is common and serious, few studies have systematically analyzed risk factors of cases in China. The objectives of the study were to identify dietary and medical risk factors for VP infection in the coastal city Shenzhen in China. **Method:** VP is one of the most common pathogens isolated from diarrhea patients in Shenzhen. We enrolled eligible case patients with VP infection from two hospitals that accounted for the largest proportion of VP cases in Shenzhen in a case-control study from April to October 2012. Control subjects were recruited through the community clinics among these who come for medical check-up and were matched to case-patients by gender, age and location. Data were collected about medical history of the patient; contact with sea water; clinical symptoms and outcome; travel history over the past week; dietary history over the past 3 days

involving around 100 potential exposures. Controls were asked about the same questions about the same time window. **Results:** Of the 500 patients with diarrhea submitted for stool culture in the two hospitals, 83 were confirmed as VP infection and enrolled in the study. Serotype O3:K6 was found to be the most common serotype. We enrolled 249 controls. In multivariate analysis, VP infection was associated with having preexisting chronic disease (odds ratio, 6.1; 95% confidence interval, 1.6-23.8), eating raw (undercooked) meat or seafood (odds ratio, 14.6; 95% confidence interval, 3.6-59.9), having food from a street food vendor (odds ratio, 7.4; 95% confidence interval, 3.2-17.3), and eating vegetable salad (odds ratio, 12.1; 95% confidence interval, 5.2-28.2). **Conclusion:** VP infection is an important enteric pathogen in Shenzhen, China. Reducing the burden of VP infection may require better education to public about risks of undercooked seafood and meat and the risks of cross-contamination, especially targeted at people with low income, transient workers, and people with medical risk factors. It is also necessary for the regulatory agency to issue guidelines for cooking food and guidelines for hand hygiene in the kitchen to prevent cross-contamination of ready-to-eat foods with uncooked seafood or meat.

Board 401. Epidemiological and Etiological Characteristics of Hand, Foot, and Mouth Disease in Henan, China, 2008-2013

X. Huang[1], H. Wei[1], S. Wu[2,3], Y. Du[1], L. Liu[4,5], J. Su[1], Y. Xu[1], H. Wang[1], X. Li[1], Y. Wang[1], G. Liu[1], W. Chen[4,5], J. Klena[2,3], B. Xu[1]; [1]Henan Ctr. for Disease Control and Prevention, Zhengzhou, China, [2]Intl. Emerging Infections Program, CDC, Beijing, China, [3]Global Disease Detection Branch, Div. of Global Hlth. Protection, Ctr. for Global Hlth., CDC, Atlanta, GA, USA, [4]State Key Lab. of Pathogens and Biosecurity, Inst. of Microbiol. and Epidemiology, Academy of Military Med. Sci., Beijing, China, [5]Key Lab. of Genome Sci. and Information, Beijing Inst. of Genomics, Chinese Academy of Sci., Beijing, China

Background: Hand, foot, and mouth disease (HFMD) is a common infectious disease of global concern mainly occurring in children aged <5 years. In China, incidence of reported cases of HFMD has sharply increased and more than 7 million cases have been reported, including approximately 2500 fatal cases, since the initiation of national surveillance for HFMD in 2008. Henan is one of the provinces most affected by HFMD in China. The objectives of this study were to investigate epidemiological and etiological characteristics of HFMD in Henan Province from 2008 to 2013. **Methods:** Epidemiological and clinical data of all HFMD cases reported in Henan Province were collected from January 2008 to December 2013; laboratory testing data was available for a subset of these cases. Descriptive epidemiological methods were used to analyze the time, region and population distribution and etiology of HFMD. A retrospective space-time scan statistic was applied to detect high risk clusters of HFMD cases based in a discrete Poisson model. The complete VP1 gene sequences from human enterovirus 71 (EV71) and coxsackievirus A16 (CA16) isolates was amplified by reverse transcription Polymerase Chain Reaction (RT-PCT), and the sequences were analyzed by bioinformatics software. **Results:** A total of 400,264 cases of HFMD were reported in Henan Province from 2008 to 2013, including 22,309 severe and 141 fatal cases. The annual average incidence rate was 70.9 per 100,000. Of reported cases, 94.5% were in children less than 5 years old, and the sporadic cases accounted for 81.8%. Incidence peaked between April and May. The spatio-temporal clusters of HFMD cases were mainly detected in northern central Henan Province. Infection was laboratory-confirmed in 27,692 (6.9%) cases of HFMD; EV71, CA16, and other enteroviruses accounted for 59.5%, 14.1%, 26.4%, respectively. Severe HFMD cases and deaths were mainly caused by EV71 infection. Phylogenetic analysis revealed that EV71 isolated from HFMD patients belonged to the C4a evolution branch of C4 sub-genotype and CA16 belonged to subtype B1a or B1b. **Conclusion:** The occurrence of HFMD in Henan Province was associated with season, age and regional distribution. Children under five were the most affected population. The major pathogens causing HFMD and their genotypes have not notably changed in Henan Province.

Board 402. Lyme Disease Surveillance in New York State: An Assessment of Patient Underreporting

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Background: Despite the mandatory nature of Lyme disease (LD) reporting in New York State (NYS), it is known that only a fraction of the LD cases diagnosed annually are reported to public health authorities. Lack of complete LD case reporting generally stems from 1) lack of report of physician-diagnosed LD cases where supportive laboratory testing is not ordered or negative (physician underreporting) and 2) positive laboratory reports only with no accompanying clinical information such that cases are considered suspect and not included in case counts (case misclassification). In an attempt to better ascertain the degree of LD underreporting in NYS, including physician underreporting and case misclassification, a two-part study was conducted in 2011 using LD surveillance data from three upstate counties. **Methods:** NYS Department of Health (NYSDOH) staff conducted LD surveillance in three counties, investigating all positive laboratory reports and all physician-reported cases. To assess case misclassification, medical records were requested on all suspect cases and cases were reclassified according to the national surveillance case definition. To assess physician underreporting, select medical providers provided NYSDOH staff with lists of patients for whom ICD-9-CM code 088.81 (LD) had been used for billing purposes. Lists were matched to the NYSDOH communicable disease case reporting system and medical records were requested on patients not previously reported. Cases were then classified according to the national surveillance case definition. **Results:** Study results indicate that there were approximately 20% (range 18.4-24.6%) more LD cases in the counties under study than were originally reported when including both case misclassification and physician underreporting. Unreported cases were more likely to have a history of erythema migrans (EM) rash with no accompanying laboratory testing (Fisher's exact, $p<0.0001$) and were more likely to be pediatric cases aged 0-10 years (X^2, $p<0.05$). **Conclusions:** Although limited to only one ICD-9 code, results of the study support the assertion that LD cases are underreported in NYS. Initiatives to increase reporting should highlight to providers the importance of reporting clinically diagnosed EM, particularly among providers diagnosing pediatric patients.

Board 403. Knowledge, Attitude and Practice Related to Malaria Inflections Among Liberian Armed Forces at Camp Edward Binyah Kesselly, Liberia

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Introduction: To reduce malaria morbidity/mortality it is important to evaluate compliance to standardized preventative measure practices. High prevalence of malaria among members of the Liberian Armed Forces (AFL) at Camp Edward Binyah Kesselly (EBK) threatens force health protection. Understanding culture and risk behaviors is crucial to enhance malaria prevention plans and help to protect both military

personnel during their deployment and the AFL personnel. Herein, we assess the knowledge and attitudes towards preventive methods as well as treatment-seeking behaviors with the goal to develop a knowledge base of current practices to improve malaria prevention measures and awareness. **Method:** A cross-sectional, self-reported survey was conducted during the last week of March 2014 at Camp Edward Binyah Kesselly. A team consists of a well-trained AFL personnel and NAMRU-3 study principal investigator introduced study objectives and methodologies to enrollees who agreed to participate in the study. **Results:** A total of 572 questionnaires were collected from the AFL, and analysis was conducted on 365 entries. The majority were males, grades E1 - E4, high school education and with median age 34 years. Seventy eight percent reported at least one episode of malaria during the previous year. One-hundred and seventy-four (48%) reported owning bed nets; however only 59% reported using nets on a daily basis. Overall 56% of the personnel were aware of at least three personal protective measures and 66% reported using topical repellents. Forty-seven percent were in need of additional information regarding malaria treatment and prevention or had little knowledge regarding malaria. **Discussion:** Our analysis indicates that a significant number of participants lacked knowledge about the disease. This represents a gap that may contribute to the high prevalence of malaria despite the availability of personal protection measures. Achieving an understanding of the military members' knowledge and concurrent practices regarding preventive measures are essential for a successful malaria control programs.

Board 404. Comparative Analysis of Culture-confirmed and Culture-independent Tests for Enteric Infections in Georgia, 2011-2013

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Background: Since 2011, culture-independent diagnostic testing (CIDT) for enteric infections has increased in Georgia (GA). The number of patients diagnosed by CIDT increased from 246 in 2011 to 542 in 2013. CIDT methods include Enzyme Immunoassay (EIA) and Polymerase Chain Reaction (PCR); test performance and specimen submission to Public Health Laboratories vary. Cases of *Campylobacter*, Shiga toxin-producing *Escherichia coli* (STEC), *Salmonella*, *Shigella*, *Vibrio*, and *Yersinia* tested by culture and CIDT are identified by active surveillance conducted by the GA Department of Public Health (GDPH) through the Foodborne Diseases Active Surveillance Network. The impact of differential patient testing on the epidemiology of these infections has not been assessed. **Methods:** Demographics and hospitalization status of GA patients infected with *Campylobacter*, STEC, *Salmonella*, *Shigella*, *Vibrio*, and *Yersinia* tested by culture, CIDT, and both methods were compared from 2011 to 2013. **Results:** From 2011 to 2013, 13,699 infections were reported to GDPH. 11,939 (87%) were diagnosed by culture only; 1,244 (9%) were diagnosed by CIDT only; and 516 (4%) were diagnosed by both culture and CIDT. 3,142 (26%) patients diagnosed by culture only and 377 (31%) patients diagnosed by CIDT only were hospitalized; 2,156 (18%) of patients diagnosed by culture only and 93 (8%) of patients diagnosed by CIDT only visited the emergency room (ER). Fifty-two percent of cases (n=649) diagnosed only by CIDT reside in northwest and southeast GA. There were no differences in race, ethnicity, and gender among patients tested by culture versus CIDT. *Campylobacter* and STEC were most often identified by CIDT, accounting for 62% and 14% of CIDT-only diagnoses respectively. Approximately 70% of CIDT diagnoses were EIA tests and the other 30% were PCR tests. **Conclusions:** CIDT use has rapidly increased in GA but adoption varies geographically. A large number of hospitalized patients are being diagnosed using CIDT, which may result in quicker treatment, but may limit GDPH's ability to conduct epidemiologic investigations and identify outbreaks. GDPH should monitor differences in CIDT testing among inpatients versus ER patients to characterize the impact on disease trends.

Board 405. Evaluation of Control and Prevention Measures for Visceral Leishmaniasis Using Mathematical Model

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Background: Visceral Leishmaniasis (VL) is a zoonosis with serious public health impacts. In some regions of Brazil the disease is spreading. In that country the transmission of VL is influenced mostly by human, dog, and vector populations. Through mathematical modeling it is possible to understand its complex interactions. The aim of this study was to understand how the different control and prevention measures could influence the hosts prevalences, using a mathematical model. **Methods:** We used an adapted VL mathematic model to simulate the use of vaccine in dogs and the dogs culling, according to different animal coverages. We also evaluated the sensitivity of the model, varying parameters (associated to the vector and hosts relationship) individually. At least, we assessed the impact generated in the prevalences of host populations. **Results:** The use of euthanasia was more effective than the vaccine, at the same coverages. These two parameters reduced significantly the prevalence of VL in both dog and human populations, especially when applied in high coverage of animals, but they were not able to eliminate the disease. The parameters related to the vector-dog contact (density of vector per dog and diary rates of bites on dogs) changed significantly both the dog and human prevalences. The parameters as density of the vector per human and diary rate of bites on humans resulted as the same, interfering slightly only in the human population. The vector mortality had low influence on both dog and human prevalences. **Conclusions:** The use of vaccine and dogs culling are good ways to control the disease if used in a high animal coverage. The variation of the parameters suggests that effective control measures are the ones that directly affect the vector-dog contact, as insecticide-impregnate collars. The use of insecticides around households interferes mostly on the vector mortality, a parameter that doesn't causes a significant decreasing on the hosts prevalence. The measures that are associated to the vector-human contact, as repellent spray, showed to be useful to prevent the diseases in humans but are not effective in blocking the VL dynamic. The evaluation of the effectiveness of control measures and the disease dynamics allow analysis of the alternatives to be implemented and assist in the development of political projects.

Role of Health Communication

Wednesday, August 26, 12:30 PM - 1:45 PM
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Board 406. The Impact of a Behavior Change Communication Intervention to Prevent Nipah Virus Transmission in Bangladesh

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Introduction: Human Nipah virus (NiV) infection is a fatal disease in Bangladesh caused by drinking raw date palm sap contaminated by *Pteropus* bats. Our study tested the effectiveness of a behavior change communication intervention to prevent NiV transmission. **Methods:** We conducted the intervention in two areas using interpersonal communication, community mobilization, print and TV during the 2012-2014 sap collection seasons. In one area, we disseminated a "do not drink raw sap" message and in the other, an "only safe sap" message. Both messages discouraged drinking sap but in the second area, we offered the option of drinking sap protected by a skirt-like barrier to stop bats from accessing the sap during collection. We encouraged sap harvesters to use skirts. We conducted baseline and endline surveys in both intervention and in a control area to measure sap consumption practices and skirt usage. In all areas, we observed raw sap consumption while harvesters were selling sap during the intervention. **Results:** Respondents' knowledge about NiV increased in the "no raw sap" (26%, p< 0.001) and "only safe sap" (24%, p< 0.001) area more than in the control area (1%). The proportion of respondents who reported raw sap consumption decreased by 24% in the "no raw sap" area, 16% in the "only safe sap" area and 9% in the control area. The reported decrease in consumption in the control area was mainly due to unavailability of sap. Observers noticed a larger decline on sap consumption in the "no raw sap" area (24%) than in the control area (8%) during the 2012-2014 sap collection seasons (p< 0.01). In the "only safe sap" area, skirt-protected raw sap consumption among community residents who reported drinking raw sap increased 40%, p < 0.001, and in the control area just 1%. Use of skirts by harvesters also increased 79%, p< 0.001 in the "only safe sap" area and decreased 9 % in the control area. **Conclusion:** Our interventions increased knowledge about NiV, the use of skirts and skirt protected sap and decreased raw sap consumption. Both interventions could be considered for future dissemination based on availability of resources.

Board 407. Chinese Social Media Reaction to Information About 42 Notifiable Infectious Diseases

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Background: Social media are increasingly used in health communication and digital epidemiology. We intend to identify what news or information trigger social media users' response regarding infectious diseases. **Methods:** Weibo contents in 2012 regarding 42 infectious diseases were obtained through a keyword search in the Weiboscope database (University of Hong Kong). Keywords were specified for each notifiable disease in China. Qualitative content analysis was performed for Weibo data of the highest peak (daily count). Similar posts were grouped and coded. **Results:** We identified five categories of information that increased Weibo traffic pertaining to infectious diseases: news of an outbreak (cholera, hepatitis C, influenza A(H1N1) and anthrax) or a case (human infection of avian influenza, epidemic hemorrhagic fever, epidemic encephalitis B, scarlet fever, malaria, echinococciosis and diarrhea); health education / information (HIV/AIDS, hepatitis A, hepatitis E, poliomyelitis, measles, typhoid, pertussis, diphtheria, tetanus, scarlet fever, brucellosis, leptospirosis, mumps, rubella, conjunctivitis and filariasis); alternative health information / Traditional Chinese Medicine (dysentery); commercial advertisement / entertainment (plague, dengue, influenza and leprosy); and social issues (SARS, hepatitis B, epidemic meningitis, gonorrhea, syphilis, schistosomiasis and hand-foot-and-mouth disease). News unrelated to the specified infectious diseases (rabies and tuberculosis) also led to elevated Weibo traffic. **Conclusions:** Our study showcases the diverse contexts from which increased social media traffic occur. Apart from outbreak news, Weibo users shared a variety of health information and discussed social issues. Our results will facilitate better health communication and advance digital epidemiology as causes underlying increased social media traffic are revealed.

Board 408. Global Handwashing Day 2012: A Qualitative Content Analysis of Chinese Social Media Reaction to a Health Promotion Event

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Background: Handwashing with soap has been shown to reduce the risk of diarrheal diseases and respiratory diseases. Global Handwashing Day (GHD) is a handwashing promotion campaign organized by the Global Public-Private Partnership of Handwashing with Soap. In China, it has been promoted by the Chinese public health authorities, international organizations and multinational corporations, through various channels, including social media. Weibo is the Chinese equivalent of Twitter. **Methods:** We conducted a qualitative content analysis of 552 Weibo posts generated on GHD 2012 by Weibo users with 1,000 or more followers with the Chinese keyword for "handwashing". The Weibo data were obtained from the Weiboscope database (The University of Hong Kong). Our samples represented the most influential Weibo users who contributed a majority of contents in the Weibo universe, and drew the most attention as far as comments and reposts were concerned. **Results:** Of the 552 posts, we identified 56 posts related to the Chinese government's official GHD promotional event, and 50 posts quoted a People's Daily's report of a survey of handwashing prevalence. 52 posts mentioned handwashing for "20 seconds" in their contents. 29 posts mentioned six steps of handwashing, including the contextualized version as the "Buddha's palm". There were Weibo posts that described the importance and benefits of handwashing and those that were creative comments in reaction to GHD. **Conclusions:** We observed the interconnections between traditional mass media and social media in handwashing promotion, as social media are amplifiers of contents provided in traditional mass media. We observed the contextualization of global hygiene messages in a unique national social media market, as in the case of "Buddha's Palm", representing the six steps of handwashing. The themes and topics identified in this study will help public health practitioners evaluate future social media handwashing promotion campaigns.

Board 409. Facts and Rumors: Social Media Reaction to Information and Misinformation on Ebola

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Background: Social media facilitate the circulation of Ebola-related information and misinformation. We aim to analyze what kinds of misinformation were circulating at the outset of the 2014 Ebola epidemic, the volume of alternative information compared to standard public health advice, and whether the alternative health information was globally present by analyzing Twitter and Sina Weibo contents. **Methods:** We retrieved Twitter and Weibo data created within 24 hours of the WHO announcement of Public Health Emergency of International Concern (Batch 1) and seven days later (Batch 2). We obtained ~1% of the Twitter universe, of which tweets containing the keyword Ebola were analyzed. We retrieved all Sina Weibo posts with either of two Chinese keywords for Ebola for analysis. Trending and fading analysis was performed for keywords, hashtags and web links. We identified alternative health information by manual coding and categorization of randomly selected sub-datasets. **Results:** Ebola-related alternative health information constituted a minority of Twitter and Weibo contents. The predominant content was information released by public health agencies and the major news agencies, channels and newspapers. Two misinformed speculated "treatment" predominated in Twitter posts. Saltwater was speculated to be protective against Ebola in the first batch of tweets, but faded a week later. "Nano-silver" was on the top 10 trending Twitter list. Chinese microblogs focused on the Chinese government sending medical assistance to Africa. **Conclusions:** Public health authorities can be assured that in the 2014 Ebola outbreak, Twitter and Weibo are platforms that help circulate outbreak news and scientific health information.

Travelers' Health

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Board 410. Increase in Paratyphoid Fever Cases Among Japanese Travelers Returning from Cambodia in 2013

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Background: Paratyphoid fever (infections with *Salmonella* Paratyphi A only, excluded with *S.* Paratyphi B or C) is one of the national notifiable infectious diseases in Japan. Approximately 20-30 paratyphoid cases had been reported annually from 2005 to 2012. Most cases had been attributed to infections in endemic Asian countries, such as India, Bangladesh and Indonesia. In 2013, an unusual increase in paratyphoid fever cases among travelers returning from Cambodia was observed in Japan. **Methods:** We assessed notified paratyphoid fever cases through the National Epidemiological Surveillance of Infectious Diseases (NESID) in Japan. We assembled clinical isolates of *S.* Paratyphi A from cases with travel history to Cambodia during 2012-2014. Isolates were phage typed, tested for antimicrobial susceptibility and pulsed-field gel electrophoresis (PFGE). **Results:** A total of 18 paratyphoid fever cases of suspected Cambodian origin (10 males and 8 females; median age, 42 years; age range, 23-76 years) were identified from December 2012 to September 2013, which peaked in May. In 2014, there were still six paratyphoid fever cases returning from Cambodia. No clear epidemiological link was identified among 24 cases with travel history to Cambodia during 2012-2014. Of the 22 isolates collected from the cases, 18 (81.8%) were phage type (PT) 2 and three (13.6%) were PT1 and one (4.5%) was untypeable. Four isolates (18.2%; two PT1 and two PT2) were nalidixic acid-resistant and the remaining isolates (81.8%) were susceptible to all antibiotics. Identified were 4 XbaI-digested PFGE patterns. Although minor variations were found in PFGE patterns, the overall picture showed a high degree of genetic similarity in all 22 isolates. **Conclusions:** It was implicated that the outbreak due to common and persistent source in Cambodia might have been continuing. Sharing information of surveillance and laboratory results targeting travelers could contribute as an international sentinel.

Vector-Borne Diseases and Climate Change

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Board 411. The Dynamics of Vector-host Interaction in Unraveling the Complexity of Eastern Equine Encephalitis as an Emerging Public Health Threat in Northeastern USA

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Eastern equine encephalitis virus (EEEV) is a highly pathogenic mosquito-borne zoonosis responsible for outbreaks of severe disease in humans and equines. During the last decade, we have witnessed annual reoccurrence of virus activity with human and equine cases, and expansion into new regions in the northeastern (NE) U.S. Entomological factors, and changes in the pathogen's abiotic and biotic environment might be responsible for the recent emergent foci. In the NE U.S., EEEV is maintained in an enzootic cycle involving the ornithophilic mosquito, *Culiseta melanura,* and passerine birds in freshwater swamp habitats. However, the role this mosquito plays in transmission of EEEV to humans and equines is not well defined. We used PCR-based methods and direct sequencing of the mitochondrial *cytochrome b* gene for profiling of blood meals in *Cs. melanura* to quantify its contact with vertebrate hosts, and to infer epidemiologic implications of its feeding behavior in four historic EEEV foci in the NE U.S. Avian point count surveys were conducted to determine spatio-temporal host community composition experienced by *Cs. melanura* and EEEV. We developed a mathematical model that simulates the dynamics of EEEV in birds and mosquitoes over a transmission season. Of 1127 blood meals identified to species level, only seven were from mammalian hosts. However, >99% of blood meals were from 65 avian species. We developed an empirically informed transmission model for EEEV in four sites using *Cs. melanura* abundance and preferred and non-preferred avian hosts. We measured strong feeding preferences for American Robin, Tufted Titmouse, Common Grackle, Wood Thrush and a few other virus competent species, quantified as the proportion of mosquito blood meals from these bird species in relation to their frequencies. Our study clarifies the host associations of *Cs. melanura* in four EEEV foci in the NE U.S. We identified vector host preferences as the most important transmission parameter and quantified the contribution of preference-induced contact heterogeneity to enzootic transmission. Our study elucidates

spatio-temporal host species utilization by *Cs. melanura* in relation to avian host abundance, and indicates that heterogeneity induced by host preference is a key mediator of vector-borne pathogen epizootics in host communities.

Board 412. Identification of Lyme Borreliosis in a Dog in Thailand

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Background: Lyme disease is a tick-borne zoonotic disease caused by spirochete *Borrelia burgdorferi*. It is transmitted from animals to humans by the bite of infected ticks of the genus *Ixodes*. There was no evidence of Lyme disease in humans or dogs in Thailand because *Ixodes* ticks are not found in Thailand. This study aimed to document for emergence of *B. burgdorferi* in dogs and ticks in Thailand. **Methods:** Blood samples were collected from dogs with visible evidence of tick infestation or with suspected signs and symptoms of blood parasitic disease from Chiang Mai (n=295) and Phuket (n=107) provinces. Samples were tested by commercial ELISA kit for *B. burgdorferi*, *Anaplasma* spp., *Ehrlichia* spp. and *Dirofilaria immitis* antibody. Positive samples were subjected to polymerase chain reaction (PCR) and sequencing to confirm the presence of *B. burgdorferi*. Ticks were collected from dogs in the same provinces and tested for *B. burgdorferi* by the same PCR. **Results:** One serum from a dog in Chiang Mai (0.3%) was positive for *B. burgdorferi*. PCR of the same sample for *fla, ospA* and *ospC* genes yielded positive result indicated that the dog was actively infected. Sequence of the PCR product showed that the dog was infected with *B. burgdorferi* sensu lato complex. Eight out of 376 *Rhipicephalus sanguineus* ticks collected in Chiang Mai (2%) were positive for *B. burgdorferi* by PCR. **Conclusion:** The results demonstrated the presence of *B. burgdorferi* in dogs and ticks in Thailand. Further investigation of the infection source and vector is needed to understand potential risks to dogs and humans in Thailand.

Board 413. Predicting the Spread of Vector-borne Disease: Chikungunya in the Americas

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Background: In December 2013, locally acquired chikungunya virus (CHIKV) infections were identified for the first time in the Americas. The potential for spread in the Western Hemisphere was immediately apparent as populations had virtually no immunity and the mosquito vectors were abundant. We estimated the probability of infected travelers arriving and local transmission occurring in specific locations to assist local preparedness and response activities. **Methods:** We developed branching process models to make probabilistic predictions of CHIKV spread using data on travel patterns, local infection prevalence, and climate-dependent transmission factors. These data and associated uncertainties were used to predict probable locations for the arrival of CHIKV-infected travelers and the initiation of local transmission. The predictions were compared retrospectively to data on cases reported to the Centers for Disease Control (CDC) and the Pan American Health Organization (PAHO). **Results:** Of the ten U.S. locations predicted to receive infected travelers by April 2014, CHIKV cases had been reported from eight. By the end of May, all ten locations had reported travelers with CHIKV infections. Of the ten countries or territories where introduced CHIKV transmission was predicted, eight had reported local cases by the end of April and the remaining two locations reported local transmission by the end of May (Puerto Rico and USVI). In the following months, CHIKV continued to spread in the Caribbean region. Transmission in the Southern Hemisphere was not predicted until September, the month when cases were first reported in Bahia, Brazil. **Conclusions:** These models have been able to predict the spread of CHIKV in the Americas with reasonable accuracy. This demonstrates the potential for branching process models to rapidly assess the probabilities of outbreak spread. Importantly, this spread can be predicted over heterogeneous transportation networks based on limited information. Updated predictions using these models are available on the CDC Chikungunya website to assist health departments in estimating their potential risk of imported and local CHIKV cases.

Board 414. Effectiveness of a Single Peridomestic Application of Acaricide to Prevent Lyme and Other Tickborne Diseases

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Background: In the northeastern US, tickborne diseases (TBDs) are a major public health concern. Identifying effective TBD prevention measures has been challenging. A single springtime application of acaricide has been shown to kill up to 95% of ticks in controlled studies. Although residential use of pesticides to control ticks is widespread, the effectiveness of pesticides to prevent human TBDs is unknown. Through a TickNET collaboration, we evaluated the effectiveness of a single residential acaricide application to prevent TBDs. **Methods:** In 2011 and 2012, we conducted a randomized, blinded, placebo-controlled trial among residential households in 8 counties in 3 states (CT, MD, NY). Households were randomly assigned to receive a single springtime yard treatment with commercially available acaricide (bifenthrin) or placebo (water). Applications were made according to public health recommendations. Tick drags were conducted 2-3 weeks post-treatment on a 10% sample to verify treatment efficacy. Four monthly post-treatment surveys were conducted to determine the number of ticks found attached to or crawling on household members. A final survey to capture TBDs was administered at 5 months. Self-reported TBDs were validated by medical record review. **Results:** Over 2 years, 2727 households were enrolled. There were no detectable differences between groups with respect to household demographics or property characteristics. Post-treatment tick drags indicated that 64.8% and 48.4% fewer ticks occurred on acaricide vs. placebo properties in 2011 and 2012, respectively. There were no significant differences between the acaricide and placebo groups in the number of tick encounters or self-reported or record-verified TBDs among household members. **Discussion:** Acaricide application was effective at controlling ticks, yet tick encounters and TBD reports were not similarly affected. Reasons for this may include: (1) residential exposure is not a principle source of TBD risk; (2) significant risk may occur in untreated areas (e.g. gardens); or (3) treatments need to be more effective at reducing tick populations to impact TBD risk. These results highlight the importance of human studies for understanding the effectiveness of TBD prevention efforts.

Board 415. Abundance and Infection Rates of *Ixodes scapularis* Nymphs Collected from Residential Properties in Lyme Disease-endemic Areas of Connecticut, Maryland and New York

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Background: *Ixodes scapularis* (the blacklegged tick) transmits *Borrelia burgdorferi* (which causes Lyme disease) and other pathogens of public health importance. In the northeastern US, risk of exposure to *I. scapularis* is considered highest peridomestically. Previous studies of tick density and infection have focused on public lands and forested research sites. We present data from residential properties obtained as part of a two-year multi-site tickborne disease intervention study. **Methods:** After providing informed consent, heads of households in freestanding homes in select Lyme disease-endemic areas in Connecticut (CT), Maryland (MD), and New York (NY) were enrolled. Tick habitat on randomly selected enrolled properties was dragged for host-seeking *I. scapularis* during peak nymphal activity in late spring-early summer in 2011 and 2012. Up to 40 30-second drags per property were conducted and ticks removed after each drag. Nymphal density was calculated as the number of *I. scapularis* nymphs collected per hour. Nymphs were tested for *B. burgdorferi*, *Anaplasma phagocytophilum* and *Babesia microti* using real-time multiplex PCR. **Results:** In total, 952 ticks were collected from 267 properties; 865 (91%) were *I. scapularis* nymphs. The overall average nymphal density was 27.4 nymphs/hour (range 0-174) in 2011 and 7.6 nymphs/hour (range 0-60) in 2012. The overall nymphal infection rate of *B. burgdorferi* was 18.5% in 2011 and 15.3% in 2012. *A. phagocytophilum* was detected from all study sites, with infection rates of 1.5%-4.8%. *B. microti* was detected in CT and NY (infection rates 5.9%-15.4%). Twenty-two nymphs from CT and NY were coinfected with *B. burgdorferi* and *B. microti*; one CT nymph was coinfected with *B. burgdorferi* and *A. phagocytophilum*. **Conclusions:** Our results document peridomestic risk for Lyme disease, anaplasmosis, and babesiosis in Lyme disease-endemic areas of CT, MD, and NY. *B. burgdorferi* infection rates were similar for both years, although the overall nymphal densities differed significantly. Nymphal infection rates in MD are consistent with previous reports but infection rates in CT and NY are lower. Coinfections in nymphs suggest the need for provider education. Additional study is warranted to determine if these pathogen rates correlate with human disease risk.

Board 416. First Detection of *Babesia microti* in *Ixodes scapularis* Ticks, Maryland, USA

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Background: Babesiosis is a parasitic infection primarily caused by *Babesia microti* and transmitted by *Ixodes scapularis* ticks. Babesiosis became reportable in Maryland (MD) in 2007 and nationally in 2011, because of the potential for transmission via blood products. In 2009, *Ba. microti* had not been detected in *I. scapularis* in MD, despite the tick's abundance and known infections with *Borrelia burgdorferi* (Lyme disease agent) and *Anaplasma phagocytophilum*. In 2009, a MD patient was diagnosed with babesiosis. Transfusion transmission of *Ba. microti* was ruled out and the patient reported no travel outside MD, suggesting local acquisition. **Methods:** MD surveillance records for 2011 (when the CSTE case definition was implemented) through 2013 were reviewed; the infection source was described for confirmed babesiosis cases. To assess where the 2009 patient acquired infection, we collected ticks at the patient's residence and nearby. Collected *I. scapularis* adults were tested by PCR by the US Army Public Health Command (USAPHC) for *B. burgdorferi*, *Ba. microti*, and *A. phagocytophilum; Ba. microti* positives were re-tested with a 2nd PCR at USAPHC. *Ba. microti* positive tick samples were sent blinded for confirmation to the CDC with nested primers targeting the s18s-rRNA gene and to Mayo Clinic using a real-time multiplex for *Ba. microti*, *Ba. duncani/Ba. duncani*-like, and *Ba. divergens/divergens*-like parasites. **Results:** Five confirmed and 9 probable babesiosis cases were reported in MD for 2011-2013. Of 4 confirmed *Ba. microti* cases, 3 were travel-associated and 1 was transfusion-acquired. Sixteen *I. scapularis* adults were collected. Eight (50%) were infected with *B. burgdorferi*, 2 of which were coinfected with *Ba. microti* and 1 of which was coinfected with *A. phagocytophilum. Ba. microti* infection was confirmed by 2nd PCR at USAPHC, CDC and Mayo Clinic. **Conclusions:** Surveillance successfully detected babesiosis cases and alerted us to potential local transmission. Our investigation resulted in the first detection of *Ba. microti* in *I. scapularis* in MD, which is remarkable given the few ticks collected. The *A. phagocytophilum* and *B. burgdorferi* infection rates are consistent with previous reports. Further investigation at this location of nymphs, the stage most likely to transmit human diseases, is warranted.

Board 417. Dengue Cluster Investigation in Two Districts, Ubon Ratchathani, January-July 2013: Epidemiological Characteristics and Key Vector Containers

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Background: Dengue hemorrhagic fever is one of important communicable diseases in Thailand. There was a large epidemic in the country in 2013. On 15th May, Bureau of Epidemiology (BoE) was notified that there were 103 cases from 4 clusters of dengue cases during 20th April to 7th July 2014 in a northeastern province, Ubon Ratchathani. The national team was sent to conducted field investigation. Objectives of this report are to describe epidemiological characteristics of the epidemic in the province particularly in two districts with highly active epidemic during June-July, identify key containers for mosquito larva control and give recommendations for disease control. **Methods:** A Descriptive study was performed. Provincial Dengue case list from Provincial Health Office, Ubon Ratchathani and Medical record (ICD-10: A90-91) from Kheungnai and Detudom hospitals during January-July were reviewed. Acute serum from currently admitted cases during 16-27 July was collected for serotype identifying container and larva surveys were conducted in villages from the two districts. **Results:** From Provincial Dengue case list, 1,642 cases were reported during January-July 2014. Provincial attack rate was 90.6 per 100,000 populations, highest among age group of 13-18 years (289.4) and followed by 5-12 years (278.7). Among those cases, 48% were male. Forty five percent of the cases were diagnosed as Dengue Fever (DF), 47% as Dengue Hemorrhagic Fever (DHF), and 8% as Dengue Shock Syndrome (DSS). In hospital of district A, 126 cases were reported. Among them, DF, DHF, and DSS were diagnose 43%, 53% and 4%, respectively. For hospital of district B, 202 cases were reported. Among them DF, DHF and DSS were diagnosed 79%, 21% without any DSS cases, respectively. Among seven

serum samples collected, 1 sample was positive for DEN-3. To achieve effective Larva survey, equalresource for vector control for both outdoor (Importance percentage 51 for district A and 43 for district B) and indoor containers (Importance percentage 51 for district A and 43 for district B) are recommended. **Conclusion:** During January to July, Dengue epidemic in Ubon Ratchathani has the highest risk among students age group. Indoor and outdoor water containers were equally important

Board 418. Human-tick Encounters as a Surrogate Measure for Disease in Tickborne Disease Intervention Studies

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Background: Indices of entomologic risk (e.g., tick density measured by drag, tick pathogen infection rates) have long been used as a proxy for human risk of tickborne diseases (TBDs). In a recent intervention study conducted by the CDC and three Emerging Infections Program sites, tick density on residential properties correlated poorly with the occurrence of TBDs among household members. To determine if human-tick encounters could serve as a more accurate surrogate of disease risk, we conducted a follow-up analysis to assess the strength of association between reported human-tick encounters and TBD diagnoses. **Methods:** Human-tick encounters (total number of ticks found crawling on or attached to household members) were measured using four monthly online surveys administered to heads of household during 2011 and 2012. Self-reported TBD diagnoses among household members were measured using a single telephone survey at the end of each study year. Self-reported diagnoses were verified by medical chart review. Logistic regression was used to evaluate the association between tick encounters and disease at the household level. **Results:** A total of 2727 households were enrolled in the study over two years: 795 (29%) reported any human-tick encounter; 680 (25%) reported ticks crawling; 434 (16%) reported ticks attached; 319 (12%) reported ticks crawling and attached; and 80 (3%) reported TBD diagnoses, 39 (1%) of which were verified by chart review. Households reporting tick encounters were more likely to have verified TBD diagnoses in the household: for any human-tick encounter, odds ratio (OR)=2.9 (95% confidence interval (CI): 1.5-5.4); for ticks found crawling, OR=2.9 (95% CI: 1.5-5.5); for ticks found attached, OR=4.2 (95% CI: 2.2-8.0); for ticks found crawling and attached, OR=4.9 (95% CI: 2.5-9.4). **Conclusions:** While entomologic outcomes measured via tick drags may not accurately represent risk of acquiring TBDs, use of human TBD occurrence as the outcome measure in interventions requires significant expense. Our findings indicate that self-reported human-tick encounters are a robust surrogate for disease risk at the household level that can be used in future intervention studies. Use of human-tick encounters as a proxy for disease in intervention studies will reduce study costs, time, and sample sizes.

Board 419. Meteorological Factors Associated with Hand, Foot and Mouth Disease in a Central Highlands Province, Vietnam: An Ecological Study

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Background: Over the years, the burden of Hand, foot, and mouth disease (HFMD) remains highly, especially in the Western Pacific Region including Vietnam. The seasonal trend in HFMD cases was reported in many areas. However, the association between HFMD and climate was not well-known/underestimated in Vietnam. This study assessed the effect of meteorological factors on HFMD in Daklak, a Central Highlands province in Vietnam. **Methods:** Monthly data on HFMD cases were collected from all commune health stations in Daklak province (total population: ~ 1.7 million) during a period of 2012-2013. The average temperature, maximum temperature, minimum temperature, humidity, rainfall, evaporation, duration of sunshine, and wind speed were recorded monthly at 5 meteorological stations throughout the province. The association between weather variables and number of HFMD cases was estimated, using a Poisson regression model. **Results:** In 2012-2013, there were 7128 HFMD patients in Daklak. The number of HFMD cases increased during the rainy season. An increased risk of HFMD was associated with higher average temperature (RR and 95% CI: 1.09; 1.03-1.15 per 1oC increase), higher minimum temperature (RR=1.09; 1.05-1.13 per 1oC increase), higher rainfall (RR=1.10; 1.05-1.15 per 200 mm increase), and higher sunshine duration (RR=1.26; 1.18-1.35 per 60 hours increase). The risk of HFMD was inversely associated with maximum temperature (RR=0.95; 0.92-0.99 per 1oC increase), and wind speed (RR=0.79; 0.75-0.83 per 1 m/s increase). Humidity and evaporation were insignificantly associated with HFMD. **Conclusions:** This study suggests that there is an obvious relationship between HFMD occurrence and climate. Temperature, rainfall, wind speed, and sunshine could be used as ecological indicators of HFMD cases in Daklak.

Board 420. Spatial Epidemiology of Lyme Disease in an Endemic County

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Background: Although Lyme disease (LD) is the most common vector-borne disease in the US, risk factors for human infection remain poorly defined. In the northeastern US, LD is thought to be acquired primarily in the home environment. We used data from one endemic county to evaluate associations of environmental and socio-demographic factors with risk of human LD according to residence. **Methods:** All households in Howard County, Maryland, were classified as a Lyme/Non-Lyme household based on surveillance reports for 2001-2011. Land use and land cover type were assessed at the geocoded household location; other environmental and socio-demographic factors were assessed at the census block group. Multilevel logistic regression models were used to describe spatial variation in risk and to examine associations of LD risk with factors ascertained at both the household and census block group. **Results:** Nearly 2% (n=1,672) of 94,303 households had at least one case of reported LD during 2001-2011; LD occurrence was spatially non-uniform. Household LD risk was primarily associated with low density residential development (adjusted odds ratio [aOR]: 1.7; 95% confidence interval [CI]: 1.4-2.1), a dominant vegetation type of red and white oak forest (aOR: 1.3; 95% CI: 1.1-1.6), and a higher amount of the census block group composed of forest (aOR per interquartile range [IQR] increase: 1.3; 95% CI: 1.1-1.6). Compared to houses without reported LD, case households were located in census block groups of higher average home value (aOR per IQR increase: 1.5; 95% CI: 1.3-1.8). Use of median odds ratios demonstrated that census block group factors accounted for more spatial variation in risk than household factors. **Conclusions:** Using a large cohort of all households in a single county, several fixed effect associations reiterated findings from earlier case-control studies. To our knowledge, this is the first analysis to associate human LD risk with a specific forest type. Variables measured at both the household

and the census block group influenced spatial differences in LD risk. However, individual behavior (not examined in this study) likely explains much variation in LD risk. Understanding the importance of various risk factors and the scale at which they influence LD risk may inform selection of appropriate interventions.

Board 421. Hunter-killed Deer as a Predictor of Notifiable Disease Rates for Lyme Disease and Babesiosis in New Jersey Counties, 1996 to 2013

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Background: This study explored the use of hunter-killed deer as a predictor of the reported incidence rates of Lyme disease and babisiosis across New Jersey counties from 1996 to 2013. While deer are not the primary reservoir of either pathogen, deer are a primary host to *Ixodes* ticks, a common vector of both babesiosis and Lyme disease. **Methods:** Data were obtained from the following sources: case data - New Jersey Department of Health; hunting data - the New Jersey Division of Fish and Wildlife; socio-demographics - the U.S. Census Bureau; and climate data - NOAA. The analysis concerned a total of 378 records across the 21 counties in New Jersey over 18-years. The association between hunter-killed deer per square mile and the reported rates of Lyme disease per 10,000 and babesiosis per 100,000 was examined by multivariate linear regression models and machine learning techniques such as support vector machines with the adjustment of socio-demographic and climate variables. **Results:** Each year, 58 cases of babesiosis and 3,111 cases of Lyme disease were reported in the state during 1996-2013. For Lyme disease, there was a strong correlation between the rate of hunter-killed deer in autumn and the rates of reported Lyme disease in the following summer ($r=0.76$, $p<0.001$). A lower but statistically significant correlation was observed for babesiosis ($r=0.15$, $p=0.003$). The multivariate linear regression model adjusting for year, average summer high temperatures, total summer precipitation, human population density, and the percent of the population under the poverty limit showed hunter-killed deer to be a statistically significant predictor ($\beta=0.87$, $p<0.001$) and yielded an R^2 of 0.62 (0.57, 0.71). **Conclusion:** The rate of hunter-killed deer in New Jersey is associated with an increase in official notification reports for both Lyme disease and babesiosis. Furthermore, Deer hunting data was predictive of the incidence rate of Lyme disease and babesiosis in the following year.

Board 422. Molecular Identification of the *Anopheles gambiae* Complex (Diptera: *Culicidae*) from Five Counties in Liberia

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Background: Members of the *Anopheles gambiae sensu lato* (Giles) complex define a group of seven morphologically indistinguishable species, including the principal malaria vectors in Sub-Saharan Africa. Members of this complex differ in behavior and ability to transmit malaria; hence, precise identification of member species is critical to monitoring and evaluating malaria threat levels. **Methods:** We collected mosquitoes from five counties in Liberia which include costal, urban, forested, and mountain/ savannah regions every other month from May 2011 until May 2012, using various trapping techniques and locations. *Anopheles gambiae* complex members were identified using molecular techniques based on differences in the ribosomal DNA (rDNA) region between species and the molecular forms (S and M) of *A. gambiae s.s* specimens. DNA was extracted from legs of each specimen. Species identification was determined by multiplex PCR using specific primers. The molecular forms (M or S) of *A. gambiae sensu stricto* (*s.s*) were determined by RFLP. Bivariate and multivariate logistic regression models identified environmental variables associated with genomic differentiation. **Results:** A total of 1696 *A. gambiae* mosquitoes were collected. Our results indicate widespread occurrence of *A. gambiae s.s.*, the principal malaria vector in the complex. We found 72.6%, 25.5%, and 1.9% of *A. gambiae s.s* specimens were S, M and hybrid forms respectively. Statistical analysis indicates that the S form was more likely to be found in rural areas, during rainy seasons and in indoor catchments. **Conclusion:** Identifying *An. gambiae* molecular forms and their distribution will enhance vector control efforts in Liberia. Previous studies have shown that the S form is highly insecticide resistant in comparison to the M form. This insecticide resistance has been linked directly to the *kdr* mutation for pyrethroid resistance and not behavioral adaptations.

Board 423. Risk Assessment for Rickettsial Pathogens in *Dermacentor occidentalis* Ticks from Southern California

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Background: *Rickettsia philipii* is an emerging cause of spotted fever group rickettsiosis in California which is differentiated from Rocky Mountain spotted fever (RMSF) by the presence of an eschar (Shapiro et al., ClD 2010). It is transmitted by *Dermacentor occidentalis,* a tick that commonly bites people in California. This tick more frequently harbors several genotypes of *R. rhipicephali* but rarely *R. rickettsii*. We investigated the prevalence of *Rickettsia* in ticks from eight sites in five counties in Southern California to assess the extent of human exposure to this rickettsial agent in a region formerly considered endemic only for RMSF. **Methods:** Questing *D. occidentalis* adults (175F, 177 M) were collected by flagging vegetation at multiple sites in February-June of 2014. Rickettsial DNA was detected with *omp*A EVA Green PCR. The rickettsial species and subtypes were identified by sequencing the 5' fragment of *omp*A and by amplification of several intergenic regions. **Results:** Ticks collected from six sites in February-March had similar prevalence of *Rickettsia* (20.2%) as in May-June at 3 sites (19.6%, one common site). Females were more frequently infected than males. *R. philipii* was only found in two sites (2 F, 1 M) and the site with both a male and female had the same genetic variant which differed from that at the other site. *R. rhipicephali* was found at all the sites and at a prevalence typically 10 times more frequent than *R. philipii* but with similar abundance per tick. The prevalence of *Rickettsia* per sample varied greatly from one site to another (4.8-33.9%, mode of 14.6%). **Conclusion:** Our studies confirm some findings found with ticks at other sites in Southern California that were collected in 2006-2007 and in Northern California in 2009. *D. occidentalis* is very widely distributed in the state in recreational areas and it is very commonly infected with *Rickettsia*. Consequently, since human bites with *Rickettsia*-infected ticks are very likely to occur, it is not surprising that increasing numbers of cases of rickettsioses are being reported in California and the public should minimize tick exposures. However, the prevalence of *R. philipii* in these sites was markedly lower than that previously reported. Whether this reduction is due to the recent extended drought in the state or the sample sites is not known.

Board 424. Characterization of the Bacterial Community of Species and Populations of *Dermacentor* Ticks

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Background: Our metagenomic analysis (*rrs* fragment pyrosequencing) of the bacterial communities present in 23 adult *Dermacentor variabilis* (Dv) ticks from Atlanta, Georgia, and southeastern Ohio identified 27 taxonomic groups; however, only 6 were present in at least 3 ticks -- 2 types of *Rickettsia*, 3 types of *Francisella* endosymbiont (FE) and a *Rickettsiella*. *Dermacentor* ticks are classic vectors for *Rickettsia* (7 ticks) while the FE was found in higher abundance and in all ticks; 15 (both sites) had two types of FE. **Methods:** In order to select other tick samples for further metagenomic analyses and to determine whether there was any relationship between the presence of *Rickettsia* and FE agents, additional Dv adults from 8 sites on a coastal barrier island in Georgia and 6 ecologically variant sites in Ohio, and *D. occidentalis* (Do) from 6 sites in southern California were collected. Their DNA was analyzed by semiquantitative EVAGreen assays (qPCR) for fragments of *omp*A (*Rickettsia*) or *rrs* (FE). The *Rickettsia* species were identified by sequencing *omp*A, *omp*B, and/or 17 Kd antigen gene amplicons. **Results:** Nearly all samples again contained FE while *Rickettsia* was found in lower prevalence and abundance irrespective of species. Primers for 11 genes commonly used in multi-locus sequence typing (MLST) for pathogenic *Francisella* (PF) were tested by PCR with the Dv FE but products were obtained for only 4 of them. Three MLST targets exhibited no genetic variation between Dv populations but they had <90% homology to PF; however, a small number of 16S genotypes were detected at each site including some new variants. While the quantity of FE detected by qPCR varied significantly between ticks and tick locations for both Dv and Do, it did not correlate with either tick sex or the presence of a *Rickettsia*. **Conclusion:** The physiological importance of the widespread dominant prevalence of different *Francisella* endosymbionts to *Dermacentor* ticks is unknown; if (and how) their presence may alter these ticks' responses to acquisition, growth and transmission of *Rickettsia* also needs experimental investigation.

Board 425. Analysis of the Metagenome of the Tick Vector *Amblyomma americanum*

Withdrawn at Author's Request

Board 426. Diagnosis of Travel Related and Locally Transmitted Chikungunya Virus in Florida

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Background: Chikungunya virus (CHIKV) is an alpha virus transmitted by *Aedes aegypti* and *Ae. albopictus* mosquitoes and has a similar etiology as dengue fever. Laboratory diagnosis of CHIKV includes detection of viral RNA by real-time reverse transcriptase polymerase chain reaction (RT-PCR) and IgM and IgG antibody by enzyme-linked immunosorbent assay (ELISA). The first local transmission of chikungunya virus in the Americas was identified in Caribbean countries and territories in late 2013 and has since spread to the USA. Florida has cruise ship ports from which tourists travel to and from the Caribbean and many residents who travel to visit family and friends living there. CHIKV assays were validated at the Florida Bureau of Public Health Laboratories (BPHL) in preparation to test for imported and potentially locally transmitted virus. **Methods:** Diagnostic and serological testing was performed at BPHL. Detection of CHIKV viral RNA by real time RT-PCR, IgM by MAC-ELISA, and IgG by ELISA were performed using Centers for Disease Control and Prevention (CDC) protocols. Patients who had traveled to endemic countries were tested for dengue virus (DENV) and CHIKV while patients who had no documented travel were also tested for West Nile Virus and St Louis Encephalitis Virus to check for Flavivirus cross reactivity in ELISA. **Results:** During 2014, the BPHL in Jacksonville and Tampa performed 474 RT-PCR assays, 568 IgM antibody-capture (MAC)-ELISA assays, and 558 IgG ELISA assays. Of the 1600 tests performed, there were 1124 negative, 90 indeterminate and 377 positive results. Of the 132 Chikungunya cases confirmed by the BPHL laboratories (122 imported, 12 locally transmitted), 124 were RT-PCR positive (23 were also IgM positive and 5 were also IgM equivocal), 2 were RT-PCR equivocal and IgM positive, and 5 were IgM positive only. **Conclusion:** Specific and sensitive testing capacity is needed in Florida due to the high volume of travelers from the outbreak area and the potential for local introduction. The BPHL provided diagnostic testing in response to suspected travel-related and locally acquired Chikungunya virus in Florida. It is important to test acute CHIKV samples with PCR in order to confirm viremic cases.

Board 427. Clinico Epidemiological Profile of Acute Encephalitis Syndrome in West Bengal, India

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Background: Recent outbreak of Acute Encephalitis Syndrome (AES) in different parts of India caused tremendous panic in general public and much media hype and furor.This is a major public health problem as it causes high morbidity and mortality. **Method:** 60 patients presented in our tertiary care hospital with clinical features of AES (WHO criteria) during monsoon period, June to September 2014, were assessed clinically using standard clinical methods and evaluated with Lumbar puncture,Viral serology and MRI brain and others. **Result:** Majority of cases were from rural area (83%) and maximum were below 5 years with male predominance. Among 60 patients Laboratory confirmed Japanese Encephalitis(JE) case-8 (13%),Probable JE case-20 (33%),AES other agent-10 (16%) among which Acute Demyelinating Encephalomyelitis (ADEM)-5, Meningoencephalitis-3, Herpes simplex virus (HSV) encephalitis-2.AES unknown agent-22 (36%).JE cases were also from 3 non endemic districts.On MRI finding all the confirmed and probable JE cases (46.66%) had typical bilateral thalamic involvement.In lumber puncture finding cell count was nearly double in JE cases as compared to Non-JE cases .Patients presented with recurrent convulsion,GCS <=6,preadmission fever duration >=5days, multiple cranial nerve involvement,abnormal posture and who were ventilated for>=5days, required multiple anticonvulsant had poor outcome in the form of death or major sequele and we found significant co relation with P-Value of<0.01. On detailed analysis of outcome death was less in JE cases (7.14%) than Non-JE cases (18.75%) but major sequele was more than double in JE (78.57%) in comparison to Non JE (31.25%).14.28% JE had minimal or no sequele while the figure was 50% for Non-JE.Prognosis of ADEM and HSV was good.Death were 3 times more in Non-JE cases but 78%JE cases had Major sequele.None of our patients were vaccinated. **Conclusion:** JE is responsible for 46% of all AES cases. Rural population is at risk mainly during monsoon. JE cases has less mortality with good standard care but

morbidity remains very high,which is a major concern.So it is better to be prevented than to be treated. Regarding prevention of JE along with control of vector and amplifying host, widespread vaccination coverage is the main weapon as breaking the geographical barrier JE cases being reported from non endemic districts also.

Board 428. Autochthonous Malaria Case in Johannesburg, Gauteng Province, South Africa, September 2014

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Background: The rarity of autochthonous malaria in non-endemic regions results in low suspicion of disease, leading to late diagnosis, delayed treatment, and high fatality rate. On 26 September 2014, the Outbreak Response Unit at the National Institute of Communicable Diseases was notified of a suspected malaria death in Johannesburg, a non-endemic malaria area. We investigated to identify the agent's possible route and transmission source. **Methods:** Interviews were conducted with the decedent's family; medical records and laboratory results were reviewed. Environmental assessments and entomological investigations were done at the decedent's home and surrounding areas. **Results:** The case was a 7-year-old female who developed fever on 21 September. On September 26 blood smear confirmed malaria parasites and the rapid antigen tests for P. falciparum were positive. The patient died before treatment could be started. Neither travel to malaria transmission areas, nor contact with residents from such areas was reported; and mechanical transmission through blood transfusion or injections was excluded. None of the adult or larval mosquitoes collected at or near the residence were malaria vectors. No other malaria cases were identified in the area. The residence was close to a road with a truck stop and cargo warehouse with potential transport links with endemic areas. Trucks from Mozambique parked in front of the decedent's residence a week before onset of illness and could have transported the infective mosquitos. **Conclusion:** It is likely that the case acquired malaria via an Anopheles mosquito transported from a malaria-endemic area. We recommend that clinicians in non-endemic malaria areas like Gauteng Province, especially during the malaria epidemic season, be reminded to test for malaria in patients showing malaria-like symptoms.

Board 429. Molecular Epidemiology and Specific Detection of *Anaplasma* sp. Related to *Anaplasma phagocytophilum* in Sika Deer and Its First Detection in Wild Brown Bears and Rodents in Hokkaido, Japan

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Background: *A. phagocytophilum* is a highly heterogenic bacterium and its strains are closely related and show unique host tropism. In Hokkaido there are several strains of *A. phagocytophilum*, one has caused disease in 2 humans and has been detected in *Ixodes ovatus* and *I. persulcatus* ticks (here, referred to as Ap-ha); however, no mammalian reservoir host has been identified for this strain in Japan until now. On the other hand, an *Anaplasma* sp. highly related to *A. phagocytophilum* (here, referred to as AP-sd) is very common in Japan as it was detected in sika deer and cattle. Here, we provided a specific detection technique for AP-sd and Ap-ha, separately. In turn, this will help us to understand the epidemiology of *A. phagocytophilum* strains in Hokkaido. **Methods:** Our study included 250 sika deer (*Cervus nippon yesoensis*), 13 brown bear (*Ursus arctos*) and 252 rodents: 138 *Apodemus speciosus*, 45 *Apodemus argenteus*, 42 *Myodes rufocanus* and 27 *Myodes rutilus* from Hokkaido island, northern Japan, during 2010 to 2014. The collected samples were examined by nested PCR and reverse line blot hybridization (RLB) to detect several strains of *A. phagocytophilum*. The positive PCR products were sequenced and statistically analyzed. **Results:** The prevalence of *Anaplasma* sp. (AP-sd) in sika deer, brown bears and rodents was 51% (128/250), 15% (2/13) and 2.4% (6/252), respectively. 84 positive 16S rRNA and 6 positive gltA gene PCR products were sequenced. Our sequences clustered with AP-sd, which was closely related to zoonotic *A. phagocytophilum* sequences. The nested PCR result was confirmed with our newly designed RLB system. Using this technique, we were able to specifically detect AP-sd separately from Ap-ha. **Conclusions:** Here, we identified two more potential reservoir hosts for AP-sd, brown bears and rodents. This suggests that AP-sd may have a broader host tropism than Ap-ha. Whereas Ap-sd has a broad infection range, and hits a number of prominent mammals in the Hokkaido ecosystem, we found no trace of Ap-ha. The most important question, then remains: what is the host for Ap-ha? An equal or greater prevalence of Ap-ha than Ap-sd in ticks were reported, so it is odd that all these animals are probably exposed to both strains but only carry Ap-sd.

Board 430. Interaction Studies of Extrinsic and Intrinsic Dengue Virus Types in Disease Affected Households of Rajasthan, India

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Background: Dengue Fever (DF) associated with Dengue Hemorrhagic Fever (DHF) is an emerging public health in India. Transmission mechanism of dengue virus especially interaction between mosquito carried extrinsic and human patients carried intrinsic DEN types of a same house hold has been studied in Rajasthan, India. **Methods:** Studies were undertaken in 39 houses of Rajasthan, India from where Dengue patients were reported. Serum samples of patients were referred to our laboratory for molecular diagnosis. We collected mosquitoes from the houses of patients and both patient serum samples and individual Aedes aegypti were subjected to Real Time PCR for dengue type specific tests using kits supplied by CDC, Atlanta, USA. **Results:** Out of 39 houses from where dengue cases were tested positive, 9 mosquitoes showed more than one DEN type. In 9 such houses showing multiple DEN types in mosquitoes, only one patient showed multiple DEN types while in remaining 8 houses, human patients showed only one of the DEN strains carried by mosquitoes of their house. **Conclusions:** The preliminary trend shows that in dengue affected houses multiple DEN types are carried by the individual mosquitoes but human systems of the patients, in majority of cases are able to eliminate multiple types allowing only one of the mosquito inoculated DEN types to manifest as disease. However, in one of the patients in present studies, patient showed multiple DEN types. Detailed studies are in progress which could reveal interesting interaction of extrinsic and intrinsic DEN types to lead to DF and/or DHF.

Board 431. Characterization of Chikungunya Virus Infections in Children in Managua, Nicaragua

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Background: Chikungunya is a viral disease transmitted by *Aedes aegypti* and *Ae. albopictus* mosquitoes. In late 2013, chikungunya virus (CHIKV) was introduced in the Caribbean island of St. Martin. Since then, over 1,250,000 chikungunya cases have been reported by PAHO and most countries in the Americas report autochthonous transmission of CHIKV. In Nicaragua, the first imported case was described in July 2014 and the first autochthonous case in September. **Methods:** We analyzed the epidemiology and clinical presentation of chikungunya in two prospective pediatric cohort studies in Managua, Nicaragua: a community-based study and a hospital-based study. Suspected chikungunya cases in both studies and cases with undifferentiated fever in the community cohort were screened by RT-PCR for CHIKV infection. **Results:** From September 2014 to February 2015, a total of 96 and 83 chikungunya cases were identified in the community cohort and the hospital cohort, respectively. In the community cohort, cases were equally distributed by sex; however, more males presented to the hospital (67%, p=0.001). Most chikungunya cases were identified from November to January (community cohort: 83%, hospital: 92%). In the first six months of the epidemic, the incidence of symptomatic CHIKV infection in children aged 2-14 years in the community cohort was 4.6 cases per 1,000 person-months (95%CI: 3.8-5.7). Clinical presentation in the community cohort ranged from undifferentiated fever (13%) to children requiring hospitalization (16%). CHIKV-positive children were older than the rest of the children in the community cohort study (9.9 vs. 8.1 years, p<0.001), and CHIKV-positive children presenting with typical chikungunya symptoms were older than those with undifferentiated fever (10.1 vs 8.1 years, p=0.03). **Conclusions:** A detailed analysis of acute symptoms in our chikungunya cases is underway. Additionally, patients with confirmed CHIKV infection will be followed longitudinally to characterize chronic symptoms associated with CHIKV infection. Finally, healthy annual serum samples collected from cohort participants in March 2014 and 2015 will be used to estimate the rate of subclinical CHIKV infections.

Board 432. Incidence of and Reasons for Hospitalization of Chikungunya Patients—Puerto Rico, 2014

F. Cruz López[1], C. H. Hsu[2], J. Perez Padilla[3], O. Lorenzi[3], A. Rivera[3], E. Lugo[4], J. Muñoz-Jordan[3], E. Hunsperger[3], J. Staples[5], M. Fischer[5], H. S. Margolis[3], B. Rivera García[6], L. Alvarado[1,4], T. M. Sharp[3]; [1]Ponce Hlth. Sci. Univ., Ponce, PR, USA, [2]CDC, Poxvirus and Rabies Branch, Atlanta, GA, USA, [3]CDC, Dengue Branch, San Juan, PR, USA, [4]San Lucas Episcopal Hosp., Ponce, PR, USA, [5]CDC, Arboviral Diseases Branch, Fort Collins, CO, USA, [6]Puerto Rico Dept. of Hlth., San Juan, PR, USA

Background: The Sentinel Enhanced Dengue Surveillance System (SEDSS) is an acute febrile illness (AFI) surveillance and research study that determines the etiology and clinical outcome in patients presenting to two hospitals in Puerto Rico. Chikungunya emerged in the Caribbean in late 2013, and chikungunya diagnostic testing was incorporated into SEDSS in March 2014. The objectives of this investigation were to estimate the proportion of chikungunya virus (CHIKV) infection in patients presenting with AFI, and estimate the incidence of and describe reasons for hospitalization of patients with evidence of CHIKV infection. **Methods:** Patients presenting with current or recent history of fever were offered enrollment in SEDSS. Demographic and clinical information were collected at presentation. Hospitalized patients were followed daily to define patient outcome. Medical records were reviewed to collect information on atypical manifestations of chikungunya. **Results:** The first patient enrolled in SEDSS with evidence of CHIKV infection had illness onset in May 2014. Of 2,380 patients enrolled during May-September 2014, 661 (28%) had evidence of CHIKV infection by RT-PCR (93%) or IgM ELISA (7%). In total, 60 (9%) patients with evidence of CHIKV infection were hospitalized, 2 (0.3%) were admitted to the intensive care unit (one with purpura and acute kidney injury, the other with congestive heart failure), and 1 (0.2%) died due to pleural effusions and respiratory failure. Of 49 hospitalized chikungunya patients for which medical records have been reviewed, 25 (51%) were female and median age was 34 years (range: 28 days-93 years). The most common admitting diagnoses were viral syndrome (69%), fever (43%), and dehydration (31%). The most common atypical manifestations of chikungunya were splenomegaly (6%) and vesiculobullous skin lesions (2%). Median duration of patient hospitalization was 4.6 days (range: 1-22). **Conclusions:** Reasons for hospitalization of chikungunya patients identified via SEDSS were most frequently associated with management of uncomplicated AFI. Atypical manifestations associated with chikungunya were rare. Next steps in this investigation will utilize a larger sample of chikungunya patients to describe their clinical course and identify risk factors for hospitalization.

Zoonotic and Animal Diseases

Wednesday, August 26, 12:30 PM - 1:45 PM

Grand Hall

Board 433. Spatial Ecology and Epidemiology of Soilborne Human and Animal Bacterial Pathogens and Their Public Health Significance in Pakistan

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Background: A multidisciplinary collaborative research funded by DTRA (HDTRA FRBAA09-8B-007) was started in 2010 to study the spatial ecology and epidemiology of soil borne human and animal bacterial pathogens and its public health significance in Pakistan. **Methods:** The first phase of the study focused on training of UVAS scientists at Penn State (GIS mapping, soil sample collection and processing, RT PCR assay and PCR DGGE), GIS workshop in Pakistan and establishing a molecular diagnostic laboratory at UVAS (standardizing RT PCR assay). The second phase of the study involves conducting a comprehensive study on distribution of soil borne pathogens in Lahore district of Pakistan. **Results:** A GIS workshop (July 25- August 7, 2011) and RT-PCR and PCR-DGGE workshop (August 8- Sept 7, 2011) was conducted for scientist from UVAS at the Penn State Laboratory. Later, a GIS workshop conducted in Pakistan (Nov 28 - Dec 3, 2011) showed that 15 of the 16 had a significant gain in knowledge. Also, a molecular research laboratory was set up at UVAS for analysis of soil samples for select pathogens. The second phase of the study involved a pilot study in and around villages of Lahore district. A total of 145 soil samples were collected and examined for pathogens and soil chemistry. Real PCR detected *Bacillus anthracis* (CapB), *Burkholderia mallei*, *Francisella tularensis* and *Coxiella burnetii* in 10, 2, 13 and 5% of soil samples. The frequency of detection of soil borne pathogens were in areas where animals were held prior to auction, transport and slaughter and these locations were along the interstate routes in Lahore. The prevalence of B. *anthracis* was found to be associated with organic matter, P, Mg, Cu, Mn, Co, Cd, Na, Fe, Ca, and P. The prevalence of *F. tularensis* and *C. burnetii* was found to be associated with P and Cu, respectively**. Conclusion:** The study provides a baseline prevalence status of selected pathogens with respect to soil characteristics, animal and human population in district Lahore of the Punjab province, Pakistan. Of much importance is the need to address public health issues raised and require appropriate interventions from public health authorities.

Board 434. Lymphocytic Choriomeningitis Virus Outbreak and Risk Assessment—Multiple States, 2012

L. Edison[1,2], C. Drenzek[2], J. Gabel[2], B. Knust[1], B. Petersen[1], P. Rollin[1], U. Stroeher[1], S. Nichol[1], J. House[3], D. Thoroughman[1,4], S. Robeson[4], K. Fowler[1]; [1]CDC, Atlanta, GA, USA, [2]Georgia Dept. of Publ. Hlth., Atlanta, GA, USA, [3]Indiana State Dept. of Hlth., Atlanta, GA, USA, [4]Kentucky Dept. for Publ. Hlth., Frankfort, KY, USA

Background: Lymphocytic choriomeningitis virus (LCMV), a rodentborne arenavirus, can cause aseptic meningitis, encephalitis, and severe birth defects among humans. In May 2012, four employees of an Indiana rodent-breeding facility experienced aseptic meningitis caused by LCMV. An epidemiologic investigation revealed exposure to LCMV infected mice originating from a Kentucky breeding facility (Facility A) as the cause. We investigated Facility A to determine the extent of the outbreak and prevent further cases. **Methods:** We performed LCMV serologic testing for all Facility A employees and conducted interviews to assess their infection control practices and potential risk factors for seroconversion. We reviewed shipping records and contacted facilities that had received potentially infected mice to encourage euthanization of the mice and assess employees' risk for exposure. Pregnant, sick, or immunocompromised pet store employees were offered serologic testing. **Results:** Among 32 Facility A employees, 11 (34%) were LCMV-seropositive, and one experienced aseptic meningitis; the one pregnant employee tested negative. Twenty-nine (91%) reported wearing gloves, and 13 (41%) using a mask. No risk factors were significantly associated with seroconversion. Feeder mice bred as reptile food at Facility A comingled with wild mice, the presumed source of infection. Among facilities from 21 states that received these mice, 264/521 (51%) pet stores and 7/11 (64%) distributors still had >500,000 potentially infected mice, which were subsequently euthanized. Thirty-five pet store employees from six states tested negative for LCMV. **Conclusion:** LCMV can pose a serious health risk to persons who work with or handle mice. Rodent breeding facilities should ensure that wild mice are separated from mice intended for distribution. Personal protective equipment and education regarding its use should be provided to employees who handle mice.

Board 435. Seroconversion and Risk Factors for Highly Pathogenic Avian Influenza A (H5N1) Virus Infection Among Live Bird Market Workers in Bangladesh During 2009-2010

S. Nasreen[1], S. U. Khan[1], S. P. Luby[1,2], E. S. Gurley[1], J. Abedin[1], R. U. Zaman[1], B. M. Sohel[1], M. Rahman[1], K. Hancock[2], M. Z. Levine[2], V. Veguilla[2], D. Wang[2], C. Holiday[2], E. Gillis[2], K. Sturm-Ramirez[1,2], J. Bresee[2], M. Rahman[3], T. M. Uyeki[2], J. M. Katz[2], E. Azziz-Baumgartner[1,2]; [1]Intl. Ctr. for Diarrheal Disease Res. (ICDDR,B), Dhaka, Bangladesh, [2]CDC, Atlanta, GA, USA, [3]Institute of Epidemiology, Disease Control and Res. (IEDCR), Government of Bangladesh, Dhaka, Bangladesh

Background: We conducted a longitudinal study to determine the incidence of seroconversion and risk factors for H5N1 virus infection among live bird market poultry workers in Bangladesh during 2009-2010. **Methods:** We enrolled poultry workers from twelve live bird markets in four districts with concurrent surveillance among poultry and environment surfaces for avian influenza A viruses and obtained poultry exposure data and blood samples. We obtained follow-up data and a second blood sample either after detection of H5N1 virus at participating markets or one year after enrolment if H5N1 virus was not detected through surveillance. Sera that had an H5N1virus microneutralization antibody titer of ≥40 and were positive in a confirmatory H5-specific Western blot assay were considered seropositive. A 4-fold rise in neutralizing antibody titer between the two serum samples with the second sample achieving a titer of ≥40 was considered evidence of seroconversion to H5N1 virus. We also collected poultry exposure data and blood samples from controls. We calculated the incidence of seroconversion against H5N1 virus and used log-linear model to assess risk factors for H5N1 virus infection. **Results:** Nine (2%, 95% CI: 1%-4%) of 404 enrolled poultry workers were seropositive for H5N1 virus antibodies at baseline. We followed 290 workers, and six (2%, 95% CI: 1%-5%) of 284 workers seronegative at baseline seroconverted. The incidence of seroconversion was 7/100 poultry-worker-years for the workers from markets with H5N1 virus identified among poultry. Workers who frequently fed poultry, cleaned feeding trays, water containers and feces from the pens, and did not wash hands after contact with sick poultry were at 7.6 times (95% CI: 2.8-20.9) higher risk of H5N1 virus infection compared with workers who infrequently performed these behaviours. All 101 controls were seronegative for H5N1 virus antibodies. **Conclusion:** Our study demonstrates that Bangladeshi poultry workers became infected with H5N1 virus while working in contaminated live bird markets. Performing poultry caring activities at the market increased the risk of acquiring H5N1 virus infection.

Board 436. Pet Ownership Increases the Risk of Encountering Ticks in the Household

E. H. Jones[1], A. F. Hinkley[2], S. A. Hook[2], J. I. Meek[3], P. B. Backenson[4], K. J. Kugeler[2], K. A. Feldman[1]; [1]Maryland Dept. of Hlth. and Mental Hygiene, Baltimore, MD, USA, [2]CDC, Fort Collins, CO, USA, [3]Connecticut Emerging Infections Program, Yale Sch. of Publ. Hlth., New Haven, CT, USA, [4]Emerging Infections Program, New York State Dept. of Hlth., Albany, NY, USA

Background: Previous reports, with limited sample size, suggest an increased risk of Lyme disease in pet owners. The association of pet ownership with tick encounters and human tickborne disease was investigated as part of a large, 2-year randomized controlled trial to evaluate a tickborne disease intervention. **Methods:** We collected data regarding pet ownership, demographics, property characteristics, tick encounters and tickborne disease. Households with and without pets were compared using Chi-squared tests. We used univariate and multivariate analyses to calculate odds ratios (OR) and 95% confidence intervals (CI) to describe the relationship between pet ownership and ticks crawling on humans; ticks attached to humans; and possible tickborne disease. **Results:** Over 2 years, 2727 households were enrolled, 1546 (56.7%) of which owned pets. Pet owning households were significantly different with respect to education (p=.0074) and race (p=<.0001). Pet owners were more likely to find ticks crawling on (OR 1.83, 95% CI 1.53-2.20) and attached to household members (OR 1.49, 95% CI 1.21-1.85). This was consistent for households owning only dogs (OR 1.82, 95% CI 1.49-2.22; OR 1.37, 95% CI 1.08-1.73), only cats (OR 1.65, 95% CI 1.19-2.28; OR 1.83, CI 1.28-2.62), and both dogs and cats (OR 2.09, 95% CI 1.58-2.76; OR 1.71, 95% CI 1.24-2.38) for ticks crawling and attached, respectively. The association between owning pets and ticks crawling (aOR 1.79, 95% CI 1.49-2.15) or attached (aOR 1.48, 95% CI 1.19-1.84) held after adjusting for potential confounders, treatment group and year. Among pet owners, finding ticks on pets increased the risk of finding ticks crawling on (OR 2.69, 95% CI 2.14-3.37) and attached to pet owners (OR 2.50, 95% CI 1.92-3.25). Pet ownership was not associated with an increased risk of tickborne disease. **Conclusion:** This is the largest evaluation of pet ownership and human-tick encounters and tickborne diseases. All pet owners, whether of cats or dogs, are at

increased risk of encountering ticks. There may have been too few cases of tickborne disease to sufficiently investigate the association between owning pets and developing disease. Pet owners should be made aware of the risk, reminded to conduct daily tick checks of both pets and family members, and to consult their veterinarian regarding tick control.

Board 437. Bat Hunting and Bat-human Interactions in Bangladeshi Villages: Implications for Zoonotic Disease Transmission

J. Openshaw[1], S. Hegde[2], H. M. Sazzad[2], S. U. Khan[2], M. J. Hossain[2], J. H. Epstein[3], P. Daszak[3], E. S. Gurley[2], S. P. Luby[1]; [1]Stanford Univ., Stanford, CA, USA, [2]Intl. Ctr. for Diarrheal Disease Res. (ICDDR,B), Dhaka, Bangladesh, [3]EcoHealth Alliance, New York, NY, USA

Background: Bats have been identified as an important reservoir for emerging zoonotic diseases. In Bangladesh, species of frugivorous bats are abundant and known to roost and forage near human settlements. The largest of these, *Pteropus giganteus*, is the natural reservoir for Nipah virus. The objective of the study was to characterize human interactions and exposures to bats to better understand what areas may be at increased risk for zoonotic spillover of bat pathogens. **Methods:** We collected data on bat-human interactions and exposures from 5,081 households in 206 villages across Bangladesh from 2011 to 2013. To focus results on *Pteropus* bats, household heads were asked about their interactions with large bats. We estimated the size of *Pteropus* bat populations at each village site by surveying roosts within a 5 km radius of each village. We used logistic regression models to determine if bat hunting was associated with environmental factors. **Results:** 11% of household heads reported seeing large fruit bat roosts around their home, 57% reported them flying overhead at night, and 15% reported finding a large bat within the boundaries of their household complex. 14% of household heads reported seeing a dead bat around their home or village with 25% reporting the carcass was thrown into a body of water. Only 1% reported family members hunting fruit bats, but 8% reported knowing of individuals hunting bats within their village. Bat hunting (either by the family or known villagers) occurred in 46% of villages and was most concentrated in western Bangladesh (Prevalence ratio [PR] 4.61, 95% CI 2.84-9.87, p<0.001). Villages where bat hunting was reported were likely to have household heads reporting bat roosts near their homes (PR 1.53, CI 1.12-2.39, p=0.018), but hunting was not associated with increased bat population density (PR 0.86, CI 0.63-1.19, p=0.32). Of those who reported hunting bats, 44% reported using them for food and 32% for medicinal purposes. **Conclusion:** Exposure of humans to bats in Bangladeshi villages is common. Bat hunting and use of bats for food and medicines occurs. Bat hunting appears to be associated with bats living in close proximity to homes. Bat hunting is most common in villages located in western Bangladesh and these areas could be further targeted for monitoring of pathogen spillover.

Board 438. Point Prevalence Survey for Tick-borne Pathogens in Military Working Dogs, Shelter Animals, and Pet Populations in Northern Colombia

M. E. McCown, A. Alleman, K.A. Sayler, R. Chandrashekar, B. Thatcher, P. Tyrrell, B. Stillman, M. Beall, A. Barbet; US Army Publ. Hlth. Command Region-Europe, Landstuhl, Germany

Background: Surveillance for exposure to tick-borne pathogens provides important information necessary for protecting local human and animal health, deployed military service members, and working dogs in various parts of the world. Based on the high tick-borne pathogen results from a 2011 surveillance study in Colombia, an in-depth point prevalence survey was conducted in July 2012. The purpose of this point prevalence study was to determine the molecular and seroprevalence of tick-borne pathogens at a specific point in time in military working dogs, shelter animals, and pet populations in Barranquilla, Colombia. **Methods:** EDTA-anticoagulated whole blood and serum samples were collected from 70 military working dogs, 101 dogs from regional and community shelters and 47 client-owned animals presenting to veterinary hospitals. Serum samples were tested for antibodies to *Ehrlichia ewingii*, *E. canis*, *E. chaffeensis*, *Anaplasma phagocytophilum*, *A. platys,* and *Borrelia burgdorferi* using species-specific peptides in an ELISA format. DNA was extracted from each sample of whole blood and tested for target DNA from *Ehrlichia* spp. and *Anaplasma* spp. by real-time PCR analysis. **Results:** Of the 218 serum samples tested, 163 (74%) were positve for *E. canis* and 116 (53%) positive for *A. platys*. Of the 218 DNA samples, 62 samples (28%) were positive for *E. canis* DNA and 35 samples (16%) were positive for *A. platys* DNA. Of the 163 dogs seropositive for *E. canis*, 60 (37%) were also positive by PCR analysis. Of the 116 dogs seropositive for *A. platys,* 26 (22%) were also positive by PCR analysis. Of the 101 samples that were seropositive for both *E. canis* and *A. platys*, 10 (10%) were also PCR positive for both. **Conclusions:** These data indicate exposure to tick-borne pathogens in the northern Colombian city of Barranquilla is extremely high with significant levels of bacteremia. This is most critical in dogs in kennel environments such as shelters or military working dog kennels (>90% samples seropositive or PCR positive for one or more organisms). Both *E. canis* and *A. platys* are primarily associated with clinical disease in dogs. However, *E. canis* infection and infection with an '*A. platys*-like' organism has been documented in people in South America and this high level of exposure warrants precautionary measures for both dogs and people.

Board 439. Long-term Impact of Chikungunya Virus Infection in Florida

K. Kendrick, D. Stanek; Florida Dept. of Hlth., Tallahassee, FL, USA

Background: Since the introduction of chikungunya virus to the Americas in December 2013, there has been a sharp increase in the number of chikungunya fever cases reported in Florida. In Africa and Asia, chikungunya virus infections have been reported to cause persistent symptoms including arthralgia and myalgia that last months after infection in some patients. Given the large number of cases and the possibility of long-lasting symptoms, the potential burden of chikungunya virus on Florida's health care resources could be significant. To better understand the impact of chikungunya virus in Florida, reported cases were followed six months after initial infection. **Methods:** The Florida Department of Health interviewed patients by telephone during the acute phase of infection as well as three months after infection onset. Those patients reporting persistent symptoms during their three month follow-up were interviewed again six months after infection onset. During each follow-up interview, patients were asked if they were still experiencing symptoms, and if so, a variety of questions about health care visits, medication use, loss of work days, and disruption to their daily routines. **Results:** Florida reported 442 imported and 11 locally acquired chikungunya fever cases with disease onset between January and October 2014. Of these 453 cases, 393 (88%) were interviewed during the acute phase of infection, and 302 (67%) were interviewed three months after infection onset. One hundred and thirty-one (43%) patients were still experiencing symptoms at three months. Among these patients, 67 (52%) sought additional care from a health care provider since their original visit, 96 (75%) took medications to manage their symptoms, 40 (31%) lost the ability to perform work related duties, and 93 (72%) reported that their symptoms disrupted their daily routines. Data from the six month follow-up of those patients symptomatic at three months will also be presented.

Conclusions: A large proportion of Florida's chikungunya fever cases are still experiencing symptoms three or more months after infection. These persistent symptoms are not only disruptive to daily lives, but also require additional medical resources to manage.

Board 440. Seroprevalence of West Nile Virus in Wild Birds in Bangladesh

A. Islam[1], M. A. Rahman[1], S. K. Paul[1], M. A. Hannan[1], A. Islam[2], M. E. Hossain[1], M. Z. Rahman[1], P. R. Hosseini[2], T. K. Dey[3], N. Zeidner[1,4]; [1]Intl. Ctr. for Diarrheal Disease Res. (ICDDR,B), Dhaka, Bangladesh, [2]EcoHealth Alliance, New York, NY, USA, [3]Bangladesh Forest Dept., Ministry of Environment and Forest, Dhaka, Bangladesh, [4]CDC, Atlanta, GA, USA

Background: West Nile virus (WNV) is the most widespread arbovirus in the world capable of causing epidemics in both humans and animals. It is transmitted by a wide range of mosquitoes and multiple species of birds can act as amplifying hosts. Migratory birds are considered to be the main vehicle for introducing WNV into new regions. In humans, the pathogenicity of WNV varies from mild, self limiting, non-fatal, febrile illness to severe encephalitis. The status of WNV in Bangladesh is currently unknown. We conducted this study to assess the prevalence of WNV among resident and migratory wild birds of Bangladesh. **Methods:** During the period of 2010 to 2012 birds were captured using mist nets and noose traps, and blood samples were taken from wild birds landing on the coastal sandbars of Cox's Bazar, Hakaluki *haor* (seasonal wetlands) of Sylhet and Moulvibazar, Tanguar *haor* of Sunamgonj and the rice paddy fields of Patuakhali, Netrokona and Guibandha. Recovered serum was tested at 50% dilution for detection of WNV antibodies using a commercially available competitive ELISA following the manufacturer's instructions (ID Screen© West Nile Competition, IDVet, Montpellier, France). **Results:** Blood samples were obtained from a total of 888 birds comprising 21 families and 80 species; 250 (28%) of them were resident and 638 (72%) were migratory. Forty eight birds (5.4%, CI 0.04-0.07) tested positive for WNV antibody. The positive birds consisted of 45 common coots (*Fulica atra*), one ferruginous pochard (*Aythya nyroca*), one fulvous whistling duck (*Dendrocygna bicolor*) and one great crested grebe (*Podiceps cristatus*). Among those birds, two common coots, one fulvous whistling duck and one great crested grebe were from the Hakaluki haor, and 43 common coots and one ferrogionous pochard were from Tanguar haor. Only one positive bird, a fulvous whistling duck, was a resident species. **Conclusions:** Both resident and migratory wild birds of Bangladesh demonstrated exposure to WNV infection. Most of the WNV positive birds were migratory common coots, which is similar to previous reports from India and Iran. Future isolation and molecular characterization of the virus will allow us to better understand the epidemiology of this virus in Bangladesh.

Board 441. Tickborne Relapsing Fever Outbreak at a High School Football Camp—Arizona, 2014

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Background: Tickborne relapsing fever (TBRF) is caused by *Borrelia* species spirochetes transmitted by *Ornithodoros* ticks. During 1982-2013, a total of 22 TBRF cases (0-3 cases annually) were reported in Arizona. In August, Coconino County Public Health Services District received a call that 5 high school students who had attended a football camp were hospitalized; several of these students had spirochetes identified on blood smears. This triggered an investigation to confirm the outbreak, identify the cause, and prevent additional cases. **Methods:** We interviewed camp staff and attendees, reviewed medical records of hospitalized patients, and inspected the campsite for evidence of rodent or tick infestation. A probable case was defined as fever, myalgias, and headache in a person attending the football camp during August 1-3, 2014; a confirmed case was spirochetemia identified in an attendee's blood smear or by isolation. **Results:** Forty (95%) of 42 male camp attendees were interviewed. We identified 6 confirmed cases (5 [83%] by spirochetes detected on blood smear and 1 [17%] by isolation) and 5 probable cases (attack rate: 26.2%). Patients were ages 15-17 years (10 students) and 33 years (1 coach). The median incubation period was 6 (range: 2-10) days. Eight (100%) of 8 patients with known treatments received doxycycline and recovered. All 10 (100%) students with known sleep locations slept in one cabin. A professional pest control company rodent-proofed the cabin in July 2014; no tick acaricides had been applied. The cabin had evidence of rodents and ticks. Trapped rodents tested positive for *Borrelia hermsii*. **Conclusions:** This is the largest recorded outbreak among Arizona residents in the last 30 years. Health care providers should consider TBRF in febrile patients who have stayed in rustic cabins in endemic areas. By removing rodents from buildings, ticks might lose their primary food source and feed on persons; therefore, acaricide spraying should be concurrent with rodent-proofing.

Board 442. Small Commercial Poultry Farmers' Perception of Avian Influenza and Biosecurity, Bangladesh, 2011-12

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Background: Highly pathogenic avian influenza A (H5N1) virus is endemic in Bangladesh. Small-scale commercial farms accounted for 44% of 549 H5N1-confirmed outbreaks in poultry farms. Biosecurity measures may reduce the spread of avian influenza. Understanding farmers' perceived risks and identifying their motivation to adopt preventive measures can help develop interventions to reduce the risk of avian influenza transmission. This exploratory study aimed to understand small commercial poultry raisers' perception of bird flu and biosecurity. **Methods:** During 2011-12, our qualitative research team conducted in-depth interviews and two group discussions with poultry farmers in 16 purposively selected small commercial farms from two districts. We reviewed and summarized emerging themes from data. **Results:** Few (4/16) farmers mentioned knowing the term biosecurity and related it with bird flu. Farmers who had experienced an H5N1 outbreak in their flock equated biosecurity with fencing. Farmers perceived bird flu as a disease that occurred at a distant time or place that could not affect their farm. More than half of the farmers either did not know or did not believe that bird flu could be transmitted to humans. Farmers were more concerned about Newcastle and infectious bursal disease, which caused mortality in their flock, than bird flu. They reported practices to prevent disease, germs, and cold. Although they did not explicitly mention bird flu prevention or biosecurity, many of these practices, such as using footbath before entering the shed and keeping gap between batches, partially or fully matched with standard biosecurity measures. Only to prevent cold, which they considered to trigger other disease and

weight loss, farmers reported aerating the litter to release gas and keeping the litter dry, since they considered damp litter or gas as the source of cold. Their main motivation was to reduce mortality and raise healthy chickens. **Conclusions:** Bangladeshi small commercial farmers are more concerned about diseases that are more common in their flocks and were less concerned about bird flu. Interventions that consider promoting biosecurity to prevent not only bird flu but also other infectious diseases they consider harmful and to keep their flock healthy may motivate these farmers to change practices.

Board 443. A Cross-sectional Study to Examine Exposure and Risk Factors for Emerging Infectious Diseases Among Febrile Patients in Kilombero, Tanzania

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Background: Three-quarters of all emerging infectious diseases (EIDs) are of zoonotic origin with the majority of these diseases originating from wildlife, particularly rodents, bats and non-human primates. **Methods:** The objective of this study is to evaluate the type, prevalence and circumstance of emerging infectious diseases among people living and working in environments that lie at the animal-human interface. This study is conducted at Illovo Sugar Estate Hospital in Kilombero, Tanzania, a rural setting under high environmental pressure where agro-industrial land use has situated human populations in close proximity to areas of increased wildlife biodiversity. From June 11th- July 12th 2014, we conducted hospital-based surveillance to determine the etiology of acute febrile illness (AFI). A case report form and epidemiological survey were administered and biological specimens collected, in order to determine potential associations with infection status. **Results:** Over the course of 5 weeks, 205 febrile patients (≥ 37.5°C, ≥ 1 year of age, with symptomatic onset of ≤ 5 days) were enrolled, including 70 children (between 1 and 15 years of age; 34%) and 135 adults (≥15 years of age; 66%). Study activities yielded 205 malaria rapid diagnostic tests (RDT), 197 blood draws, and 115 nasopharyngeal/oropharyngeal swabs. Of the adult participants, 75 (56%) work in sugarcane fields, while 18 (13%) work in a factory setting. Among all febrile participants, 115 (56%) are members of families that own livestock, 155 (76%) and 119 (58%) have recently observed rodents and bats *in* their homes, respectively, and 121 (59%) observed primates *near* their homes. Of all enrolled fever cases, 119 (58%) were malaria positive as determined by RDT. Biological specimens are currently being analyzed using AFI TaqMan Array Cards (TAC)_a multi-pathogen detection assay used for targeted syndromic surveillance. **Conclusions:** Preliminary findings have indicated a high degree of animal-human interaction with known reservoirs of emerging pathogens. While RDTs detected biomarkers for malaria (*P. falciparum* predominately) among the majority of participants, nearly half of all febrile cases tested negative for malaria infection; thus warranting further testing for other etiologic agents of fever that may be prevalent in this area.

Board 444. Human Brucellosis and Goat Farms in Ratchaburi, Thailand, 2013

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Background: Brucellosis is a disease caused by *Brucella* spp., a facultative intracellular gram-negative cocco-bacillus. It is an important infectious disease among goats and transmissible to human. In April 2013, Ratchaburi Provincial Health Office notified Bureau of Epidemiology (BoE) that a goat farmer was diagnosed with brucellosis in Chombeung and Saun Pheung districts. BoE investigation team investigated the outbreak, from 7 to 10 May 2013 to find additional cases in human, describe the epidemiology and implement control measure. **Methods:** The investigation team collected goat farms and keepers information in affected area using Snowball technique. Brucellosis laboratory with Rose Bengal Test (RBT) results of the goats, residing in the same farms with human cases, were obtained from Ratchaburi provincial livestock office. Social network of goat farms was analyzed with Ucinet6 program. **Results:** The investigation team interviewed 54 people in 34 farms. Two goat farmers were positive. Network of goat farms showed linkage between the positive farms and other farms, merchants and slaughterhouses, which conformed to the progress of disease spreading. Chombeung district had positive goats in farm since 2012 and may transmit the disease to other farms in the network. **Conclusions:** The index goat farm was difference from the index human case although they are related with activities and time sequence. Information of network can be used to support disease control when resource is limited.

Board 445. Community-based Rotavirus Surveillance Among Pigs and the Children of Pig-raisers in Bangladesh, 2013-2014

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Background: Group A rotavirus is the most common cause of diarrhea in young children, while rotaviruses are found in a variety of animal species including pigs. However, limited data are available for rotavirus strains in pigs, which serve as reservoirs for novel human strains. We aimed to detect and characterize rotavirus genotypes circulating among piglets and the children of pig-raisers to investigate putative interspecies transmission. **Methods:** Rotavirus surveillance was conducted in two backyard pig-raising communities in rural areas of Rajshahi district from June 2013 to June 2014. We enrolled 240 households raising at least one pig each. Community health workers visited households twice a week to screen piglets (aged 0-8 weeks) and children (aged 0-59 months) with diarrhea. Fecal swabs were collected from piglets and stools samples from children with diarrhea. Specimens were analyzed for group A rotavirus RNA by rRT-PCR using rotavirus VP2-specific primers. The G (VP7) -encoding genes were characterized by dideoxynucleotide sequencing using consensus primer sets Beg9-End9 and P(VP4) - encoding gene were characterized by using consensus primer sets Con2-Con3. **Results:** We identified 23 piglets (median age: 3 weeks; range: 1-7 weeks) with diarrhea;10 (43%) had rectal swabs positive for rotavirus and 5 (50%) of these were genotyped as G9, 3 (30%) as G1 and 2 (20%) were untypeable. Ten (100%) P-genotypes were untypeable. Among 12 children with diarrhea (median age: 8 months; range 1-48 months), all had stool specimens positive for rotavirus; 3 (30%) of these were genotyped as G1, 1 (10%) as G2 and 6 (60%) were untypeable. One (10%) P-genotype was P8 and nine (90%) were untypeable. G1 strains detected from pigs and children in the same community were closely related (>99% partial VP7 identity), though the isolates with G1 genotype in pigs and children came from different households; in addition, piglet diarrhea

occurred on February but children diarrhea occurred on March, April and September 2014. **Conclusions:** This study provides important baseline data on genetic characterization of rotavirus strains in pigs and children of pig-raisers. Further analysis, including complete genome characterization, is ongoing to understand the full spectrum of genetic diversity of rotavirus strains in pigs and children.

Board 446. Human *Salmonella* Serotype Dublin Infections and Antimicrobial Resistance, United States

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Background: *Salmonella enterica* is estimated to cause 1.2 million illnesses each year in the United States. *Salmonella enterica* serotype Dublin infections commonly cause bloodstream infection and require antimicrobial therapy. Ineffective treatment due to antimicrobial resistance is of increasing concern, especially for invasive infections. We describe the epidemiology of Dublin with particular focus on resistance among clinical isolates. **Methods:** We analyzed data from five CDC enteric disease surveillance systems to summarize demographic, clinical, and antimicrobial resistance characteristic of Dublin infections. We compared Dublin with other non-typhoidal *Salmonella* (NTS) infections. **Results:** During 1968-2012, 3,679 Dublin infections were reported to CDC. The incidence of Dublin was 6.6 times higher in 2012 than in 1968; the incidence of other NTS was only 1.5 times higher. Forty-eight percent of Dublin isolates were from blood, compared with 5% for other NTS (P<.0001). From 1996-2012, hospitalizations (74%) and deaths (4%) were more common for Dublin than other NTS (38% and 0.5%, respectively; P<.0001 for both comparisons). During 1996-2004, 68% of Dublin patients were hospitalized and 3% died. During 2005-2012, 81% were hospitalized and 5% died. Ninety-five clinical isolates were analyzed for antimicrobial resistance from 1996-2012. Forty-five (47%) were multidrug resistant (MDR), defined as resistant to ≥3 classes. Among MDR isolates, 33 (73%) were resistant to ≥5 classes and 23 (51%) were resistant to ≥7 classes. During 1996-2004, 29% of isolates were resistant to at least one antimicrobial and the median number of classes against which these isolates were resistant was 4. During 2005-2012, 78% were resistant and the median number of classes was 7. **Conclusions:** Infection with *Salmonella* Dublin is often severe, with higher hospitalization and mortality rates compared with other NTS infections. The incidence and severity of Dublin infections have increased in recent years. At the same time, the percentage of resistant isolates and the number of drug classes to which Dublin isolates were resistant also increased. These data demonstrate the need for targeted prevention efforts and guided treatment of Dublin infections.

Board 447. Environmental Contamination with *Salmonella* Species in Homes with Reptile Pets, Minnesota 2003-2014

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Background: Of the 1.2 million *Salmonella* infections that occur annually in the U.S., 6% are thought to be reptile-associated; in Minnesota 3.5% of salmonellosis cases can be attributed to reptiles. *Salmonella* bacteria can persist in the environment for months, maintaining a source of infection. We sampled household surfaces in homes of reptile-associated salmonellosis (RAS) cases in Minnesota to evaluate reptiles as a source of environmental contamination by *Salmonella*. **Methods:** The Minnesota Department of Health performs active population-based surveillance for laboratory confirmed *Salmonella* infections. Salmonellosis cases are interviewed with a standard questionnaire; cases reporting reptile exposure are asked to submit a reptile stool sample for *Salmonella* testing. Cases were eligible for household sampling if the reptile was found to carry the same *Salmonella* serotype and pulsed-field gel electrophoresis subtype as the case isolate. **Results:** From 2003 to July 2014, 12 households were sampled. Median time from RAS case specimen collection to household sampling was 21 days (range, 5-78 days). Two hundred twenty-one samples were collected from the 12 households (median, 14.5 samples per household; range, 9-38). *Salmonella* was found in all 12 households; overall, 38% of samples were positive for *Salmonella* (range, 18% - 70% per household). The RAS case *Salmonella* serotype was found in all 12 households; overall, 16% of samples matched the RAS case serotype (range, 3% - 70% per household). Kitchen and bathroom sinks were most commonly contaminated; *Salmonella* was found in 7 (78%) vacuum cleaner bags, 86% matching the RAS case serotype. **Conclusions:** Contamination of household surfaces with *Salmonella* bacteria was common in RAS households. *Salmonella* strains matching by serotype were found in the RAS case, the associated reptile, and the household environment, indicating that *Salmonella* contamination is not limited to the reptile habitat. Household surfaces are important reservoirs of *Salmonella*, allowing for indirect transmission of *Salmonella* from reptiles to humans. This study supports previous findings that vacuum cleaners are effective collectors of bacterial contamination from the household environment.

Board 448. Chikungunya Virus Infections in Florida, 2014

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Background: In December 2013, the first local transmission of chikungunya virus was reported in the Americas. Since then, the United States has seen an increase in chikungunya cases among travelers returning from endemic areas, particularly the Caribbean and South America. In July 2014, Florida reported the first local transmission of chikungunya virus in the continental United States. **Methods:** Cases were reported and interviewed by the Florida Department of Health. The Council for State and Territorial Epidemiologists case definition for chikungunya virus was used to classify cases as either probable or confirmed. Surveillance related to local introductions of chikungunya virus included 50-100 meter cluster investigations around a patient's residence, enhanced syndromic surveillance, and medical record review. Awareness was increased through media coverage, reverse 911 dialing, and targeted mailings. **Results:** From January 2014 to February 2015, Florida reported 11 locally acquired and 492 imported chikungunya fever cases with onset in 2014. All 11 locally acquired cases and 215 (44%) imported cases were confirmed, most by polymerase chain reaction (PCR). All 11 locally acquired cases were Florida residents while imported cases included 457 Florida residents and 35 non-residents. Among imported cases, the most common reason for travel was to visit friends and relatives, reported by 359 (77%) of those responding. The most common country of exposure was Puerto Rico, reported by 128 (26%) patients, followed closely by Haiti, reported by 109 (22%) patients. The 11 locally acquired cases were reported in four South Florida counties: one case in Broward, two cases in Miami-Dade, and four cases each in Palm Beach and St. Lucie. Three of these counties, Broward, Miami-Dade, and Palm Beach, have reported 237 (48%) of the 492 imported cases. Overall, the 503 cases reported in Florida were 60% female, 46% white, and 51% non-Hispanic. The median age was 51; 23% of cases were 65 or older and 7% were 18 or younger.

Conclusions: Disease activity in the Caribbean and the Americas can have a significant public health impact on Florida residents. Awareness of the situation in Florida can help inform surveillance activities and control efforts throughout the United States.

Board 449. Leptospirosis Surveillance—Using Dogs as Sentinels for Human Infection in New York City, 2006–2014

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Background: Leptospirosis is reportable in humans and animals in New York City (NYC). Human leptospirosis is rare, with 0-3 cases annually. The Department of Health and Mental Hygiene (DOHMH) began laboratory-based surveillance for canine leptospirosis in June 2006 to assess the use of dogs as sentinels for human infection, better define the ecology of leptospirosis in NYC, and identify clusters. **Methods:** DOHMH investigates human leptospirosis reports by interviewing the physician and patient. Canine reports from a major veterinary laboratory and veterinarians are investigated by interviewing the veterinarian and dog owner. Clinical and demographic characteristics and risk factors were summarized. As different animal species are known to harbor specific serovars, predominant serovar(s) were compared with animal exposures. ArcMap was used to visualize space-time clusters. **Results:** In 2006-2014, there were 20 human cases, most from the borough of the Bronx (n=7, 35%). Serovars were identified in 13 patients; 12 were infected with *L. icterohaemorrhagiae* and 1 with *L. bratislava*. Eight patients were exposed to rodents. From June 2006-2014, there were 129 canine cases. Most resided in Manhattan (n=53, 41%) or Brooklyn (n=39, 30%). Twenty-six cases (20%) traveled and likely acquired their infections outside NYC. Among cases with no travel, the predominant serovars (serovar(s) with the highest titer) included *L. bratislava* (n=36), *L. icterohaemorrhagiae* (n=30), and *L. grippotyphosa* (n=27). Serovars of canine cases were associated with exposure to animal reservoir hosts: 93% of dogs with *L. icterohaemorrhagiae* or *L. bratislava* were exposed to rodents and 78% with *L. grippotyphosa* were exposed to raccoons, opossums, or skunks. Two clusters were detected in 2007 (n=2) and 2008 (n=3). Canine cases were not geographically representative of human cases. **Conclusions:** Human and canine leptospirosis infections in NYC are attributable to serovars associated with rodents and other small mammals, reflecting the resident animal reservoir species. Human and canine cases were distributed throughout NYC but no clustering was seen, suggesting that canine surveillance did not predict human infections. However, investigating canine cases and sharing reports has enhanced our relationship with the veterinary community.

Board 450. Development and Implementation of One Health Surveillance and Research Activities at the Animal-Human Interface in Vietnam, 2009-2015

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Background: One Health identifies opportunities and challenges of zoonotic disease prevention and control within existing human, animal and environmental health systems, requiring multi-sector cooperation. Regional epidemics and global pandemics have occurred because of challenges at this animal-human interface (AHI). We developed and implemented a multi-sector mechanism for conducting joint human and animal surveillance and research activities at the AHI in Vietnam. **Methods:** Leveraging existing partnerships and creating new collaborative mechanisms, the U.S. Department of Health and Human Services and Centers for Disease Control and Prevention (CDC), and the Vietnam Ministries of Health (MOH) and of Agriculture and Rural Development (MARD), signed bi-lateral and multi-sector agreements supporting a One Health approach to zoonotic disease activities in Vietnam. **Results:** Over 6 years, CDC established cooperative agreement partnerships with MOH and MARD and conducted joint One Health surveillance and research activities in people, pigs and poultry. Accomplishments included human and animal influenza virus identification, prevalence and seasonality; risk factor determination for virus transmission between species; and evolution of poultry and human influenza viruses over time. Influenza A viruses of interest included human seasonal H1N1, H1N1pdm09, and H3N2; avian H5N1 (multiple clades), H5N6, H7N9, and H9N2; and swine H1N1, H3N2, and vH3N2. **Conclusions:** CDC, MOH and MARD established a One Health partnership mechanism through inter-agency agreements and joint activities. With 10 international conference presentations and manuscripts in development, MOH, MARD and CDC have increased Vietnam capacity for multi-sector One Health activities, provided scientific and evidence-based data for zoonotic disease prevention and control, strengthened One Health collaboration and coordination between ministries, and enhanced public health and animal health partnerships between two countries. Global increase in the transmission of emerging zoonotic diseases from animals to humans and the ease and speed of global travel causes major concerns for both animal and human health. Continued One Health surveillance and research at the AHI may help to prepare for, control and reduce this global threat.

Board 451. Early Indicators of Fatal Leptospirosis During an Epidemic in Puerto Rico: A Case-control Study

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Background: Leptospirosis, a potentially fatal zoonosis caused by *Leptospira* spp. bacteria, is endemic in Puerto Rico. Leptospirosis has a broad clinical presentation, and delayed diagnosis and treatment may lead to increased mortality. A case-control study of human leptospirosis was performed to identify demographics, clinical characteristics, and medical interventions associated with fatal outcome. **Methods:** Fatal leptospirosis cases that occurred in 2010 were identified through enhanced surveillance for fatal acute febrile illness. To identify nonfatal leptospirosis cases, suspected dengue cases reported via passive surveillance but had no evidence of dengue virus infection, and were further tested for evidence of infection with *Leptospira* spp. Specimens were tested by microscopic agglutination test, immunohistochemistry, and PCR. Fatal and non-fatal cases were matched 1:1-3 by age and status of hospitalization. Records were reviewed from all medical visits. **Results:** In total, 170 leptospirosis cases were identified; 21 (12%) were fatal. Leptospirosis cases occurred predominantly in males (80%), in both urban and rural areas, more frequently during the rainy season, and in all age groups; highest incidence was in 40-69 year-olds. Prevalence of chronic medical conditions and day post-illness onset of first presentation were similar between fatal and non-fatal cases. Fatal cases had more medical visits than nonfatal cases, but were more likely to be diagnosed as leptospirosis and admitted at first presentation. Non-fatal cases were more likely to have fever and cough at first presentation. Fatal cases were associated with elevated white cell count, neutrophil counts, total bilirubin, BUN, and creatinine, and decreased

albumin and bicarbonate at first presentation. During hospitalization, fatal cases were more likely to remain afebrile and develop hemoptysis, jaundice, altered mental status, or seizures. Analysis by multivariate logistic regression is ongoing. **Conclusions:** This study identified a high incidence (0.6 per 100,000 residents) of fatal leptospirosis in Puerto Rico in 2010. Symptoms and laboratory parameters were identified that predicted fatal versus nonfatal but severe leptospirosis. These factors may enable early recognition and appropriate treatment of severe cases.

Board 452. Investigation of Q Fever in Dairy Farms in Mae-On District, Chiang Mai, Thailand

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Background: Q fever is a zoonotic disease caused by the intracellular bacterium *Coxiella burnetii*. Although acute disease in humans is usually self-limiting, chronic infection may lead to endocarditis and death. Infections commonly result from inhalation of infectious particles from cattle, sheep, and goats, the primary reservoirs of *C. burnetii*. Although a previous study has identified *C. burnetii* as a common cause of infectious endocarditis in Thailand, the specific reservoirs responsible for these infections are not known. Mae-On district in Chiang Mai is one of the major cow milk producing areas in Thailand. A previous investigation in 2012 showed that two out of six cattle dairy farms (33%) were positive for Q fever by ELISA with 15% prevalence at the individual animal level in this district. Three out of 12 farmers (25%) were tested positive for Q fever serum antibodies by ELISA. This investigation was conducted to explore the potential role of dairy cattle and dairy farm environmentin Mae-On district as a reservoir of *C. burnetii*. **Methods:** In September 2013, the investigating team visited sixcattle dairy farms in Mae-On district including twoQ fever positive farms.At each farm, five environmental samples were collected, as well as serum, milk and vaginal swabs from each cow. Serum samples were tested for antibody against *C. burnetii* by IFA while other samples were tested for the presence of *C. burnetii* by PCR. **Results:** No environmental samples (n=30) were positive for *C. burnetii*. Although none of the vaginal swabs were positive for *C. burnetii*, four out of 60 milk samples (7%) and 13 out of 82 sera (14%) were positive. Both PCR and IFA positive proportions were higher in farms with previously infected farmers. **Conclusion:** These data identify dairy cows as a potentially important reservoir of *C. burnetii* in Thailand that could shed the bacteria in milk. A prospective study is planned for Mae-On district to determine the incidence of Q fever in dairy farmers and the disease impact on dairy production.

Board 453. Canine and Livestock Husbandry Practices Among Ohio Farmers and Potential for Zoonotic Disease Transmission

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Background: Dogs are often on livestock farms, where they serve important management and companion roles. However, they may also be involved in disease transmission between livestock and people. The increase in canine raw diets, canine companions as family members and an increasing population of immune-compromised people make this understudied disease pathway particularly important. The objective of this study was to quantify and qualify dog ownership among livestock producers, their husbandry and biosecurity practices, and concern for zoonotic disease potential. **Methods:** A 10-minute questionnaire was developed. Household and individual-level data were collected - demographics, number of livestock owned, dog ownership and husbandry practices, and attachment level to and preventive veterinary care for the dogs. It was mailed to 2000 Ohio livestock owners randomly selected from a farming magazine mailing list. Of respondents who had both dogs and livestock, a dog fecal sampling kit was mailed. Returned kits were tested for *Salmonella* spp. and ESBL-producing organisms using standard enrichment and selective media. **Results:** The survey response rate was 33%, of which 223 (73%) were livestock dog-owners (LDO). Approximately 55% of LDO households included at least one high-risk individual (i.e., < 5 yrs, ≥ 65 yrs, diagnosed with an immunocompromising condition). Dog-owning respondents frequently reported higher-risk husbandry practices: 54% had outdoor-only dogs, 50% never leashed or fenced their dogs, 75% rarely/never pick up their dogs' feces. Dog-livestock contact was often reported (73%), of which 70% indicated high-risk management practices (e.g., access to sick pens, new arrivals). Raw meat or animal products were fed in 24% of the households. Many respondents had little/no concern of the dog transmitting a disease to livestock or family members. Households with high-risk members reported similar husbandry, biosecurity, and concern levels (all p>0.05). Fecal sample testing is on-going. **Conclusions:** Dog ownership and close dog-livestock contact were frequently observed. High-risk practices were regularly reported and level of zoonotic disease concern was low, indicating a need for improved education and outreach for the livestock dog owning community, particularly for high-risk households.

Board 454. Changing Trends in Backyard Flocks: Review of Outbreaks of Human Salmonellosis Linked to Contact with Live Poultry—United States, 1990-2013

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Background: Ownership of backyard poultry flocks has increased in popularity concurrent with the increase in live poultry-associated salmonellosis (LPAS) in humans. These increases highlight the need to better understand practices that contribute to this emerging public health issue. We reviewed outbreak reports to describe the epidemiology of LPAS in the U.S.A., examine changes in trends, and inform prevention campaigns. **Methods:** LPAS outbreaks were defined by having ≥2 culture-confirmed human *Salmonella* infections with a combination of epidemiologic, laboratory, or traceback evidence linking illnesses to live poultry contact. Outbreak data was obtained through CDC's outbreak database, CDC's National Outbreak Reporting System, and literature review. Additionally, standardized poultry exposure questionnaires administered during 21 multistate outbreak investigations during 2008-2013 were analyzed to identify high-risk practices. **Results:** During 1990-2013, 51 LPAS outbreaks were documented, involving 2,188 illnesses, 306 hospitalizations, and 5 deaths. The median outbreak size was 25 case-patients (range: 4-356). Outbreak onsets ranged from January-July; duration averaged 4.2 months; 79% of outbreaks began during February-April. The median patient age was 9 years (range <1-92). Sixty percent (374/619) of case-patients reported exposure to chicks and 27% (170/619) to ducklings. The median time between obtaining poultry and illness onset was 17 days. Since 2007, outbreaks increased in size, occurred year-round, and were more frequently linked

to backyard flock ownership. High-risk practices included keeping poultry inside households [51% (194/381)] and kissing birds [14% (52/373)]. **Conclusions:** Live baby poultry remain an important source of human salmonellosis in the U.S.A., particularly among children. Recurring LPAS outbreaks highlight the need for strategies to prevent human illness associated with live poultry contact through a comprehensive One Health approach involving human, animal, and environmental health.

Board 455. Shiga-toxin Producing *Escherichia coli* O157 Infections in England 2009-2011: Effects of Climate and Land Use

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Background: This study examined the relationship between human cases of shiga-toxin producing *E. coli* O157 infection and land use, animal density, rainfall, sunlight, and temperature. **Methods:** Observational design using spatial and temporal visualisation, spatial exploration and logistic regression. Human case data was obtained from national surveillance systems for STEC in England, animal and land use data was taken from the 2010 agricultural census performed by the UK Department for the Environment, Food and Rural Affairs and climate data was obtained from the UK Met Office. **Results:** Increased odds of infection were associated with higher levels of cattle density, residence in the north of England and higher minimum temperature. Decreased odds were associated with land being used for horses. **Conclusions:** We conclude that higher cattle density levels result in an increased risk of infection either through direct contact with animals or as a result of environmental contamination.

Board 456. Novel PCR Exclusion Assay to Detect Pathogenic Spotted Fever Group *Rickettsia* in the Lone Star Tick (*Amblyomma americanum*)

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Background: While the lone star tick (*Amblyomma americanum*) is the most common and abundant human-biting tick in the southeastern United States where spotted fever rickettsioses are frequent, the role of this tick in transmitting and maintaining pathogenic rickettsiae remains poorly defined. The low pathogenicity spotted fever group *Rickettsia* (SFGR) *Candidatus* "Rickettsia amblyommii" (hereafter *R. amblyommii*) is commonplace in most populations of *A. americanum*. Many assays commonly employed to detect rickettsiae use PCR primers that target highly conserved regions in the SFGR and thus also detect *R. amblyommii*. Amplicons from these conserved assays must be sequenced to differentiate the abundant *R. amblyommii* infections from the less common SFGR, but the low abundance agents may not be detected in the presence of *R. amblyommii*. It is also not cost- or time-efficient to test for low prevalence rickettsial agents with multiple specific probe-based assays. **Methods:** Using the more than 50 available *Rickettsia* genomes, we identified a chromosomal region in *R. amblyommii* containing large deletions relative to the chromosomes of other SFGR. PCR-based assays were designed which detect the intact gene region in most SFGR, but not *R. amblyommii*. **Results:** We evaluated the assays against a variety of sample types, including DNAs derived from isolates of many pathogenic SFGR and *R. amblyommii* from multiple states, laboratory-maintained tick colonies of known infection status, and field-collected ticks, and found that they were successful at detecting pathogenic SFGR in a background of *R. amblyommii*, including *R. parkeri* and *R. rickettsii*, of most interest for their human pathogenicity. **Conclusions:** The use of a Ramb-Ex (*R. amblyommii* exclusion) assay in future studies will provide more accurate estimates of the prevalence of less common SFGR in *A. americanum* and thus clarify the role of this tick in the maintenance and transmission of the SFGR commonly responsible for human rickettsioses.

Board 457. The Ecology of Nipah Virus in its Natural Reservoir, *Pteropus giganteus*, in Bangladesh

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Background: Nipah virus (NiV) is an emerging zoonotic virus that has caused seasonal outbreaks of encephalitis in Bangladesh with greater than 75% mortality. *Pteropus giganteus* is the putative reservoir in Bangladesh, though little is understood about NiV in these bats. The primary route of spillover appears to be date palm sap consumption. We describe the ecology of NiV in *Pteropus giganteus*. **Methods:** Between 2006 and 2012 we collected urine, blood, feces, and saliva from 100 *P. giganteus* from each of 4 districts within and 4 outside the "Nipah Belt." 100 bats were also sampled quarterly from a population near recurring outbreaks. Urine, saliva and fecal samples were screened for NiV RNA by nested PCR. Serum was screened for anti-NiV IgG antibodies using an indirect ELISA, a recombinant expressed NiV-N antigen ELISA, and Luminex. An SIR model was used to test serological data from the longitudinal study for seasonal trends. **Results:** Nipah virus RNA was detected in 0 - 3.8% of bats, depending on time and location, which included locations outside the Nipah Belt and times of year beyond human NiV season. IgG-positive bats were found throughout Bangladesh (seroprevalence: 20% - 56%). The SIR models show seasonal infection in juvenile bats, peaking in July, with no apparent transmission among adult bats. Phylogenetic analysis of a 224bp segment in the NiV N-gene from 13 samples from the same population but across different time points showed >98% sequence homology. A divergent strain was identified in eastern Bangladesh. **Conclusions:** Our data support the conclusion that *P. giganteus* is the reservoir for Nipah virus in Bangladesh. NiV detection in bats was not limited by location or time of year, suggesting spillover would be possible anywhere in Bangladesh if a suitable bat-human interface was present. Seasonal and location-specific human activities such as date palm sap harvesting, rather than infection dynamics in bats, probably drive human epidemiology. The divergent N gene sequences in different locations, but N gene stability in one location over time, suggests that there may be localized strains circulating in bats. The genetic diversity observed in previously reported human cases from various locations in western Bangladesh may be a reflection of the strain circulating in the local bat population at the time of spillover.

Board 458. High Resolution Genotyping of *Bacillus anthracis* and Spatio-temporal Patterns of an Anthrax Epizootic in White-tailed Deer, *Odocoileus virginanus*

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Background: Anthrax, caused by the bacterium *Bacillus anthracis*, is enzootic in areas of North America. Despite the disease's long history, transmission dynamics during outbreaks among wildlife are poorly understood. Previous studies indicated clustering and directionality of anthrax outbreaks at regional levels; none have examined outbreak dynamics at the level of the individual carcass or compared such analyses to the genetic diversity of *B. anthracis*. High resolution spatio-temporal analysis and genotyping were used to investigate a single outbreak among white tailed deer, *Odocoileus virginanus.* **Methods:** Location and date of death or date found were obtained for 41 carcasses during the outbreak period. Spatial clustering and directionality were analyzed using *K*-function analysis and a direction test, respectively. Spatial clustering was compared with deer movement data obtained on the ranch during the outbreak season. Isolates from 16 carcasses and adjacent soil samples were genotyped using multiple locus variable number tandem repeat analysis (MLVA) and single nucleotide repeat (SNR) analysis; spatial and genotyping results were compared. **Results:** Carcasses were clustered at a distance of 680 meters, within the maximum daily activity space (1259 meters) of deer during the outbreak period. The directionality of the outbreak paralleled dry river beds. Isolates from the outbreak had identical MLVA genotypes. Four SNR sub-genoptypes (SGTs) were identified; two SGTs were isolated from each of two carcass sites. High SNR diversity occurred where carcasses were in closest proximity. **Conclusion:** The clustering of carcasses suggests ongoing transmission through environmental pathways initiated as each new carcass contaminates the immediate environment. Carcass locations were within the activity space of adjacent cases; deer had opportunity to encounter nearby carcasses sites and, potentially, freshly contaminated soil, browse contaminated by necropahgous flies, or biting flies. The direction test indicated river beds, which had denser browse and higher fly densities than the surrounding landscape, were areas of active transmission. SNRs did not provide clear evidence of linear transmission; however, areas of high diversity could indicate landscape features supportive of high transmission.

Board 459. Outbreaks of Cutaneous Anthrax Among Humans in Bangladesh: Understanding the Risk Factors from a Case-control Analysis

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Background: Though exposure to infected ruminants has been identified as a major risk for cutaneous anthrax, individual susceptibilities have not been fully investigated. The objective of this study was to determine risk factors that could guide measures to prevent anthrax in humans. **Methods:** During 2012-2013, we investigated 7 anthrax outbreaks in 4 districts. A case was a person with an acute skin lesion developing from a papular through vesicular to central black eschar over 2-6 days and exposed in the past 2 weeks to raw meat, carcass, body fluid or by-product of sick or dead ruminants with clinical and/or laboratory evidence of anthrax. All persons from outbreak communities who did not develop clinical illness within 2 weeks of exposure were controls. For a case-control study, we recruited one control from each of the four households nearest to an enrolled case. Odds ratios (OR), 95% confidence intervals (CI) and p-values were estimated by logistic regression. Multivariate logistic regression was done using variables significant at P<0.05. **Results:** Overall, 207 (15%) cases were identified among 1,359 exposed individuals. Compared to controls on univariate analysis, cases were more likely to have raw meat exposure while slaughtering or butchering (OR=36.0), have observed animal slaughter (OR=5.0), had a cut injury on exposed body parts (OR=26.0), have skipped ≥2 meals per week (OR=5.0), be aged ≥18 years (OR=3.0), and to smoke tobacco (OR=7.0); they were less likely to wash hands after handling raw meat or observing a slaughter (OR=0.5). On multivariate analysis, raw meat exposure (adjusted OR [AOR]=36.7, CI=11.3-118.7), observing animal slaughter (AOR= 4.0, CI=1.3-12.0), skipping meals (AOR=4.0, CI:1.2-10.9), smoking tobacco (AOR=2.0, CI:1.2-3.2) and washing hands (AOR=0.5, CI:0.3-0.8) were independently associated with anthrax infection. **Conclusions:** Exposure to raw meat while slaughtering or butchering was identified as the strongest risk factor, underscoring the need to ensure livestock vaccination. However, this is difficult to accomplish in resource-poor countries like Bangladesh. Meanwhile, implementation of a hand washing intervention could ameliorate risk. Smoking and skipping meals may increase susceptibility by lowering host immunity; these novel risk factors warrant future studies.

Board 460. Use, Characterization, and Potential Zoonotic and Antibiotic Resistant Organisms Among Dogs Using Dog Parks in the Minneapolis/St. Paul Metropolitan Area

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Background: Dog parks are increasingly popular venues for dog owners. In 2010, there were an estimated 2200 dog parks in the United States. Within the 7 county metropolitan area of Minneapolis/St. Paul there are more than 60 dog parks. Considering the large numbers of dogs visiting these parks there are opportunities for increased dog to dog and dog to human interactions. These frequented areas can permit the spread of disease causing organisms among dogs and potentially people. Our aim was to characterize dog parks, owner practices, and the dogs visiting metropolitan dog parks. **Methods:** Owners were surveyed to determine the frequency of visits, vaccination and deworming status, and health of their dog(s). Site visits were done to collect information on the size and topology of the park and posted park rules/recommendations. Up to 10 owners were surveyed at each park and asked to provide feces from their dog. Fecal samples were cultured for *Campylobacter*, *Salmonella*, and *Escherichia coli*. Antibiotic susceptibility testing was performed on *E. coli* isolates using the Sensititre System. *E. coli* samples were tested for the presence of AmpC and ESBL production using disk diffusion for five antibiotic combinations. **Results:** 22 dog parks were visited during July and August, 2013. Dog poop bag dispensers were available at most (91%) parks. 42% of owners stated that they visited a dog park 5 or more times per week. 175 (96%) owners reported that their dog's rabies

and routine vaccination status was up to date. 186 fecal samples were collected. 58 (53%) of 109 fecal samples were *Campylobacter* sp. positive and 1 (.5%) of 186 samples was culture positive for *Salmonella*. 46 of 50 *E. coli* samples resistant to cefotaxime were AmpC positive and 4 *E. coli* isolates were extended spectrum beta-lactamase (ESBL). A number of these isolates were multidrug resistant, harboring plasmids that confer the phenotype. Isolates from different dogs in the same dog parks harbored similar antimicrobial susceptibility profiles. **Conclusions:** Dog owners who visit metropolitan dog parks did frequently over a given week. Potential zoonotic agents and antimicrobial resistant organisms were isolated. Veterinarians need to be aware of the potential for infectious disease transmission of zoonotic and antibiotic resistant organisms among dogs using dog parks.

Board 461. Self-reported Acute Health Symptoms and Exposure to Companion Animals

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Background: In order to understand the burden of disease associated with acute health symptoms (e.g. gastrointestinal [GI], respiratory, dermatological), it is important to study how common exposures influence these symptoms. Contact with familiar and unfamiliar animals can result in a variety of health symptoms related to zoonotic infections and allergic responses; however, few studies have examined this association in a large-scale cohort setting. **Methods:** Cross-sectional data collected from 50,507 beachgoers at 9 beach sites in the United States from 2003-09 were used to examine associations between animal contact and acute health symptoms during a 10-12 day period. Fixed effects multivariable logistic regression estimated adjusted odds ratios (AOR) and 95% confident intervals (CI) for associations between animal exposures and outcomes of GI illness, respiratory illness, and skin/eye symptoms. **Results:** Two-thirds of the study population (63.2%) reported direct contact with animals, of which 7.7% had contact with at least one unfamiliar animal. Participants exposed to unfamiliar animals had significantly higher odds of self-reporting all three health symptoms, when compared to non-animal exposed participants (GI: AOR=1.4, CI=1.2-1.7; respiratory: AOR=1.6, CI=1.3-1.9; and skin/eye: AOR=1.8, CI=1.5-2.2), as well as when compared to participants who only had contact with familiar animals. Specific contact with dogs, cats, aquarium fish, or pet birds was significantly associated with at least one acute health symptom; AORs ranged from 1.1-1.4, when compared to participants not exposed to each animal. **Conclusions:** In a survey of >50,000 respondents, contact with animals, especially unfamiliar animals, was significantly associated with GI, respiratory, and skin/eye symptoms. Such associations could be attributable to zoonotic infections and allergic responses associated with animal contact. Etiological models for acute health symptoms should consider contact with companion animals, particularly exposure to unfamiliar animals. Prevention of pet-associated zoonotic diseases includes practical, commonsense measures like hand washing, but are often overlooked by pet owners and non-pet owners alike. *This abstract is of a proposed presentation and does not necessarily reflect EPA policy.*

Board 462. Molecular Characterization of Zoonotic Poxviruses Circulating in the Amazon Region of Colombia, 2014

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Background: Poxviruses cause exanthematous lesions in humans and animals. Orthopoxviruses gained much attention as smallpox caused by *Variola virus* killed millions of people before its eradication in 1980. In addition, *Vaccinia virus* (VACV) was used for vaccination during the eradication of smallpox. Before the 1970s VACV zoonotic outbreaks were associated with smallpox vaccination campaigns. However, recent VACV outbreaks have occurred with no such association in countries including Brazil and India. Parapoxviruses such as *Pseudocowpox virus* (PCPV) have been scarcely reported in South America. **Methods:** Following reports of cutaneous lesions in farmworkers caring for dairy cattle in rural areas of the department of Caquetá, Colombia, a public health investigation identified 5 persons with clinical disease compatible with poxvirus infection**.** Serum and lesion-derived samples were collected following standard procedures. Anti-orthopoxvirus IgM and IgG were tested by ELISA. Molecular characterization was achieved by PCR amplification and sequencing of the A25R and A56R genes for orthopoxviruses, and the p37K gene for parapoxviruses. Phylogenetic analysis identified specific poxvirus strains and established their relationships with previously characterized strains worldwide. **Results:** Lesions in humans were associated with contact with infected cattle. These were typically papular or vesicular, becoming ulcerative and accompanied by localized pain, fever, and lymphadenopathy. Three patients had both anti-orthopoxvirus IgG and IgM antibodies and were found infected with a VACV strain closely related and ancestral to the previously described Group I strains which circulate in Brazil. Another patient had anti-orthopoxvirus IgG alone. This patient was found infected with PCPV. The fifth patient was also found infected with PCPV. **Conclusions:** This is the first study that describes the molecular detection and characterization of zoonotic VACV and PCPV in Colombia. Our findings, together with previous evidence of similar outbreaks uncharacterized by laboratory in Colombia, stress the need for the establishment of intensified poxvirus surveillance in humans and livestock, as well as identifying hosts and reservoirs in the nature which may be involved in sylvatic transmission cycles.

Board 463. Spatial-temporal Distribution of Rodent-borne Hantavirus Infection (*Oligoryzomys fulvescens*) in Tonosi—Panama

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Background: Hotspot detection and characterization has played an increasing role in understanding the maintenance and transmission of zoonotic pathogens. Most recent studies are performed at macro-scale and describe broad temporal patterns of population abundances while few have been conducted at a microscale over short time steps that better capture the dynamical patterns of key populations. These finer resolution studies may better define the likelihood of local pathogen persistence. This study characterizes the patterns, spread and spatio-temporal dynamics of *Oligoryzomys fulvescens*, an important mammalian reservoir in central America. **Method:** Information collected in a longitudinal study of rodent populations in the community of Agua Buena in Tonosi, Panama,

between April 2006 and December 2009 was analyzed using non-spatial analyses (box plots) and explicit spatial statistical tests (correlograms, SADIE, and LISA). A 90 node grid was built (raster format) of base map. The area between the nodes was 0.09 km^2 and the total study area was 6.43 km^2 (2.39 x 2.69 km). The temporal assessment dataset was divided into four periods: the dry and rainy months and the months of April and December were considered transition months during each year. **Results:** There were heterogeneous behavior patterns in the densities and degrees of dispersion of *O. fulvescens* that varied across seasons and among years. Moran's I showed a strong positive spatial autocorrelation up to distances of 300 - 600 m - indicating the geographic extent of local populations. SADIE analyses identified spatial clusters (the *Pa* index for all periods were highly significant ($p<0.01$)). While LISA, characterized changes in the configuration from one period to another in all the analyzed periods ($p<0.05$), but not in all areas studied. **Conclusion**: *Oligoryzomys fulvescens* shows a well-defined spatial pattern, that evolves over time, and leads to a pattern of changing aggregation. Thus, hot spots of abundance show a generally shifting pattern that helps explain the intermittent risk from pathogens transmitted by this species. Drivers of this variation is associated with seasonality , as well as anthropogenic pressures that occur with agricultural activities.

Board 464. Influenza A Prevalence in Two Swine Populations in Guatemala, 2012

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Background: Swine influenza A viruses are important due to their potential impact in swine production and as a zoonotic disease. Surveillance efforts in Guatemala are limited. **Methods:** A cross-sectional study was carried out to estimate the virological and serological prevalence of influenza A in swine in two municipalities in Guatemala (Santa Rosa and Quetzaltenango) in 2012. One nasal swab and one serum sample were taken from each animal. Swabs were tested by RT-PCR essays using primers directed at the influenza A matrix gene. The presence of antibodies against influenza A in serum was tested using a commercial competitive ELISA essay (IDEXX Influenza A Ab test). We investigated associations (prevalence risk ratio [PRR] with 95% confidence intervals [95% CI]) between different exposures and viral infection, including sex, age, density, farm type, presence and report of other swine in the same farm with respiratory infection signs during the last month, and presence of poultry in the same farm. **Results:** Two hundred pigs were sampled in each municipality; 293 (73%) male, 326 (82%) 2- 6 months old, 319 (80%) from smallholdings. A total 400 nasal samples and 399 serum samples were processed. The estimated virological prevalence in swine in Santa Rosa was 19% (95% IC 95: 14% - 23%), and 14% (IC 95%: 12% - 16%) in Quetzaltenango, and the serological prevalence was 0% (IC 95%: 0% - 0%) in Santa Rosa and 9% (IC 95%: 7% -11%) in Quetzaltenango. None of the positive pigs presented respiratory signs at the time of sampling or belonged to a farm that reported pigs with signs during the previous month. Swine that were farmed with domestic ducks or geese were found to have 5 times greater risk of being infected with influenza A (PRR: 5, IC 95%: 2.5 - 9.7) in Santa Rosa, and a borderline association in Quetzaltenango (PRR: 1.9, IC 95%: 0.9 - 3.8) was observed. Other borderline associations were animal age and sex, rearing density and being farmed with chickens or turkeys. **Conclusions:** Although results are limited by data available for some variables and knowledge of the time of exposure, the observed associations should be further investigated. These results will help to better understand the circulation of influenza A viruses in Guatemala and support the development of a long term surveillance and hypotheses that could help characterize viral circulation.

Board 465. The Results of Epizootic Studies on Plague and Tularemia in the Plague Natural Foci of Transcaucasian Plain-foothills

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Background: Subspecies of tularemia, *Francisella tularensis holarctica* circulates in the territory of Azerbaijan. First time tularemia was isolated in 1941 and further in 1948, 1949, 1955, and 1958 in Azerbaijan. *F. tularensis* was identified in about 15 water reservoirs located in the country. Tularemia epizootics were reported among wild rodents in 34 administrative regions of Azerbaijan during the period of 1958-2013 and 201 human cases were reported in 22 administrative regions from 1943 to 2013. Before Soviet Union was collapsed Republican Anti-Plague Station (RAPS) conducted yearly monitoring for identification of epizootics among rodents, implement anti-epidemic measures towards elimination of sources of infection. In 2013 the STCU Partner Project "Research of natural plague and tularemia foci and development of sanitary arrangements complex in Azerbaijan" was started in collaboration with Armed Forces Biomedical Research Institute. **Methods:** During two years, complex of measures directed on identification of tularemia epizootics in Jeyranchol region and partially in Ganja - Kazakh plain and foothill of the Lesser Caucasus mountains. Overall 2.525 samples from rodents and other mammals, 13.647 ectoparasite samples, including 11.914 samples of 11 flea species and 1.760 samples of 10 tick species were tested for presence of tularemia agent using bacteriological and biological methods in the laboratory while carrying out the tasks over a period of two years. **Results:** 418 bioassay animals were infected (white mice). All strains were virulent for white mice and guinea pigs and showed agglutination with a specific tularemia serum. Prepared extracted DNA from pieces of internal organs of 394 rodents was tested using Real Time PCR instrument and 7 positive results were obtained. It's also notable that, this was determined using molecular tests, as well as for the first time for this region, agent cultures were isolated from *Libyan jirds* and *Ixodic ticks* (*İxodes ricinus* and *Rhipicephalus bursa*), collected from sheep and goats. These strains belonged to holarctic race of tularemia microbe. **Conclusions:** The results of the two-year monitoring are valuable by the reason that new areas were identified during the task conduction process, where previously the epizootics of tularemia were not observed.

Board 466. Comparison of Highly Pathogenic Avian Influenza A(H5N1) Viruses Isolated From Humans in Vietnam Provides Evidence for Recent Reassortment and Emergence of a Novel Clade 1 Genotype

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Background: Highly pathogenic avian influenza (HPAI) A H5N1 virus is considered endemic in Vietnamese poultry and has caused human infection since 2003. Human infections with HPAI H5N1 are a public health concern due to a high mortality rate and the potential for emergence of pandemic viruses with sustained human-to-human transmission. Since their detection in 2003, HPAI H5N1 viruses isolated from birds and humans in southern Vietnam have been classified as clade 1 with a single genome constellation (VN3) while viruses isolated recently from central and northern provinces were classified as clade 2.3.2.1c (VN48). We provide evidence of continuing evolution of the HPAI H5N1 virus in Vietnam. **Methods:** HPAI H5N1 virus was identified by the Institute Pasteur, Ho Chi Mihn City in 4 human cases from 2012 and 2 human cases from 2013. Virus isolation and full genome sequencing was successful for two of the 2012 cases and both cases from 2013. Phylogenetic and antigenic characterization of these viruses was performed. **Results:** Comparison of these viruses revealed the emergence of a unique reassortant virus in 2013 composed of clade 1.1.2 hemagglutinin and neuraminidase surface protein gene segments but internal gene segments derived from clade 2.3.2.1a viruses (VN12), which have circulated in Vietnam since 2012. Closer analysis revealed mutations in multiple genes of this novel genotype previously associated with increased virulence in animal models and the potential for adaptation to mammalian hosts. Despite the changes identified between the 2012 and 2013 genotypes, virulence in the ferret model was similar. Antigenically, the 2013 viruses were poorly cross-reactive with ferret antisera produced to the clade 1 progenitor virus, A/Vietnam/1203/2004, but reacted strongly to antisera produced against a newly proposed clade 1.1.2 WHO candidate vaccine virus with comparable hemagglutination inhibition titers as the homologous antigen. **Conclusions:** This study indicates a shift in the genome of clade 1 H5N1 viruses circulating in poultry in southern Vietnam and shows their ability to successfully reassort with viruses from other H5N1 clades and to infect humans. Continuous surveillance of HPAI H5N1 and other avian influenza viruses in Vietnam is essential to monitor virus evolution, to assist in control and prevention strategies, and to identify viruses of pandemic potential.

Board 467. Prevalence of and Risk Factors for Q Fever in Dairy Animals and Agricultural Workers in the Central Lowland Regions of Azerbaijan

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Background: The prevalence of rickettsial infections (including Q fever) in humans and animals in Azerbaijan is unknown, due to lack of research over the past 35 years. The last available data from 1960 describe Q fever outbreaks in Absheron, Nakhchivan and the Jeyranchol plain. Recently, cases of abortion have been widespread in cattle with 503 undiagnosed cases documented in the Central Lowlands in 2012-2014. Due to the serious public health implications of Q fever, a potential cause of the abortions, the Republican Veterinary Laboratory and Anti-Plague Station are planning to conduct a joint One Health project to evaluate the prevalence and risk factors of Q fever in select regions of Azerbaijan. The project's objectives are to 1) compare the seroprevalence among those with high and low exposure to ruminants, 2) identify the presence of Q fever in ruminants of the volunteers, and 3) to analyze the potential risk factors associated with being exposed to or infected with this pathogen. **Methods:** Farms and people in four regions of the central lowlands (Sabirabad, Saatli, Imishli, and Beylagan) will be evaluated. Blood samples will be collected from people who have close contact with ruminants and those who have limited contact with ruminants and tested by ELISA for the presence of anti-*Coxiella burnetii* antibodies. Vaginal swabs, and fecal and milk samples will be collected from ruminants of volunteers and tested using real time PCR. Potential risk factor information will be collected at the time of sampling and data analyzed to assess whether specific risk factors are associated with being seropositive. **Expected Results:** We expect that the seroprevalence of *C. burnetii* in people with high exposure to milk-producing animals will be greater than in those with low exposure. Risk factors involving close contact with reproductive fluids and raw dairy products will be associated with increased risk of exposure. In addition to collecting information on the disease, this study will provide an opportunity to educate people on the zoonotic disease, including anti-epidemic and prevention measures. As a One Health project, the cooperation between the Ministries of Health and Agriculture will be strengthened in Azerbaijan and a model established for joint projects in the future.

Board 468. First Incidence of Detection of Infection with a Zoonotic Parapoxvirus in Humans in the Country of Georgia

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Background: The genus Parapoxvirus (PAPV), in the family Poxviridae, is composed of the orf virus (ORFV), pseudocowpox virus (PCPV) and bovine papular stomatitis virus (BPSV). Infection with PAPV can manifest with skin lesions similar to infection with *Bacillus anthracis* or novel orthopoxvirus (OPXV). *Bacillus anthracis* is endemic in Georgia and novel OPXV strains have recently been discovered in-country. Infection with members of PAPV is likely under-recognized because of a lack of clinical suspicion and available molecular diagnostics in the country. Therefore, rapid detection of parapoxviruses is extremely important for exclusion of other febrile rash-causing illnesses in humans. Previously, no detection of parapoxviruses has been reported in Georgia. In this study, we report the findings of the implementation in Georgia of a rapid, real-time PCR assay for the detection of PAPV. **Methods:** Archived DNA samples (n=130) extracted from human clinical cases presenting with skin lesions from 2011 to 2013 were screened by RT-PCR for detection of PAPV. The assay was used to conduct differential diagnosis between infections with PAPV or B. anthracis and OPXV. A Taqman based RT-PCR assay for detection of PAPV was used and ran on an ABI 7500 Fast RT-PCR machine per manufacturers' instructions. **Results:** Results showed that 40% (n=52) out of 130 samples tested positive for PAPV infection. In light of these findings, we began screening patients suspected of having infections with *B. anthracis* or OPXV for the presence of PAPV. Based on this approach, in November and December of 2014, we identified two additional sporadic cases of PAPV infection in humans. Both patients were females from parts of Georgia: one from west (Khoni, Imereti Region) and the other from east (Gardabani, Kvemo Kartli). Both patients were exposed to an infected animal. Furthermore, PAPV infection is confirmed in several more clinical samples obtained from different parts of the country since January 2015. **Conclusions:** In this study we demonstrate that PAPV is present in Georgia and has spread in both Eastern and Western Georgia. These results may explain the etiology of undiagnosed clinical cases seen in patients presenting with skin lesions. Due to this enhanced awareness there has been an observed increase in reported cases of poxviruses in humans and animals in Georgia. Acknowledgements: To Neil Vora and Yu Li from CDC Atlanta for supporting this.

Board 469. Global Dissemination of *Bartonella* Infections by Invasive *Rattus* Rats

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Background: The most of *Bartonella* spp. detected in the Old World rats (genus *Rattus*) belong to a defined phylogenetic lineage. This group of *Bartonella* spp. is hypothesized to have emerged from Asia with *Rattus* rats due to human activity before becoming common and widespread in urban and rural environment around the world. **Methods:** The study of distribution and diversity of *Bartonella* spp. in rats from 17 countries of Asia, Africa, Europe, and North and South Americas was conducted. Gene sequence variations were analyzed among >600 isolates obtained from rats, and complete genome sequences were compared between isolates from the 5 continents. **Results:** The investigations of aboriginal *Rattus* spp. from Bangladesh, Nepal, Thailand, Vietnam, and southwestern China have revealed very high diversity of bartonellae. Those included several recognized species (*B. elizabethae, B. tribocorum, B. rattimassiliensis,* and *B. queenslandensis*) along with a number of unnamed strains. In contrast, the diversity of bartonellae in invasive *Rattus* rats in America, Africa, and Europe was reduced thought the prevalence can be high. Not all rat populations within US carry bartonellae. Populations of rats were highly infected with bartonellae in Atlanta, Baltimore, New Orleans, Oakland, and Los Angeles; while all examined rats in Denver, Chicago, Los Vegas, New York, and Phoenix were *Bartonella*-free. Most rat isolates obtained from US and Canadian cities were phylogenetically close to *B. tribocorum*, the most common species in rats from Thailand. Several rats collected near San Francisco Bay carried *B. coopersplainsensis*, a species described in rats from Australia. In Salvador (Brazil), the most common species identified in rats was *B. queenslandensis*, a bacterium also described in rats from Australia. The analysis indicated that likely there were numerous events of introduction of bartonellae from Asia to other regions, with the apparent global dispersal of six major clades containing Asian isolates. **Conclusions:** The genetic and genomic analyses of *Bartonella* strains obtained from rats from many countries have demonstrated that this bacterial complex evolved and diversified in Asia before being disseminated by rats to other parts of the globe. It was hypothesized that the presence of a specific *Bartonella* sp. in a particular location is largely dependent on the characteristics of the founding or subsequently introduced rat populations.

Board 470. Epidemiological Characteristics of Brucellosis on the Territory of Municipality of Veles for the Period Between 1990-2014

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Background: Brucellosis is one of the most important zoonosis according to its meaning and expansion in Republic of Macedonia. The continuous and long term of work with antyepidemic activities for its prevention didn't give the expected results. That is why we still registry new cases every year. **Methods:** The material for work is based of the continuous analyses of the information from Public Health Center Veles using analytical and descriptive method. The analyzed information is got from the checked cards for transitive diseases, epidemiological interview and the information from terrain research and the hospital histories of the patients from Infective department of Public hospital, Veles. **Results:** According to the way of spreading 65,4 % of the patients had contacts with infected animals and they consumed unprocessed milk products. 24,1% only consumed unprocessed milk products, 7,1 % had contacts with infected animals and 3,4% with unknown way of transmission. According to the source of infection: 3,9% had contacts with infected cow, 61,5 % with infected sheep and 34,6 % with infected goat. Consummation of the unprocessed milk product leads us to: 50,4 % with infected sheep, 45,3% with infected goat and 4,3 % with infected cow. The infected patients are 68,6 % men and 31,4 % women by gender. There is a seasonal spreading of the infection, between third and the ninth month of the year. The distribution by age is: 18,7 % between 10 and 19 y.old, 19,8 % from 60 y. and up, 17,6 % between 20 and 29 y.old and 16,3 % people between 40 and 49 years. According to profession, the distribution is: 20,0 % are housekeepers, 37,8 % are cattle-breeders, 13,6 % are pensioners with cattle, 13,8 % are students, 6,4 % are farmers, 6,7 % are unemployed. We registered high fever in 98 % of the patients, perspiration in 85 % of the patients, pain in joints in 85 % of the patients. Also there is headache in 82 %, splenomegaly in 3 % and lymphadenitis in 3 % of the patients. **Conclusions:** On the territory of municipality of Veles and 35 of surroundings, there are 635 infected patients between 1990 and 2014. The sources of infection are infected sheep, goat, and cow. The way of transmission is by contact and alimentary mode.The illness is spreading much more in professionals. By taking the particular antyepidemic activities and prevention there is reduction of the number of patients with brucellosis in Veles, but every year we have new cases and the continuance prevention never stops.

Board 471. Active Surveillance for Avian Influenza A/H7N9 Virus in Poultry in the North of Vietnam, 2013 - 2014

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Background: On 31 March 2013, China reported low pathogenic avian influenza (AI) A/H7N9 virus illnesses among Chinese patients. AI H7N9 also was detected in China among domestic poultry and other avian species. As the north of Vietnam shares a long border with China where daily activities involving human and animal movements are very dynamic, this poses a high potential risk of the introduction of AI H7N9 virus into Vietnam. We conducted active surveillance of domestic poultry for AI H7N9 virus in three provinces in northern Vietnam during a 3-month period known to have increased production, transportation and consumption of poultry. **Methods:** Between 05 December 2013 and 06 March 2014, 30 oropharyngeal swab samples from domestic poultry (chickens, ducks and muscovy ducks) and 5 environmental (faeces and water) samples were collected weekly at 10 live bird markets (LBM) and one poultry culling area, selected purposely in high risk poultry transportation areas. Surveillance sites included Ha Noi province, where there is high demand for broiler chickens and spent hens, and Lang Son and Quang Ninh provinces that border China. Samples were tested for influenza type A and the matrix (M) gene, and then for H7 subtype virus using real-time RT-PCR at the national veterinary laboratory. **Results:** No samples were positive for the H7 subtype virus. A total of 1,292 samples (1,279 chickens, 7 ducks and 6 muscovy ducks) were collected and tested. Of all tested samples, 311 (24.1%) were influenza A positive, including 213 positive oropharyngeal swabs, 52 faeces and 46 water samples. All M gene positive samples were collected from LBMs; none from poultry culling area. The prevalence of influenza A virus was highest in Lang Son (44%) and lowest in Hanoi (17%). A total of 200 representative positive samples were sent to the US Centers for Disease Control and Prevention in Atlanta for further identification (results pending). **Conclusions:** AI A/H7N9 virus was not detected in poultry in Vietnam. However, large numbers of the

samples were positive with influenza type A virus. Continued surveillance for H7N9 virus in domestic poultry at traditional and none-traditional LBMs is critical for timely detection and response in Vietnam. This surveillance also is very important for identification of poultry that are potentially transported illegally into Vietnam.

Board 472. Rabies Prevalence in Iraq: Diagnostic Efforts of Iraqi Central Veterinary Laboratories

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Background: Since 2010, Iraq has focused on building its diagnostic and prevention capabilities for rabies, one of the important zoonotic diseases in Iraq. Data on the country-wide prevalence of rabies was collected from 2010-2014 showing that the disease is widespread in the country. **Methods:** 350 brain samples were collected from farm animals and stray dogs in Iraqi governorates, not including the Kurdistan region. A major stray dog eradication campaign was completed from 2012-2013 and brain tissue samples were collected and sent to the Rabies Diagnosis Laboratory-Histopathology Unit at the Central Veterinary Laboratories (CVL). Farm animals with suspected cases of rabies were sent by state veterinary hospitals and private sector units to the CVL. A questionnaire was prepared by the Rabies Diagnosis Lab and sent to veterinary hospitals to help them identify potential rabies cases for sampling. All samples were sent to the CVL in clean, iced, double-sealed packages inside thick, labeled plastic boxes. The samples were divided into three groups to undergo different laboratory testing. The first group of brain samples was fixed into 10% buffered formalin for histopathology tests. The second group was frozen under -20 C for direct Immunofluorescence Antibody Test (dFAT). The third group was preserved for future PCR testing. **Results:** The laboratory results from the tests performed on the 350 brain samples showed that rabies has a high rate of infection in most Iraqi regions among farm animals and stray dogs. Farm animal samples included cows, calves, sheep and buffalo. The highest rate of infection between 2010 and 2014 was in cows and positive tests for rabies were found in samples from almost all Iraqi governorates where sample collection was possible. **Conclusions:** In the future, PCR testing, Direct Rapid Immunohistochemistry Tests (DRIT) and mice inoculation tests will be used in addition to dFAT and Histopathology tests. Plans are also underway to transition to a capture, vaccinate and release policy for stray dogs. For full rabies eradication to be accomplished, there must be increased laboratory diagnostic capacity, updated equipment, increased training of lab personnel and expanded biosafety and biosecurity measures in all veterinary laboratories in the Iraqi governorates.

Board 473. Detection and Genetic Analysis of Norovirus from Dogs in South Korea

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Background: Noroviruses are the most predominant viral agent of acute gastroenteritis outbreaks in human worldwide. Many researchers have strengthened the hypothesis for the emerging zoonotic transmission because of norovirus cross-species infection to human through domestic animals. Recently, noroviruses have been detected from dogs in Portugal, Italy, Greece, United Kingdom, and Hong Kong. In most industrialized countries, companion animals have become an integral part of family life, sharing our lifestyles, bedrooms, and beds. Therefore, the purpose of this study was to detect and to analysis the genetic characteristics of canine norovirus in South Korea. **Methods:** During July 2014 to February 2015, a total 421 fecal samples were collected from pet animal hospitals and animal shelters in South Korea. **Results:** Nucleic acid was extracted by using the QIAamp viral RNA mini kit and tested for the presence of norovirus by RT-PCR assays. Canine norovirus specific primers were designed on a partial RdRp region of the viral genome from previously reported canine norovirus sequences (GenBank). For genetic analysis, partial VP1 region was amplified and phylogenetic trees were generated by the neighbour-joining method with the maximum composite likelihood model. Results: We detected canine norovirus in 5% (19/421) fecal samples. All canine norovirus sequence on RdRp region showed high nucleotide identity with recently reported canine norovirus strains. The phylogenetic analysis demonstrated that most canine noroviruses from South Korea are close to Norovirus dog/FD53/2007/Ita strain from United Kingdom. **Conclusion:** Our findings emphasize that intensive monitoring for canine norovirus infection in companion animals is needed to investigate the potential for the emergence of a zoonotic virus. This is the first announcement of the presence of canine norovirus in South Korea. Although the positive rate among dogs is relatively lower than that of data from other countries, additional studies are need to demonstrate the prevalence of canine norovirus including serologic studies.

Board 474. Comparing Seasonality of Bats' Feeding Behavior to Seasonality of Nipah Virus Transmission to Humans in Bangladesh

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Nipah outbreaks occur during the winter in Bangladesh and have been linked with the consumption of either fresh or fermented date palm sap presumed to be contaminated with bat (*Pteropus giganteus*) urine or saliva. Date palm sap is usually harvested during the winter and a fraction of fresh sap is consumed by people. A few communities collect date palm sap throughout the year to ferment and consume. This study's objective was to characterize *Pteropus* bats' date palm sap feeding behavior round the year to identify potential for sap contamination with bat excreta. We used infrared cameras to observe bats' feeding behavior for 28 tree-nights per month for 22 months from March 2013 to December 2014. We placed the cameras at 4 sap producing date palm trees focused at the sap producing surface and collection pot from 5:00 PM to 6:00 AM for seven consecutive nights. We extracted the number and duration of bat visits (flying and/or landing on and around the tree) and duration of contact (landing, licking, or urinating either on shaved surface or collection pot) with date palm sap from the images. We described the frequency of bat visits during four seasons: winter (December-February), spring (March-May), monsoon (June-September), and post-monsoon (October-November). We recorded a total of 26,870 bat visits (5% *Pteropus*, 90% non-*Pteropus* and 5% unidentified) from 616 observation tree-nights. Median duration of each visit was higher for *Pteropus* bats than non-*Pteropus* bats (8 versus 0.03 minutes, P< 0.001). Median duration of contact with date palm sap was higher for *Pteropus* bats (0.67 versus 0.03 minutes, P<0.001) for each visit. The average number of *Pteropus* bat visits per night was the highest during spring (17) followed by winter (14), post monsoon (6) and monsoon (3). Even when date palm sap is harvested year-round, *Pteropus* bats visit the date palm trees more frequently during the spring and winter, perhaps due to lack of other available food. Feeding behavior could be one reason why the risk of Nipah infection to people has been concentrated in the winter season, even when fermented sap is consumed year-round. Sap harvesters should regularly use skirts to prevent bats from contaminating the date palm sap to prevent Nipah virus and other bat associated zoonoses.

Board 475. Human Exposures to Ferret-badgers and Gem-faced Civets after Reemergence of Wildlife Rabies—Taiwan, 2014

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Background: In 2013, Taiwan agricultural authorities confirmed rabies among 276 ferret-badgers collected since May 2012, ending rabies-free status since 1961. During December 2014-February 2015, four gem-faced civets were tested rabies-positive. We characterized and compared human exposures to these two rabies-affected carnivores. **Methods:** We identified rabies postexposure prophylaxis (PEP) recipients from the national PEP registry. Recipients exposed to ferret-badgers or gem-faced civets in 2014 who received ≥1 dose of rabies vaccine were enrolled for a telephone interview using a pre-tested questionnaire to collect information on demographics, exposure circumstances, and postexposure medical management. Bivariate analyses and multivariable logistic regression were used to compare characteristics of exposures. **Results:** Among 74 enrolled PEP recipients, 57 (77%) completed interviews. The median age was 51 years (range 17-82); 38 (67%) were males. The most common circumstance leading to exposures was provoked attack (n=31, 54%), including hunting, capturing, repelling, feeding, nursing, and petting animals. Twenty-nine (51%) respondents did not wash wounds with clean water for ≥ 15 minutes. Compared with respondents exposed to ferret-badgers (n=33, 58%), respondents exposed to gem-faced civets (n=24, 42%) had significantly higher proportion of being male, younger, exposed in towns where rabies was not confirmed, and exposed due to provoked attack. In multivariable analysis, younger age (OR [odd ratio] 1.1, 95%CI [confidence interval] 1.001-1.123 per 1-year decrease) and male gender (OR 31.9, 95%CI 3.39-301.76) were significantly associated with exposure to gem-faced civets but provoked attack was not (OR 2.2, 95%CI 0.30-15.43). **Conclusions:** Exposures to gem-faced civets, the latest rabies-positive wildlife in Taiwan, varied from exposures to ferret-badgers in characteristics and occurred more frequently in younger male adults. Half of the respondents did not wash wounds adequately after exposures. Educational and prevention efforts should be targeted to young men to avoid provoked attack of rabies-affected carnivores and ensure appropriate postexposure wound management.

Board 476. The Human-animal Interface in Peri-urban Slums of Kenya

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Background: As many emerging and reemerging infectious diseases worldwide are zoonotic, novel research on the relationship between man and animal must be considered in a One Health context. In Kisumu, Kenya several peri-urban 'slums' have serious issues surrounding water, sanitation, and hygiene leading to high rates of childhood diarrhea. This study examines whether households experience close contact with animals in the environment and engage in behaviors that present a risk for zoonotic or reverse zoonotic disease transmission. By determining the purpose and type of animal contact and the species most often associated with these interactions, we can assess possible zoonotic enteric diseases exposures at the household and compound. **Methods:** Between June 2014 and April 2015, focus group discussions, household surveys, and household and environmental sampling was conducted in three peri-urban slums of Kisumu, Kenya. Randomly selected households were chosen from the villages of Nyalenda A, Nyalenda B, and Obunga. Within the multiple measures utilized, key questions focused on household animal ownership, purpose and type of animal contact, common animal species, GPS points of animal prevalence in the communities, and samples of animal waste. **Results:** Initial findings show that animals are very common within the compounds of all three communities. Observational data shows that 76% of compounds had at least one animal present during the time of sampling. Of the compounds with animals present, 44% had only one species visible at the site during sampling while 56% compounds had two or more different animal species present. In terms of animal waste present in the compounds, 78% of compounds had fresh stool inside the compound. Additional data on the frequency of enteric pathogens in animal waste will be presented.**Conclusions:** Peri-urban communities that practice animal husbandry may be at elevated risk for zoonotic and reverse zoonotic enteric disease. Understanding the purpose of animal contact and the type of animal for which close contact occurs is critical in assessing exposure risk and instituting proper interventions. Future research in this area is necessary to prevent zoonotic enteric disease while respecting the cultural importance of the human-animal relationship within these communities.

Tropical Infections and Parasitic Diseases

Wednesday, August 26, 12:30 PM - 1:45 PM

Grand Hall

Board 477. Population-based Surveillance for Bacteremic Melioidosis in Northeast Thailand: An Update on Incidence and Case Fatality Rate, 2006-2013

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Background: Melioidosis incidence and mortality have reportedly been increasing in endemic areas of Thailand but little population-based data on culture-confirmed *Burkholderia pseudomallei* infections exist. We update estimates of melioidosis bacteremia incidence and case fatality rate (CFR) in Nakhon Phanom (NP) province since automated blood culture became available in all 12 hospitals in the province in 2006. **Methods:** Data were reviewed from population-based surveillance for community-acquired pneumonia and bloodstream infections in NP from 2006 to 2013. A case of bacteremic melioidosis was defined as a hospitalized patient with *B. pseudomallei* isolated from blood culture; patients with evidence of pneumonia on chest x-ray (CXR) were considered to have melioidosis pneumonia. Patients with repeat positive *B. pseudomallei* cultures within 20 weeks were counted once. **Result:** From 2006-2013, 882 bacteremic melioidosis (BM) cases were identified including 457 (52%) from NP provincial hospital. The annual incidence of BM ranged from 12 to 16 per 100,000 people from 2006 to 2013 (p=0.30). The CFR among patients with known outcomes declined from 17% to 12% (p=0.40) and the population mortality decreased from 2.04 to 1.84 per 100,000 people (p=0.68). The highest annual incidence was among persons aged 50-69 years (41 per 100,000); significantly more cases occured in the rainy season (July-October) compared to the dry

season (March-June) (p=0.032). Overall case fatality among BM cases in provincial hospital was greater than in district hospitals (22% *vs* 4%; p<0.001). Additional details were available for the 57% (499/882) of BM cases captured by pneumonia surveillance. Among these patients, 62% (310) had a CXR performed, of whom 49% (152 of 310) had radiographic evidence of pneumonia. The annual melioidosis pneumonia incidence was 2.54 per 100,000 people (95% CI, 2.15-2.98). Among melioidosis patients who had a CXR performed; 26% of those with evidence of pneumonia died in-hospital versus 16% without pneumonia (p=0.03). **Conclusion:** The continued high incidence of bacteremia, pneumonia and deaths from *B. pseudomallei* in an endemic area, despite a potential declining case fatality, highlight the need for early diagnosis and treatment and further interventions for melioidosis prevention and control in Thailand.

Board 478. Survival Estimates of *Lutzomyia longipalpis* in an Endemic Area of Visceral Leishmaniasis in São Paulo State, Brazil

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Background: Visceral leishmaniasis is a zoonotic disease of great importance in public health in Brazil. Since the introduction of VL in the northwestern region of São Paulo state at the end of the 90s, it has spread continuously into new areas. Its etiologic agent, *Leishmania infantum*, is transmitted mainly by the sandfly *Lutzomyia longipalpis* (Diptera: Psychodidae), the domestic dog being the main host. The gonotrophic cycle and vector survival are parameters related to the vectorial capacity therefore their estimation could provide information to support the design of surveillance and control measures. The present study sought to estimate the survival rate and the duration of the gonotrophic cycle of *Lutzomyia longipalpis* in an endemic VL area of São Paulo state, Brazil. **Methods:** The study was carried out in Panorama municipality in São Paulo state, Brazil. The daily survival was estimated by using the capture-mark-release-recapture method. The sandflies were captured in animal sheds, counted, marked with fluorescent powder and released after 24 h. The recaptures were extended for 8-15 successive nights with a Castro aspirator and CDC light traps. The sandflies collected were observed under the stereomicroscope and UV light. To estimate the duration of the gonotrophic cycle engorged females were marked and released and those recaptured were dissected to observe the eggs' development. **Results:** The daily survival of *Lu. longipalpis* males varied from 0.69 to 0.84. For the females the survival was estimated on the basis of three experiments and varied from 0.59 to 0.92. The recapture rates of males ranged between 7.7 % and 20% and of the females between 2.2% and 12.8%. The gonotrophic cycle's duration varied from 4 to 8 days. **Conclusions:** High male and female survival rates of this species were observed, which together with the gonotrophic cycle estimated at an average of 4 days, highlight the epidemiological importance of *Lu. longipalpis,* since it could sustain two or more gonotrophic cycles. The high recapture rate of males could be explained by the aggregation pattern on the host as described for other Brazilian regions. This behavior could be exploited by designing control measures such as pheromone traps or environmental management that could decrease the survival of the species and thus the risk of human infection.

Board 479. Prevalence and Factors Associated with Buruli Ulcer in Ayamelum Local Government Area of Anambra State, Nigeria

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Background: Buruli ulcer represents an important and re-emerging public health problem in many African countries. It is a neglected tropical disease caused by *Mycobacterium ulcerans* which affects all age groups causing serious morbidity and disability. In Nigeria Buruli ulcer disease has been documented from different areas, however in all these studies, no detailed assessement of the magnitude of the disease has been done. This study was therefore carried out to determine the prevalence of Buruli ulcer, determine the knowledge of buruli ulcer among respondents and identify the factors associated with the disease in Ayamelum Local Government Area of Anambra State, Nigeria. **Methods:** It was a cross-sectional study of 4 communities in Ayamelum Local Government Area of Anambra State through a multi stage sampling method. An interviewer administered questionnaire was used to collect data on socio-demographic variables, knowledge/ perception, clinical presentations and factors associated with the infection. Swabs and fine needle aspirates were also collected and subjected to Ziehl Neelson microscopy technique to determine prevalence. Data analysis was done using Epi Info version 3.5.1. **Results:** A prevalence of 5.6% for Buruli ulcer was established in the Local Government Area. The age range <15 years recorded the highest prevalence of 37.5% while Ifite Ogwari community recorded the highest prevalence of 40%, whereas over 80% of respondents have good knowledge of the disease. Living close to a river OR=4.63(1.57-13.70, farming in a swampy farmland OR=3.21(1.08-9.57), fishing OR=3.03(1.35-6.78) and swimming OR=2.40(1.18-4.88) were identified as factors associated with infection while BCG vaccination OR=0.16(0.08-0.35) and putting on protective wears to the farm OR 0.09(0.04-0.22) were protective. **Conclusion:** The study area constitutes a focus of endemic Buruli ulcer of considerable magnitude and recommends that the Local Government Authorities should intensify health education/awareness campaign, BCG vaccination, and implementation of control strategies of Global Buruli Ulcer Initiative.

Board 480. Description of Dengue-related Hospitalization and Disease Severity from an Enhanced Dengue Surveillance System in Puerto Rico

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Background: Dengue is an acute febrile illness (AFI) that is endemic in Puerto Rico. The clinical spectrum of dengue ranges from mild AFI to a life-threatening illness. Although timely identification of dengue patients can reduce medical complications and mortality, this is complicated by clinical manifestations that overlap with other AFI. **Methods:** To identify early clinical features that can be used as predictors for severe dengue, we evaluated the clinical course of laboratory-positive (i.e., DENV nucleic acid detected by RT-PCR or anti-DENV IgM antibody detected by ELISA) dengue patients enrolled in the Sentinel Enhanced Dengue Surveillance System (SEDSS) site located in Ponce, Puerto Rico. Patients were those presenting with AFI during May 7, 2012 to May 6, 2013 that were hospitalized (n = 262) or were out-patients that returned for follow-up evaluation (n = 120). **Results:** Of all 382 patients, there were no significant differences in age or sex between hospitalized and non-hospitalized patients. Admitted patients sought care later than non-hospitalized patients (mean day of presentation = 4 vs.2 days), and

had a mean hospital stay of 4 days. Clinical findings associated with hospitalization were anorexia (p = 0.002), diarrhea (p = 0.021), and dengue warning signs of persistent vomiting (p < 0.001), abdominal pain (p < 0.001), and bleeding (p = 0.013). Laboratory findings at presentation associated with hospitalization were leukopenia (p = 0.021) and thrombocytopenia (p < 0.001). Mean platelet count was significantly lower in hospitalized than non-hospitalized patients (mean = 81,000 vs. 151,000) (p < 0.001). Patients that presented 4-7 days after illness onset had greater odds of having thrombocytopenia (OR = 2.18; CI: 1.24-3.83) or elevated liver transaminases (OR = 4.74; CI: 1.53-19.45).**Conclusions:** Enhanced dengue surveillance revealed that hospitalized dengue patients presenting late for clinical care were more likely to present with dengue warning signs, and were hospitalized more frequently. Further analysis will assess correlation between early presentation and ultimate disease severity.

Board 481. Investigation of Visceral Leishmaniasis Caused by *Leishmania martiniquensis* in Non-endemic Area of Thailand

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Background: In Thailand, most leishmaniasis cases were reported from southern Thailand. On 5 September, 2013, suspected leishmaniasis patient in northern Thailand was notified to the Bureau of Epidemiology. Therefore investigation team performed case investigation, active case finding, and search for reservoir and vector. **Methods:** Epidemiological investigation was performed by medical record reviewing, history taking and physical examination. Active case finding was done on villagers, who lived in the same village since the patient's onset date within 200 meters radius from patient's residence. Reservoir search was done by serum and blood collection from human, domestic mammal animal, rodents and adult vector trapping by light traps method to find sandflies in the same areas. **Results:** A 38-year-old man infected with HIV had been living in villages A and B presented with chronic papule for 3 years. He received treatment as fungus infection but showed no improvement. Then patient was worked up for leishmaniasis by Bone marrow biopsy, and the result showed many kinetoplast containing in bone marrow, amastigote form of leishmania, later identified as *Leishmania martiniquensis* by Polymerase Chain Reaction (PCR). For active case finding, we found 12 suspected cases from 123 persons and result of Direct Agglutination Test (DAT) and PCR showed negative for all. For reservoir study, all blood samples test from 111 humans were negative. The results of DAT on 20 animals were positive, but all of their PCR were negative. We found 2 rodents in Village A but there was no *Leishmaniasis spp.* from PCR. Five sandflies were trapped and 2 of them were female. The result of female sandflies PCR were negative for *Leishmania spp*. We co-operated with Lamphun provincial health office and municipality to control vectors by deltamethrin fogging. **Conclusions:** Visceral leishmaniasis with co-infected HIV was confirmed by bone marrow biopsy and PCR in a patient from northern Thailand. There were no human and animal reservoirs found in this event. Sandflies were detected. Immunocompromized host who develop symptom of lieshmaniasis should be aware in northern Thailand.

Board 482. Evaluation of a Novel Intervention to Improve the Clinical Management of Patients with Dengue—Puerto Rico, 2012-13

Withdrawn at Author's Request

Board 483. A Helminthiasis Prevalence and Ecological Study in the Aragacotn Region of Armenia, 2013

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Background: Soil-transmitted helminthes are endemic in Armenia. Children are particularly susceptible to infection. A prevalence study was conducted in preschool and school age children in the Aragacotn region in Armenia. An ecological study was conducted in parallel to determine risk factors and their effects on the prevalence of helminthiasis. Methods: Twenty six settlements in the Aragacotn region were included in the study. The region was divided into zones according to access to water, sewage facilities, distance from health facilities, and gardening type. Parasitological testing using salt flotation method of Fulleborn modified by Kalantaryan and anal swab examination was conducted among 899 preschool age (3-5 years) and 3,137 school age (6-9 years) children. Results: Among the 3,137 school age children, 53 (1.69 per 100 population) were infested with helminthes. Helminthes infections were observed in 5 (0.56) of the 899 preschool age children. The majority of the infections, 32 cases, were with *Enterobius* vermicularis: 29 cases (0.92) in school age children and 3 cases (0.33) in preschool age children. Infection with Ascaris lumbicodies was observed in the other 26 cases: 24 cases (0.76) in school age children and 2 cases (0.22) in preschool age children. Villages with access to water supplies 18-24 hours a day had a prevalence of 0.34%, while those with access to water for < 6 hours a day had a prevalence of 4.5%. A prevalence of 3.7% was observed in villages where vegetable and strawberry gardening is prominent (50-75% of the territory) verses 0.25% in villages where this type of gardening is not predominant (<50%). The prevalence of helminthiasis in villages with and without centralized sewage facilities was 0.84% and 2.56%, respectively. In villages where the distance to a health facility (parasitological laboratory) is > 21 km, the prevalence ranged from 2.8-8.5%, whereas a prevalence of 0.7% was observed in villages where the distance is < 21 km. Conclusions: Approximately 1.4% of children had soil-transmitted helminthes infections. Inadequate water supply, sewage facilities, and access to health facilities are important risk factors for infection. Vegetable and strawberry gardening also contributed to a high prevalence since this type of harvesting is primarily done by children.

Board 484. Trends of Visceral Leishmaniasis in Armenia, 1999-2014

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Background: Leishmaniasis is caused by intracellular protozoan of the genus *Leishmania* and transmitted by phlebotomine sandflies. The disease is a major health problem, especially in its visceral form. The first visceral leishmaniasis (VL) case in Armenia was registered in 1913.

According to the World Health Organization, 919 cases of VL were registered in Armenia between 1926 and 1969. No cases of VL were reported from 1970-1998. In 1999, a case of VL was recorded in a 4 year old child. Since then, cases of VL have been reported each year, with the exception of 2000. **Methods:** We reviewed all VL cases reported to the National Center of Disease Control and Prevention from 1999-2014. The case files, including medical and laboratory records, were analyzed for demographic data, clinical manifestation, and diagnostic data. **Results:** From 1999-2014, 81 cases of VL were reported. Two fatal cases occurred in 2008 and 2010. The main clinical manifestations were fever (83%), weakness (65%), and weight loss (56%). Before the introduction of serological methods in 2008, 21% of the cases were diagnosed by clinical signs and epidemiological criteria; 79% were confirmed microscopically. After 2008, all cases were confirmed by microscopy, serology, or both. Between 1999 and 2005, cases were registered only in the northern regions of the country. After 2006, cases were also reported in southern Armenia. More than 50% of cases were in children less than 2 years old. **Conclusions:** After a 30 year interval without incidence of disease, VL has re-emerged in Armenia. This is likely due to a lack of vector, rodent, and canine control programs, which halted in the 1970s. Case definitions were introduced in 2010, but there is still a low awareness of the disease among doctors. This leads to delays in diagnosis. Delays are also due to a lack of trained personnel and modern laboratory diagnostics in distant regions. Although cases are reported throughout the country, diagnosis and treatment is only available in Yerevan. Further investigation is required to determine the reporting differences among regions. Educational programs and trainings are required to improve awareness of the disease among doctors and the public. There is also a need to implement vector and reservoir control programs and make rapid diagnostics available, particularly in distant regions.

H1N1

Wednesday, August 26, 12:30 PM - 1:45 PM
Grand Hall

Board 485. Active Surveillance for Respiratory Pathogens Among DoD Beneficiaries

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Background: In 2007, NHRC was asked to provide support pandemic avian influenza preparedness by both DoD Global Emerging Infections Surveillance and Response System (GEIS) and upper echelon Navy Commands.[1,2] One goal was to evaluate new diagnostics that may rapidly identify avian flu. Surveillance was expanded into DoD dependent clinics to better represent the general population, allowing NHRC to conduct studies useful for clearance of diagnostics. Furthermore, these studies will increase the number of influenza strains examined by NHRC, which in turn will result in more data being included in Centers for Disease Control and Prevention surveillance. Of note, NHRC's FRI surveillance team identified one of the first two cases of pandemic H1N1 in April 2009. **Methods:** Subjects are recruited from multiple Naval Medical Center San Diego clinics and the Captain James A. Lovell Federal Health Care Center. The case definition includes a subjective fever or temperature ≥ 100.5°F with a cough/sore throat. An eligible patient must be a beneficiary at least 6 months old with the symptoms described above. Up to two samples nasal, throat, nasopharyngeal swab, or a combination thereof are collected. *Routine Testing***:** Each specimen will be evaluated with a College of American Pathologists accredited flu A/B polymerase chain reaction assay and viral culture for flu A/B. Flu A positive samples are subtyped. Samples are also tested for other community acquired respiratory illnesses. *Diagnostic Testing***:** Rapid diagnostic tests may be performed at the clinic site or NHRC. **Results:** We have studied a total of approximately 4,463 subjects to date, and 548 of these have been flu positive (12.2%). We have studied 773 subjects in 2014. Of these, 75 subjects (9.7%) have been flu positive to date. **Conclusions:** This study provides valuable information regarding circulating influenza rates and strains in a population of military dependents, representing a wide demographic and multiple geographic regions. Study data contribute to public health surveillance and vaccine effectiveness evaluation, as well as provide an early warning system for influenza outbreaks. Finally, the established surveillance infrastructure has augmented US pandemic preparedness by facilitating the development and FDA approval of influenza diagnostic technologies with promise to enhance detection of seasonal, novel, and highly pathogenic influenza.

Board 486. Epidemiology of Fatal Cases Associated with Pandemic Influenza Reported in Yemen

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Objectives: This study describes the incidence of all fatal cases associated with Pandemic Influenza A (H1N1) in Yemen. It sets out to highlight the factors associated with poor prognosis to enhance the implementation of prevention and control programs. **Methods:** The study is based on retrospective analysis of available data until 14 March 2010, as compiled by the disease control and surveillance team in Yemen. **Results:** Between 16 June 2009 and 14 March 2010, a total of 33 laboratory-confirmed death cases associated with pandemic influenza A (H1N1) were reported to the Diseases Control and Surveillance in the Ministry of Public Health and Population. During this period, a total of 6049 suspected influenza A (H1N1) cases were recorded. With this denominator, the case fatality rate (CFR) was 0.54%. During June through August, H1N1 confirmed cases were infrequently detected, including only 30; however, from September through December, over 200 confirmed cases were reported each month. Of the 33 cases recorded, 25 were male (76%) and 8 were female (24%), male to female ratio being 3:1. Overall median age of the death cases was 30.8 years (range 1 - 55). The most common diagnosis upon admission was pneumonia. Out of the deaths, twenty five (75.8%) had no documented underlying diseases. Chronic cardiovascular disease (9.1%) was the most commonly reported disease and 2 deaths (6.1%) were recorded as pregnant women. **Conclusions:** The most common diagnosis upon admission was pneumonia. Chronic cardiovascular diseases were the most commonly reported underlying conditions, while the most identified risk factor was pregnancy. These findings should be taken into consideration, when vaccination strategies are employed.

Board 487. Molecular Characterization and Phylogenetic Analysis of Circulating Strains of Influenza A (H1N1) pdm09 and Influenza B from 2013-2014 in Egypt

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Background: Influenza viruses are associated with a range of clinical presentations and can lead to fatal disease. Monitoring genetic changes of influenza viruses is crucial for vaccine strain selection, detection of drug resistance and virulence markers. We analyzed the hemagglutinin (HA) and neuraminidase (NA) genes of influenza A pdm09, as well as

HA gene of influenza B viruses circulating among influenza-like illness (ILI) patients in Egypt during the period from January 2013-February 2014. **Methods:** Oropharyngeal swabs (n=2382) collected from seven governorates in Egypt were screened by real-time RT-PCR to determine type and subtype of circulating influenza strains. The detected viruses were propagated on MDCK, and isolates representing seven governorates were chosen for sequencing and phylogenetic analysis. **Results:** Influenza A virus was identified in 10% of ILI cases, whereas influenza B was detected in 8% of cases. Fifty percent of influenza A cases were of pdm H1N1 subtype. The HA of 25 representative pdm09 isolates had 11-16 amino acid (a.a) differences from vaccine strain (A/California/07/2009), whereas NA gene of sequenced isolates had 6-11 a.a differences. The HA and NA phylogenetic trees showed similar topology; samples collected from Jan-May 2013 clustered within genetic clade 6C, whereas samples collected from Nov 2013-Feb 2014 clustered within clade 6B with the exception of one that clustered within clade 6C. This sample had an exclusive mutation at two antigenic sites in the HA (A186T, R205K). This change was not found in any of the other isolates. The D222G mutation, previously found to be associated with increased virulence, was not detected in the HA. The mutations (H275Y, N295S, and Y253H), previously shown to be associated with resistance to neuraminidase inhibitors (NAIs), were not detected in the NA. Sequence analysis of 15 influenza B sequences revealed B/Yamagata lineage viruses predominated over B/Victoria lineage at a ratio of 4:1, respectively. **Conclusion:** Phylogenetic analysis of pdm H1N1 and influenza B viruses isolated from Egypt during this period were similar to other circulating strains worldwide; no clade seven pdm viruses were isolated. Our findings will guide the treatment of severe cases of influenza A (H1N1) pdm09 viruses in Egypt.

Board 488. Pandemic Influenza (A/H1N1pdm09) in Older Adults in Kashmir, India: Did the Population Not Get Exposed to Earlier Epidemics?

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Background: Surveillance reports of cases of A/H1N1pdm09 virus infection have typically been shown to occur in children and adults; those born prior to 1957 seem to have low prevalence. This is postulated to be related to pre-existing, cross-reactive antibodies believed to have originated from previous infections with antigenically related viruses of 1918 and 1957. We undertook an extensive surveillance in all age group including those &gt60 yrs. **Methods:** Prospective surveillance data from Kashmir region of the northern Indian state of J&K, was collected from January 2011 to November 2013. Kashmir is a valley surrounded by the Himalayan range of mountains with people remaining largely confined (even cut-off), with minimal interaction with outside world, especially during winters. Epidemiological and clinical data was recorded from patients with influenza-like illness (ILI) and severe acute respiratory infection (SARI) attending outpatient/inpatients at SKIMS, a tertiary care center. Combined throat and nasal swabs were collected in viral transport medium and tested by real-time RT-PCR for influenza viruses. All influenza A positive samples were further subtyped using primers and probes for A/H1and A/H3. **Results:** Of the 4635 samples collected, 794 (17.2%) tested positive for influenza. Percentage positivity among various age groups included 7.6% (113/1477) in those <5 yrs, 27.8% (103/370) in those 5-18 yrs, 24.4% (451/1851) in those18-60 yrs and 15.2% (127/835) in those >60 yrs. Of the 127 elderly influenza positive cases, 43 tested positive for A/H1N1pdm09, 41 for H3N2 and 41 for influenza B. Most (76%) of the elderly required admission for pneumonia or respiratory failure. Clinical features among the elderly affected by different strains of influenza virus were not significantly different from one another. The patients were treated with routine antibiotics, supportive management as well as oseltamivir. Two patients with influenza B succumbed to their illness whereas others had uneventful recovery. **Conclusions:** Unlike other populations, A/H1N1pdm09 influenza is not rare among older adults in Kashmir. This pattern of age distribution could be rooted in the population being largely unexposed to previous outbreaks, and needs scrutiny in other similarly confined populations.

Board 489. Air and Railway Travels Accelerated Spatial Spread of 2009 Pandemic Influenza A (H1N1) in Mainland, China

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Background: The geographic spread of 2009 pandemic influenza A (H1N1) substantially affected the lives of ten thousands of people in the world. Very few studies have investigated the effects of domestic travel on the spatial spread of pandemic influenza within a country. **Methods:** We collected 174,675 individual cases in mainland China from May 2009 to April 2010. Arrival days and peak days from prefecture-specific epidemic curves were used to analyze the spread of pandemic influenza between prefectures. Mann-Whitney U test was applied to determine whether significant differences in arrival days and peak days exist between prefectures grouped by the existence of airports and railway stations. Passenger volume on domestic travel and road network data for 281 prefectures were obtained to explore their power of predicting arrival days. Univariate regression was performed for each variable and its log-transformed form to measure the explanatory power. All variables with $P < 0.05$ and $R^2 > 0.1$ in conjunction with their interactions were selected into the multivariate regression model by a stepwise algorithm. **Results:** The median arrival day of prefectures with airports or railway stations was significantly less than that of remaining prefectures (105 vs. 119 days, $P = 0.0052$ for airports; 110 vs. 127 days, $P < 0.001$ for railway stations); however, no significant difference in median peak day was found (178 vs. 178 days, $P = 0.71$ for airports; 178 vs. 177 days, $P = 0.72$ for railway stations). The difference in median arrival days between groups from either airports or railway stations was about 2 weeks. Approximate 1 week lag was observed when comparing the median arrival days of railway stations group to those of airports group. Travel-related variables were opted into final multivariate regression model, which showed strong ability to explain the variability of arrival days ($R^2 = 0.62$). The regression coefficients indicated passenger volumes by air and railway were significantly negative associated with the invasion timings of pandemic influenza. **Conclusions:** Both air and railway travels accelerated the spatial spread of pandemic influenza between prefectures in mainland China by an amount of about 2 weeks, but railway travel had a time lag of approximate 1 week compared to air travel. The predictive power of our model highlighted the strategy of regulating air and railway travels to mitigate the spread of pandemic influenza within mainland China.

Board 490. Circulation Dynamics of Seasonal and Pandemic Influenza Viruses in Nigeria (2009-2013)

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Background: In 2006, the Highly Pathogenic Avian Influenza- H5N1 (HPAI) virus spread to the Nigeria and affected the poultry population with a fatal human case. A National Influenza Sentinel Surveillance (NISS) system with four sentinel sites and a laboratory with molecular capacity to diagnose the virus, were established to monitor the infection and the trends in human population. We report a five-year influenza surveillance activity among cases with Influenza-like-illness (ILI) and Severe Acute Respiratory Infection (SARI) in Nigeria. **Methods:** Oropharyngeal and nasopharyngeal samples, including epidemiological information, were taken from each case fitting into standard case definitions of ILI and SARI at the respective out-patient and in-patient wards of each site. The samples were investigated for influenza A and B types, and subtypes of Influenza A using real-time reverse transcriptase polymerase chain reaction (rRT-PCR). Both the epidemiological and virological data were analysed and linked using EPI-INFO 3.5. **Results:** Between March 2009 and December 2013, a total of 8,257 ILI and 1966 SARI samples were tested for influenza with 804 (9.7%) and 113 (5.8 %) positive respectively. Children 0-9 years had the highest positivity in ILI (11%) and SARI (5.9%). Adults (>65 years) had a lower positivity in ILI (5%) and comparable positivity (5.3%) in SARI. Influenza A infection was higher in ILI (6%) than SARI (2.7%) whereas Influenza B infection in both were comparable (3.8%; 3.1%). Influenza virus activity occurred in both cases throughout the year with yearly bimodal phases- January/February and November/December. In ILI, A/H3 predominated in 2009 (69.8%) but A(H1N1)pdm09 infection was higher in 2010 (76.6%) after which a decline occurred subsequently with Influenza B and A/H3 taking over. A(H1N1)pdm09 also was prominent in SARI in 2010 (61.1%) than in other years. **Conclusions:** ILI and SARI cases in Nigeria have recorded low to moderate influenza activity with children mostly affected. There is no defined season for influenza but peak activities cluster around the dry season. The dominance of influenza (H1N1)pdm09 in 2010 coincided with its pandemic occurrence in West Africa with the restoration of seasonal activity thereafter. Efforts are being intensified to determine the burden of the disease in the population.

Board 491. Not a Total Failure: Influenza Vaccine Associated with a Reduction in Symptom Severity Among Patients with Influenza A/H3N2 Disease

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Background: The moderate level of protection (~60%) conferred by influenza vaccines is well-known, but the vaccine's ability to attenuate symptom severity among vaccinated individuals (i.e., vaccine failures) has not been established. **Methods:** From 2009-2014, otherwise healthy adults (>18y) presenting with influenza-like illness (ILI) were enrolled in an observational, longitudinal study in five US military hospitals. Influenza was diagnosed and subtyped by PCR. Recent receipt of seasonal influenza vaccine and type of vaccine received was collected by self-report. Using self-administered diaries, patients categorized symptoms as absent (0), mild (1), moderate (2) or severe (3) daily for ten days after ILI onset. Individual and composite severity scores were compared between those who had vs. had not received the seasonal influenza vaccine >14d prior to enrollment. **Results:** A total of 147 cases of influenza (A/H1N1, n=66; A/H3N2, n=62; A/untyped, n=3; B, n=16) were identified, of whom 111 (76%; A/H1N1, n=44; A/H3N2, n=52; A/untyped, n=3; B, n=12) had been vaccinated. The median (interquartile range, IQR) age of patients was 31 (25, 38) years, and did not differ between vaccinated and unvaccinated groups (p=0.90). Women were significantly less likely to be vaccinated than men (56% vs. 89%; p<0.01). The median (IQR) interval since receipt of seasonal influenza vaccine was 132 (102, 158) days and did not differ by subtype (p=0.06). Among those vaccinated, 54% had received inactivated influenza vaccine (IIV). The proportions who had received IIV did not differ by subtype (p=0.80). Differences in the severity of symptoms between vaccinated and unvaccinated groups were not observed for influenza overall. However, among patients with A/H3N2, the severity of upper respiratory (median score: 5 vs. 8), lower respiratory (4 vs. 6.5), GI (2 vs. 5) and total (15.5 vs. 23) symptoms two days post-onset was lower among those who had been vaccinated as compared to those who were unvaccinated (p<0.05 for all comparisons). Differences in lower respiratory, GI and total symptom severity were observed four days post-onset. No such differences were observed among those with A/H1N1 or B infection. **Conclusions:** Among patients with A/H3N2 infection, receipt of seasonal influenza vaccine was associated with reduced symptom severity.

Board 492. Quantifying the Mortality Impact of the 1918-1920 Influenza Pandemic in Arizona

Withdrawn at Author's Request

Board 493. Analyzing the Adverse Side-effects of the Influenza A/H1N1 Vaccine in Health Care Staff in Selected Provinces of Afghanistan

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Background: In 2010 there was widespread public mistrust of the Influenza A/H1N1 vaccine in Afghanistan. To encourage vaccination, the Ministry of Public Health undertook a study to analyze the risks involved in vaccination. The purpose of this study was to demonstrate to the public that the adverse side-effects did not pose any serious health threat. **Methods:** A total of 27,100 health care workers received the A/H1N1 monovalent vaccine in the four provinces of Kabul, Nangarhar, Balkh and Herat. OpenEpi was used to draw a randomized sample of 417 people for participation in this study, which was conducted over 4 weeks in March-April 2010. Interviewers were trained in questionnaire administration and assigned districts in the four regions. 370 people interviewed were included in the final study: 25% were female, 75% male; mean age was 36 years, and range was from 16-65. Standardization of injection procedure was ensured by using best practices of injection safety for vaccination. **Results:** 53% of those interviewed reported pain at the injection site, 40% reported fever in the first three days after immunization, 39% reported body pain, 33% reported tiredness, 29% reported swelling at the injection site and 28% reported redness at the injection site. More females than males suffered adverse reactions; the rates varied across provinces, ranging from 79% of females in Balkh reporting adverse side-effects to 23% in Kabul. **Conclusions:** While the results demonstrated that a high percentage of vaccine recipients experienced adverse side-effects, all were mild, non-life threatening and resolved within a few days. No serious lasting side-effects were reported. The results of this study were shared with over 20 governmental and non-governmental

stakeholder institutions and publicized through media interviews and announcements. As a result, reports from vaccination teams showed daily increases in the number of people vaccinated to the point at which Afghanistan suffered from a vaccine shortage.

Board 494. Risk Factors for Death from Influenza A(H1N1)pdm09 in Pregnant Women, State of São Paulo, Brazil, 2009

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Background: In April 2009, influenza A(H1N1)pdm09(pH1N1) emerged in North America and on June 11, the World Health Organization announced the onset of an influenza pandemic. In São Paulo, 12,002 cases were confirmed and 578 deaths, with 678 cases and 53 deaths in pregnant women, according to the Information System for Notifiable Diseases-SINAN, in 2009. The SINAN was used to select the cases and controls for this study. **Methods:** This case-control study aimed to assess the risk factors for death from influenza pH1N1 in pregnant women, hospitalized in 2009, with laboratory confirmation, and severe acute respiratory illness hospitalized in 2009. Medical charts of all 48 pregnant women who died (cases) and 185 randomly selected patients who recovered (controls) were investigated in hospitals. Household interviews were conducted. Clinical and socio-demographic characteristics comparisons were performed using the Mann-Whitney U or chi-square tests. Odds ratio-OR and confidence intervals (95%-CI) were calculated. **Results:** There was no significant difference in socio-demographic distribution between cases and controls. The demand for medical care prior to hospitalization demonstrated an increased risk for death, OR 8.03(2.38-27.09). When evaluating others risks conditions for complications, there were no differences. Use of antiviral treatment was a protective factor, OR 0.31 (0.13-0.74) and, when started in the first 48 hours of onset of symptoms and between 48 and 72 hours it was more protective, OR 0.14 (0.05-0.37) and OR 0.13 (0.02-0.68) respectively. There was a higher risk among pregnant women in the 3rd trimester, OR 4.45 (1.15-29.25). Among the cases, 45.8% of the women had live births, 54.1% stillbirths/miscarriages. Among the controls, 98.8% of the women had live births, 1.2% miscarriages/stillbirths, considering also information fromo the interviews. **Conclusion:** Antiviral treatment, within the first 72 hours of onset of symptoms was an important protective factor for death, emphasizing the need to warn pregnant women with an influenza-like illness, about the importance of seeking early care. Training of health professionals is required for adequate clinical management. Maintaining high vaccine coverage among pregnant women is important to reduce infection, and consequently hospitalization and deaths, also preventing unfavorable neonatal outcomes.

Challenges in Controlling Respiratory Infections in Special Settings

Wednesday, August 26, 12:30 PM - 1:45 PM

Grand Hall

Board 495. Pneumonia Associated with *Chlamydia pneumoniae* Infection at a US Army Training Installation

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Background: Over 300,000 *Chlamydia pneumoniae* (*C. pneumoniae*) infections occur in the US annually; about 10% result in pneumonia. There is no seasonal pattern. Outbreaks often occur in close-contact settings like long-term care facilities, prisons, and military training sites. During Jan-Jun 2014, trainees at a large Army installation experienced increased C. pneumoniae infections and pneumonia, prompting a site assistance visit (SAV) by the US Army Public Health Command (USAPHC) in June 2014. **Methods:** Respiratory disease surveillance data were analyzed for Jan 2013-Jun 2014. Data sources included the site's surveillance system and databases of the USAPHC Acute Respiratory Disease Surveillance Program (ARD-SP) and the Naval Health Research Center (NHRC) Febrile Respiratory Illness (FRI) Program. **Results:** During Jan-Jun 2014, 225 cases of x-ray confirmed pneumonia were diagnosed in trainees, three times the number that occurred in Jan-Jun 2013 (n=67). The 2014 cases occurred throughout the trainee population, affecting at least 34 of 45 units; 70% were in advanced training units. The ARD-SP also identified increased streptococcal ARD in Mar 2014. NHRC laboratory surveillance revealed 130 trainees were tested for respiratory pathogens during this time and *C. pneumoniae* (38%, n =50) was the most common organism identified, followed by Rhinovirus (6%) and Influenza (5%); 80% of those with *C. pneumoniae* had x-ray confirmed pneumonia. Declines in morbidity occurred in Jun 2014, with a subsequent return to baseline. **Conclusion:** The high percentage of *C. pneumoniae* positive lab tests and large number of *C. pneumoniae* positive cases with x-ray confirmed pneumonia support the conclusion that *C. pneumoniae* was the primary pathogen in this outbreak. Similar *C. pneumoniae* clusters have occurred in trainees at this site with no discernable pattern, most notably in a 2009 outbreak associated with two trainee deaths from *Streptococcus pneumoniae* meningitis. There is less evidence of *C. pneumoniae* emerging at other military sites. Clinicians must consider *C. pneumoniae* in their differential diagnoses when pneumonia is suspected. Data from this and other respiratory disease outbreaks in military trainees suggest interaction between respiratory pathogens, which deserves further study.

Board 496. Acute Respiratory Infection Outbreaks in Postpartum Nursing Centers: An Emerging Public Health Threat—Taiwan, 2007-2014

H-Y. Wei, W-T. Huang, W-C. Chen, Y-C. Lo; Ctr. of Disease Prevention, Taipei, Taiwan

Background: Postpartum nursing centers (PNCs) are institutions offering full-day short-period accommodation and nursing care to postpartum women and their babies. Residing mothers and babies are cared in separate rooms and have contacts with each other in the breastfeeding room or during rooming in. Acute respiratory infection (ARI) might be transmitted from mothers to babies through infectious

droplets and easily spreads out. We characterized ARI outbreaks in PNCs and identified etiology and source of the outbreaks. **Methods:** In Taiwan, PNCs are mandatory to report suspected outbreaks to the corresponding local public health departments. Verified outbreaks are registered to the Epidemic Investigation Report Files Management System (EIRFMS). An ARI outbreak was defined as ARI in ≥2 persons with interval of onset ≤10 days. Pharyngeal swabs were collected from 2–29 cases in each outbreak and tested for influenza virus, respiratory syncytial virus (RSV), *Bordetella pertussis*, or other respiratory pathogens. We conducted descriptive analyses by extracting epidemiological data, infection source and control measures of EIRFMS-registered ARI outbreaks in PNCs from January 2007 to September 2014. **Results:** We identified 26 ARI outbreaks in PNCs (total 401 cases, median outbreak size 13 cases, range 2-45 cases). The annual number of ARI outbreaks ranged from 0-10, and 17(65%) occurred after January 2013. RSV (n = 21), *Bordetella pertussis* (n = 1), and influenza B virus (n = 1) were identified as the etiologic agents. All cases comprised 342 (84%) babies, 38 (9%) mothers, and 21 (5%) staff member. Of 342 babies with ARI (median age 17 days, range 0-40 days), 128 (37%) were hospitalized and mostly attributed to RSV (n = 125). During the outbreaks, the first known case-patient was mother (n = 10), staff member (n = 3), or unspecified (n = 13). Described infection control measures included isolation of ill babies (n = 8), rooming in all babies (n = 4), or closure of PNCs (n = 2). **Conclusions:** ARI outbreaks have been increasingly identified in PNCs but infection control measures were inadequately taken. RSV, likely transmitted from ill mothers, was the leading cause and accounted for substantial morbidity among PNC babies. We recommend enhancing surveillance of maternal ARI symptoms and quarantine the babies if mothers experience ARI.

Board 497. Outbreak of 2009 Pandemic Influenza A (H1N1) Caused by Over Crowded Party at a Valve Production Company, Samutprakan Province, Thailand, 2014

Withdrawn at Author's Request

Board 498. An Outbreak of Respiratory Syncytial Virus Pneumonia in an Orphanage Home, Thailand, July - August 2014

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Background: Young children with underlying diseases are at high risk of severe pneumonia. On July 17, four babies from Orphanage Home A developed severe pneumonia. An investigation was promptly initiated to verify diagnosis, identify pathogen(s) and risk factors and control the outbreak. **Methods:** Active case finding was conducted among all 241 children. An acute respiratory illness (ARI) case was defined as a child who stayed in Orphanage Home A and had at least 2 of following clinical criteria: fever, cough, sputum, difficult breathing/fast breathing, abnormal lung sign during July 1- August 6, 2014. A severe pneumonia case was defined as a child who had pneumonia with respiratory failure. Nasopharyngeal and throat swab specimens were collected from patients. A retrospective cohort study was carried out by recruiting children in the 3 dormitories with highest attack rates. An environmental survey and laboratory study were done. **Results:** Totally, 74 children met the ARI case definition (attack rate=31.5%), 46 children (62.2 %) had pneumonia, 6 children (8.1%) developed severe pneumonia. Ninety one percent (42/46) of specimens were positive for RSV by RT-PCR technique. Co-infection with Mycoplasma and Chlamydophila were found. Three out of eight environment swabs were RT-PCR positive for RSV. From multiple logistic regression, being a boy (adjusted OR=3.23, 95%CI=1.1-9.4) and having cardiopulmonary disease (adjusted OR=11.64, 95%CI=1.3-107.2) were identified as independent risk factors of pneumonia. Moreover, increasing age was found as a protective factor (adjusted OR=0.93, 95%CI=0.8-0.9). A ratio of caregivers to children was 1:8 in toddlers and 1:14 in older children which is about 2 times greater than the standard. In dormitories, there was no space between children's beds. After July 29, no new cases were found. **Conclusions:** This outbreak of RSV pneumonia occurred in high risk population who lived in a crowded orphanage home. Co-infection with atypical bacteria was observed. Hand hygiene, early screening of sick children and cases isolation were implemented to control the outbreak. It is recommended to increase number of caregivers to meet the standard and to administer necessary vaccines in addition to those required in EPI to children and caregivers.

Board 499. Containing Influenza Outbreaks with Antiviral Use in Jails and Prisons in Taiwan, 2005-2014

H-Y. Cheng, W-C. Chen, W-T. Huang; Taiwan Ctrs. for Disease Control, Taipei, Taiwan

Backgrounds: Influenza can spread rapidly in a concentrated population. In Taiwan, prisons and jails are not considered populous institutions that are eligible for free influenza vaccination. The close living conditions and high turnover of inmates and staff members expedite the spread of influenza virus and make containment extremely difficult. We characterized influenza outbreaks in these high-risk settings and assessed the use of antiviral mitigating strategies. **Methods:** Taiwan Centers for Disease Control used a symptom surveillance system to monitor outbreaks in populous institutions. Local public health authorities verified outbreaks and registered reports to the Epidemic Investigation Report Files Management System (EIRFMS). An influenza outbreak was defined as 3 cases of influenza-like illness occurring within 48 hours in close proximity and influenza disease was confirmed by PCR test. We reviewed EIRFMS-registered reports of influenza outbreaks in jails and prisons during September 2005-September 2014. The antiviral interventions included treatment for influenza cases before outbreak notification and prophylactic use for contacts afterwards. Univariate analysis was performed to compare size and duration of outbreaks with different interventions. **Results:** We identified 25 influenza outbreaks; influenza A virus was the etiologic agent in 22 (88%) outbreaks. The median days from outbreak onset to notification was 3 (range 0-10) and the median duration was 18 days (range 0-54). Median outbreak size was 47 cases (range 5-311). Of 12 outbreaks with known influenza vaccination coverage, the median vaccination rate was 6.5% (range 0-100%). Control measures such as enhancing personal hygiene, environmental cleaning and case isolation were applied in 24 (96%) outbreaks. Antiviral prophylaxis was used in 7 (28%) outbreaks with median 4 days after notification but it did not influence the duration and size. However, initiating antiviral treatment before notification (n = 11) significantly decreased the risk of resulting in an outbreak with ≥10% attack rate or ≥80 cases (OR 0.04, p=0.002). **Conclusions:** Early initiation of antiviral agents significantly reduced the size of influenza outbreaks in prisons and jails. Influenza vaccination should be provided for inmates and staff members for prevention.

Board 500. Detection of Non-influenza Viruses in Acute Respiratory Infections in Children Under the Age of Five in Côte d'Ivoire

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Background: Approximately 2.2 million children die every year of acute respiratory infections (ARI) worldwide and nearly 40% of these deaths occur in Africa. The role of viruses other than influenza as a cause of ARI is not well documented in Africa because of limited diagnostic capacity. We conducted a study to describe the epidemiological and virological patterns of ARI due to non-influenza respiratory viruses in children under five years in Côte d'Ivoire. **Methods:** Between January and December 2013, nasopharyngeal specimens were collected from children <5 years of age presenting for care and who met the WHO case definitions for influenza-like illness (ILI) or severe acute respiratory infection (SARI). We used three multiplex conventional RT-PCR assays to test specimens negative for influenza for other viruses as follows: human respiratory syncytial virus (hRSV), human metapneumovirus (hMPV) by multiplex RT-PCR-1, parainfluenza viruses (PIV) type 1, 2, 3 and 4 by the multiplex RT-PCR-2, human coronaviruses (HCoV) OC43 and 229E, influenza C, rhinovirus (hRV), enterovirus (Env) by multiplex RT-PCR-3. Hemi-nested singleplex PCR was used to detect rhinoviruses. **Results:** During the study period, 1340 specimens were collected from patients under five years. Of 1,059 influenza negative specimens 29% (307/1059) were positive for at least one pathogen; coronavirus 229E was found in 39.1% (120/307), RSV in 24.4% (75/307), PIV in 20.5% (63/307), hMPV in 6.2% (19/307), rhinovirus in 4.9%(15/307), coronavirus 0C43 in 1% (3/307) and enterovirus in 1% (3/307). Of the 1059 specimens, 917 (87%) were in patients with ILI and 142 (13%) with SARI. The proportion of specimens positive for at least one virus was 30% (273/917) in ILI and 24% (34/142) in SARI cases. Coronavirus 229E was most commonly detected in ILI cases with 39% (107/273) positive, while RSV was most commonly detected in SARI cases with 10% (14/142) positive. RSV circulated throughout the year with peaks during the period June - August corresponding to the rainy season and peak circulation of influenza. **Conclusions:** A wide range of respiratory viruses other than influenza was detected in a substantial proportion of cases of ILI and SARI in children. Further work is needed to better define the epidemiology of these viral infections in Côte d'Ivoire.

Board 501. Possible Evidence of Antibody-dependent Enhancement of Illness During Influenza Pandemic of 1918 in Military Officer Trainees

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Background: The great mortality observed during the 1918-19 influenza pandemic remains poorly understood. Besides its unique ability to preferentially kill young adults, the different waves of the 1918 pandemic may have interacted in a non-protective manner. In order to gain insight into the events of 1918, records from US Military Academy, West Point (USMA) and US Naval Academy, Annapolis (USNA) were examined for sequential respiratory illnesses that might be evidence of antibody-dependent enhancement (ADE). **Methods:** Individual cadet (n=511) / midshipman (n=1190) records for those training during all of 1918 at USMA and USNA were collected from prospective clinical reports counting influenza-like illness (ILI) for 3 years. **Results:** At USMA there was no association between ILI experience during the first wave period (Feb-Apr 1918) (illness attack rate 24.1%) and ILI during the second wave period (Sep-Oct 1918) (illness attack rate during fall 1918, 30% among previously ill vs. 32% among not previously ill; RR=0.95, 95% CI (0.70, 1.29) p=0.72). However, of the 227 cadets who had been at the academy throughout both 1917 and 1918, those who were treated for ILIs during the winter-spring 1917 were 3-times more likely than their counterparts to be treated for ILI during the fall 1918 (illness attack rate during fall 1918, 67% among those with ILI in 1917 vs. 22% among those with no ILI in 1917; RR=3.10, 95% CI [2.13, 4.52], p < 0.0001). At USNA midshipmen who had clinically significant ILIs anytime between October 1917 and April 1918 (13.5% illness attack rate) were twice as likely as their counterparts to be affected by influenza during fall 1918 (illness attack rate in fall 1918, 48% among those with prior ILIs vs. 24% among those with no prior ILIs; RR=2.03, 95% CI [1.65, 2.50], p < 0.0001). No cadets present during all of 1918 died at USMA; ten midshipmen died at USNA despite similar illness rates to USMA. **Conclusions:** ILI prior to the pandemic wave of late 1918 appears to have predisposed to an increased risk of illness in late 1918 which might be explained by ADE and may be similar to Canadian observations when the 2009 pandemic was preceded by seasonal immunization. The unusual epidemiology of the 1918 pandemic may be partially explained by diverse preceding respiratory infections.

Board 502. A One Health Approach for Studying Swine Influenza Virus Transmission at Pig Farms, China

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Background: Rapid rises in domestic pork consumption have resulted in the expansion of China's pork industry. To meet demand, producers have shifted to larger, more efficient production facilities called confined animal feeding operations (CAFOs). Such facilities, however, create suitable environments for the mixing and generation of novel pathogens. Current surveillance methods to detect zoonotic pathogens among swine are invasive, unilateral, and require extensive resources to operate. Alternative methods that embrace a One Health approach and incorporate human, animal, and environmental testing strategies could be a novel way to overcome such challenges. Hence, we aimed to use a One Health approach, incorporating human, animal, and environmental sampling, to survey 5 swine production facilities for influenza A virus in Guangdong Province, China. **Methods:** In 2014, we performed a cross-sectional serosurvey of 130 swine-production workers and 115 non-exposed controls, weekly bioaerosol sampling at 5 test sites during summer and winter, and a weekly collection of swine oral secretion specimens. Environmental swab samples were also collected in winter only. Sera were tested using hemagglutinin inhibition assays against various influenza A virus subtypes, and other samples were tested using an influenza A real-time RT-PCR assay. **Results:** Twenty-three of 130 (18%) swine-exposed and 8 of 115 (7%) controls were sero-positive against swine H3N2 virus. Seven of 28 (25%) pig oral secretion and none of the bioaerosol samples collected during the summer were positive for influenza A virus. Nine of 95 (9%) bioaerosol, 14 of 86 (16%) pig oral secretion, and 38 of 95 (40%) environmental swab samples collected in the winter were positive for influenza A virus. **Conclusions:** Overall, study data reveals considerable detection of influenza A virus, with bioaerosol samples having a higher rate of detection during the

winter. Cross-sectional serosurvey data suggests greater exposure to swine H3N2 among pig workers compared to unexposed controls. While data analyses are ongoing, our concomitant human, animal and environmental sampling methods (One Health approach) may be a new way forward to better understand influenza transmission.

Board 503. Characterization of Viral Load and Persistence of Influenza A Virus in Air and on Surfaces of Swine Production Facilities

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Background: Little is known of the mechanisms of transmission of influenza A viruses (IAV) in swine production facilities, including the levels of exposure for both humans and swine from aerosols and on surfaces. We performed longitudinal field sampling of swine facilities for the presence and persistence of IAV in aerosols and on surfaces. **Methods:** Farms were identified by veterinarians as having suspected influenza outbreaks in the swine herd. Site visits were conducted to sample influenza virus in aerosols using high volume samplers, and on surfaces using wipe sampling, as well as in swine oral fluids using cotton ropes. Herds were visited every 3 to 7 days until the outbreaks had resolved. Viral load was determined using a quantitative RT-PCR for IAV. Clinical measures of swine health including coughing and sneezing scores were recorded during each visit. Farms were visited between day 0 and day 42 after the reported onset of clinical signs. **Results:** IAV was detected in indoor aerosols and on surfaces. Thirty three (47%) air samples collected inside the barns were positive for IAV by PCR. In 22 visits (63%) IAV RNA was detected in at least one air sample and IAV was detected in all the farms of the study. Estimates of viral load in aerosols ranged from 0 to $1.25x10^6$ RNA copies/m^3 of air while on surfaces estimates ranged from 0 to $6.65x10^5$ RNA copies/ml. Viable virus was cultured from aerosols but not surfaces. Virus levels peaked in the first week of an outbreak and declined over the next 10-14 days. Our model predicted IAV could be found for 21 days in the air from infected environments during an acute outbreak. **Conclusions:** We concluded that during outbreaks of IAV infection in swine, aerosols in barns contain significant levels of virus particles representing an exposure hazard to both swine and swine workers. These findings support enhanced measures to prevent zoonotic aerosol transmission of swine influenza virus in production facilities.

Board 504. Influenza Surveillance in the Tropics: A United States DoD Perspective

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Background: Influenza is prevalent during the winter in temperate regions; however, its seasonality is less well defined in the tropics. We aimed at evaluating the distribution of influenza subtypes worldwide as part of a US military network of partners developed to identify strain subtype circulation, genetic shifts/drifts and improve match for vaccine development. **Methods:** A website-based data repository and analysis tool was designed and data collated on patients with influenza-like illnesses (ILIs) from 32 countries with matching strain subtype, date and patient location between October 2011 and March 2015. Laboratory confirmation was done by reverse transcriptase polymerase chain reaction (RT-PCR) or culture. Trends were arrived at by influenza subtype (H1N1, H3N2 and B) and geographic region in the tropics (South America, sub-Saharan Africa and Southeast Asia). **Results:** A total of 51,768 ILI patients were tested, 11,927 (23%) of which were laboratory confirmed. 2671 (22.4%) patients were positive for H1N1, 4604 (38.6%) were positive for H3N2, and 4556 (38.2%) were positive for B (954 patients were not subtyped). Influenza isolation rates were higher during the months of July through October. H3N2 strains predominated worldwide, except during July through October 2013, when H1N1 strains predominated. Influenza B strains circulated throughout each of the four seasons. Interestingly, in August through October 2014, H3N2 strains began to predominate in the southern hemisphere preceding the increased H3N2 activity in the northern hemisphere. **Conclusions:** Notwithstanding previously described year-round influenza activity in tropical regions, we noticed peaks in influenza circulation during late summer and early fall months of 2011-2015. This peak in activity preceded well-defined peaks in the northern hemisphere. Most saliently, H3N2 activity was shown to peak in these regions approximately 2-3 months prior to its predominance in the northern hemisphere. This information is critical in the timely assessment of influenza strain circulation for adequate vaccine development.

Board 505. Incidence of Influenza and Influenza Re-infection in a Cohort of Nicaraguan Children

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Background: Influenza causes substantial morbidity and mortality worldwide, especially among children. In tropical and developing countries, little is known about the burden and epidemiology of seasonal influenza. **Methods:** To examine the incidence of influenza, characterize risk factors for infection and disease severity, and investigate determinants of reinfection, we conducted a prospective cohort study in children aged 0 to 14 years in Managua, Nicaragua. The primary outcomes of this study were laboratory-confirmed influenza and influenza-like illness. All children were provided with primary medical care through the study, and data from each visit was systematically recorded. Children meeting the study definition of a possible influenza case had a respiratory sample collected at presentation that was tested for influenza virus by qRT-PCR. **Results:** Between January 1, 2011, and December 31, 2013, 1,933 children participated in the cohort study. Overall incidence of influenza during the three-year period was 13.6 cases per 100 person-years (95% CI: 12.6, 14.7). Incidence of influenza varied by age, ranging from 26.0 cases per 100 person-years in one year old children to 4.7 per 100 person-years in ten year old children. Eighty-nine children presented with two laboratory-confirmed influenza illnesses, and 9 children presented with three laboratory-confirmed influenza illnesses over the three-year period. The mean number of weeks between influenza episodes was 87.5 with a range of 2 to 203 weeks. The effective reproductive number of each seasonal epidemic was 1.3 in 2011 and 2012 and 1.4 in 2013. **Conclusions:** We found a significant burden of influenza, with an incidence of 13.6 cases per 100 person-years. The basic reproductive number for our seasonal influenza epidemics was within the range of those observed for seasonal influenza in temperate settings.

Prevention Challenges for Respiratory Diseases in Community and Healthcare Settings

Wednesday, August 26, 12:30 PM - 1:45 PM
Grand Hall

Board 506. Hospitalization for Respiratory Infections, ICU and Mechanical Ventilation in the United States, Using Medical Claims Data

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Background: To aid hospital resources allocation and planning, we characterized and examined intensive care unit (ICU) and mechanical ventilation use associated with respiratory hospitalizations and identified risk factors associated with mechanical ventilation uses. **Methods:** We analyzed health care insurance claims data in the MarketScan Database. Respiratory hospitalizations, ICU admission and mechanical ventilation were identified by using ICD9 discharge codes, billing and procedure codes respectively. Underlying medical conditions were determined from outpatient and inpatient discharge codes in the preceding year. We estimated rates per 100,000 person-years for respiratory hospitalization, ICU admission, mechanical ventilation and deaths. We used log-binomial regression to estimate the relative risk of underlying medical conditions on mechanical ventilation use. **Results:** During 2009-2012, we identified 626,654 respiratory hospitalizations associated with 190,081 (30%) ICU admissions and 42,568 (7%) uses of mechanical ventilation. Among 190,081 ICU admissions, 35,604 (19%) received invasive mechanical ventilations and 11,944 (6%) died. Rates of respiratory hospitalizations per 100,000 person-years were highest in patients aged <=2 years and >=65 years (1,027 and 2,399 respectively) and were lowest in those aged 18-49 years (163). Among patients hospitalized for respiratory illnesses, 75% had at least one underlying medical condition. The lowest rate of underlying medical conditions was in children aged <=2 years (36%) and the highest (91%) in adults aged >= 65. Compared to those without underlying medical conditions, children under 18 years of age with at least one underlying medical condition were 2.9 times (95% CI: 2.6-3.1) to be mechanically ventilated. Adults with pre-existing medical conditions were 1.1 times (95% CI: 1.1-1.2) more likely to be mechanically ventilated than those without such conditions. **Conclusions:** The burden of respiratory hospitalizations is highest for very young children and older adults. However, the greatest burden of ICU and mechanical ventilation is in older adults. Children aged <18 years with underlying medical conditions are at higher risk for ICU and mechanical ventilation use compared to children without conditions.

Board 507. Middle East Respiratory Syndrome Coronavirus Infection of New Zealand Rabbits

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Background: Middle East respiratory syndrome coronavirus (MERS-CoV) is an emerging zoonotic infectious disease in humans. The virus causes acute respiratory distress syndrome associated with high mortality, calling for an urgent need to develop prevention strategies. Small animal models are valuable for evaluation of candidate vaccines and antivirals drugs. We investigated the ability of MERS-CoV to infect adult male New Zealand rabbits by the intranasal route. **Methods:** Virus titers were measured using quantitative reverse transcriptase-PCR (qRT-PCR) assays targeting the MERS-CoV envelope (upE) and nucleocapsid (N2 and N3) genes. Pulmonary pathology of the rabbits was examined using histopathology and immunohistochemistry (IHC). Sera were tested for the presence of antibodies that neutralized MERS-CoV. **Results:** On primary infection, rabbits displayed no clinical signs of disease but virus replication was detected in the nasal turbinates, trachea and lungs in a dose-dependent fashion. Infection was restricted to the respiratory tract, where peak infectivity was noted on day 3 post-infection. Histopathology and immunohistochemistry of lung tissue revealed intense focal viral antigen in the alveolar epithelium with minimal inflammation in the airways or alveoli. Primary infection did not elicit a serum neutralizing antibody (NtAb) response. When previously infected rabbits were re-challenged with MERS-CoV, viral nucleic acid was still detected in the lungs, indicating that primary infection failed to protect against reinfection. Lung histopathology and IHC revealed lower viral antigen load but many foci of prominent inflammatory infiltrates, interstitial congestion and perivascular cuffing. Because reinfected rabbits developed serum NtAb, they were challenged again to determine whether NtAb would confer protection. We observed reduced viral load and lower viral antigen by IHC and minimal inflammation in the lungs. **Conclusions:** New Zealand rabbits are moderately permissive to experimental infection with MERS-CoV and NtAbs confer partial protection from reinfection. Pulmonary viral load and histopathology can be followed in the evaluation of candidate MERS-CoV vaccines and antivirals in rabbits.

Board 508. Mathematical Model to Calculate Cost-effectiveness of Vaccination Against Influenza in the Republic of Kazakhstan, 2014

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Introduction: In Kazakhstan, the incidence of ARVI and influenza varies by region and by age, however, no assessment of economic damage by geographic distribution and age of cases had been performed. We have developed a mathematical model to calculate the cost-effectiveness of vaccination against influenza, which demonstrated effectiveness of the intervention, with due account of factors that may impact vaccination effectiveness. **Methods:** The study adopted following variables: influenza vaccine efficacy - 50%, non-specific immunity to ARVI - 25%, vaccine cost - US $ 10, share of influenza among all ARVI cases - 30%, proportion of patients seeking medical care in case of ARVI: in children - 81%, in adults - 32%; contagiousness - 1.3, proportion of hospitalized patients - 0.9%, cost of a doctor's home visit - US $ 6.90, cost of doctor's consultation in clinic - US $ 4.5. Medication costs in outpatient setting: US $ 16.5 for adults, and US $ 13.8 for children. The study determined that cost of hospital care for ARVI in 2012-2013 for adults comprised US $ 116, and for children - US $ 184.4. **Results:** Vaccination cost-effectiveness calculations for children under 1 in Almaty demonstrated that 1 dollar invested will generate 2.35 dollars in savings. **Conclusions:** The model we used for economic cost-effectiveness evaluation is a fully automated tool which runs in Excel, it allows changing various parameters, including the incidence rate, vaccine efficacy, cost of treatment, etc. The model enables calculations of the actual cost of the vaccine, as well as prediction of the amount of savings, and is recommended for use in calculating the cost-effectiveness for different population groups.

Board 509. Laboratory Monitoring for Influenza Under the Influenza Sentinel Surveillance During the 2013-2014 Epidemic Season in West Kazakhstan Province, Republic of Kazakhstan

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Introduction: Sentinel surveillance (SS) for influenza was introduced in Uralsk, West Kazakhstan province, in 2008, with the aim to improve and standardize all measures for rapid response to epidemic situation. **Methods:** Sentinel surveillance for influenza in Uralsk is performed in two hospitals for patients with severe acute respiratory infection (SARI) and two outpatient clinics for patients with influenza-like illness (ILI). These records are entered into an electronic database for subsequent analysis in EpiInfo. Collected samples are examined in virology laboratory by PCR using AmpliSence, a Russian test-kit. Samples for the study were collected from 173 patients with SARI and 98 patients with ILI. **Results:** Total number of PCR tests positive for influenza virus in ILI patients comprised 28 (28.6%), including 24 (86%) for influenza A, and 4 (14%) for influenza B. Influenza A/H1N1-09 subtype was identified in 21 patients (87.5%), and influenza A/H3N2 in 3 patients (12.5%). The first positive result was recorded at week 6 of 2014. During weeks 7-10, the percentage of positive results peaked at 64%. The highest percentage of PCR+ was observed in the age groups of 15-29 - 36%, and 30-64 - 32%. PCR results for non-influenza viruses were positive in 37.5% of cases. The morbidity was caused by the RS virus in 75%, and rhinovirus in 25% of cases. In SARI patients, PCR identified 24 (14%) cases positive for influenza, of which influenza A subtype was responsible for 100% of cases. Subtype distribution: influenza A/1N1-09 in 21 patients (87.5%), influenza A/H3N2 in 3 (12.5%) patients. The first PCR+ result for influenza was recorded at week 6, the highest number of PCR+ cases was registered during weeks 7-10 - 18 cases (75%). Maximum percentage of positive tests - 56.5% - was recorded in the age group of 0-4. PCR investigation for non-influenza viruses returned positive results in 56.3% of cases, majorly caused by RS-virus - 38.9%, and parainfluenza - 22.2%. **Conclusions:** In 2013-2014 season, most actively circulating viruses were influenza A/H1N1-09, influenza A/H3N2 in a few cases, and only 4 cases of influenza B in ILI patients. Of the non-influenza virus, RS virus was detected in the majority of cases.

Board 510. Influenza Trends in an Urban Area of Indonesia, 2011–2014

S. Misriyah[1], M. Amalya[2], M. Ester[2], A. D. Iuliano[3], K. Lafond[3], C. Y. Praptiningsih[2], G. Samaan[4], T. Uyeki[3]; [1]Ministry of Hlth. of Indonesia, Jakarta, Indonesia, [2]US-CDC, Jakarta, Indonesia, [3]CDC, Atlanta, GA, USA, [4]Indonesia FETP, Jakarta, Indonesia

Background: Seasonal influenza in Indonesia has not been well-described to-date. An improved understanding of influenza virus activity and population impacted can benefit disease prevention and control strategies. A three-year enhanced surveillance effort was implemented at ten health care facilities in East Jakarta District of the Java Province to describe the impact of seasonal influenza in this community. **Methods:** Surveillance was conducted at four government health centers and six hospitals in the East Jakarta District. At health centers, all outpatients with influenza-like illness (ILI: temperature ≥38°C plus cough or sore throat) and at hospitals all inpatients with severe acute respiratory infection (SARI: fever or subjective fever plus cough or sore throat or shortness of breath) were enrolled. For all enrolled ILI and SARI patients, demographic, clinical and exposure data and respiratory specimens for influenza testing were collected. Data from October 2011_September 2014 were analyzed to describe influenza disease trends by patient age, time of year, and viral subtype. **Results:** We enrolled 6,080 (1%) ILI cases from 475,952 outpatients. Of ILI cases tested, 1,884 (31%) were positive for influenza viruses and of those 44% were influenza B, 32% were A(H3N2), and 24% were A(H1N1)pdm09. Among ILI cases with influenza virus infection, 918 (49%) were in children aged 5-17 years, 977 (52%) were in females, and none were in pregnant women. We enrolled 4,178 (2%) SARI cases from 184,373 inpatients. Of SARI cases tested, 571 (15%) were positive for influenza viruses, and of those 42% were influenza B, 31% were A(H3N2), 26% were A(H1N1)pdm09, and one was A(H5N1). Of SARI cases positive for influenza, 111 (19%) were in children aged 5-17 years, 310 (54%) were in males, and 5 (0.88%) were in pregnant women. Influenza activity consistently increased from December to February each year, corresponding to the rainy season. **Conclusions:** Influenza viruses were commonly detected among both ILI and SARI patients, demonstrating a substantial burden in this urban community. Influenza circulation consistently peaked during the rainy season each year. These findings can inform the target audience and timing of influenza disease control strategies such as vaccination.

Board 511. Tailoring the Timing of Influenza Public Health Measures to Local Needs: Experience from East Jakarta District in Indonesia

S. Misriyah[1], M. Ester[2], M. Amalya[2], A. D. Iuliano[3], K. Lafond[3], C. Y. Praptiningsih[2], T. Uyeki[3], G. Samaan[4]; [1]Ministry of Hlth. of Indonesia, Jakarta, Indonesia, [2]US-CDC, Jakarta, Indonesia, [3]CDC, Atlanta, GA, USA, [4]Indonesia FETP, Jakarta, Indonesia

Background: Influenza virological surveillance is needed to determine viral strains for yearly vaccine composition and to provide evidence for disease control policies including vaccination and health education timing. Indonesia conducts national influenza surveillance but sub-national trends are not well established. To inform local disease control policies, this study describes two-year influenza virological surveillance findings from the East Jakarta District in Java Province. **Methods:** Influenza surveillance was conducted for outpatients with influenza like illness (ILI) in 4 primary health centers and inpatients with severe acute respiratory infection (SARI) in 6 hospitals from August 2011-July 2013. WHO case definition for ILI and SARI was used in the system. All ILI and SARI patients had nasal/throat swabs collected along with epidemiological data. Proportion positive for influenza by virus type/subtype was calculated and compared to national surveillance findings based on WHO FluNet data. Virus strains were compared to strains in the WHO vaccine composition. **Results:** Of 5,081 ILI and 3,085 SARI cases, 25% were influenza-positive. From total 1,996 influenza-positive cases during this two-year period, 46% (n=924) were detected in December 2011_February 2012, and 21% (n=419) were detected in December 2012_February 2013. Influenza peak activity and subtypes circulating were similar to that observed in the national surveillance system, with A(H1N1)pdm09 and A(H3N2) dominating from December_January while influenza B dominating in February. Strains detected from October to February matched strains in WHO's nothern hemisphere vaccine composition and strains detected in July matched the southern hemisphere vaccine composition. **Conclusion:** Influenza virus infection is a common cause of ILI and SARI indicating the need for prevention and control measures. The temporal and subtype findings suggest that East Jakarta District should consider vaccination or influenza health education before December each year. The District should use the latest-available WHO-recommended northern hemisphere vaccine composition since it is available before the peak in activity. For vaccination conducted by clinicians at other times of the year, the latest-available vaccine composition should be used.

Board 512. Healthcare Seeking Behavior for Respiratory Illness in a Northern Province of Vietnam

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Introduction: While progress has been made towards defining the epidemiology of influenza-associated illness in Vietnam, sentinel surveillance systems capture only cases presenting to select sites, limiting our understanding of community burden of disease. We conducted a survey to identify self-reported cases of influenza-like illness (ILI) and severe acute respiratory infection (SARI) in a community serving one sentinel site and describe healthcare utilization to better estimate the burden of influenza-associated illness. **Methods:** A cross-sectional survey was conducted in one urban and one rural area of Thai Binh Province, Vietnam. A two-stage cluster sample was used to select households. Standardized questionnaires were used to screen households for episodes of self-reported ILI (fever and cough or sore throat) in the previous month and SARI (fever and cough or sore throat and hospitalized at least one night) in the previous 12 months, and health seeking behavior for each episode. **Results:** During May 2013, we surveyed 2,100 households and 6,760 residents, including 1,470 households and 4,666 residents in rural Kien Xuong District and 630 urban households and 2,094 residents in Thai Binh City. Overall, we identified 582 (9%, 95% CI: 6-11) residents who self-reported episodes of ILI and 121 (2%, 95% CI: 1-2) residents who self-reported episodes of SARI. The proportions of persons who self-reported ILI and SARI were significantly ($p< 0.05$) lower in Thai Binh City than in Kien Xuong District. Overall, the proportion of participants that reported seeking healthcare outside the home for an ILI episode within the last month was 89% (95% CI: 84-94) and for SARI was x%. **Conclusions:** In both urban and rural communities of Thai Binh Province the majority of cases with self-reported ILI sought healthcare outside the home. Less than 1/5 of self-reported ILI cases presented to a national ILI surveillance sentinel site. For SARI, 1/4 of cases sought healthcare at a SARI burden study site. National sentinel surveillance and facility-based research studies that depend on healthcare seeking behavior and are not adjusted for healthcare utilization will underestimate burden of influenza-associated disease in Vietnam.

Board 513. Seasonality of Circulating Influenza Types and Subtypes in a Rural Indian Community Under Active Surveillance

S. Broor[1,2], S. Saha[3], W. M. Sullender[4], K. Fowler[5], V. Gupta[2], A. Krishnan[2], S. Kant[2], V. Raghuram[2], K. Lafond[6], M-A. Widdowson[6], R. B. Lal[6]; [1]SGT Med. Coll., Gurgaon, India, [2]All India Inst. of Med. Scis., New Delhi, India, [3]CDC, New Delhi, India, [4]Univ. of Colorado, Denver, CO, USA, [5]Univ. of Alabama at Birmingham, Birmingham, AL, USA, [6]CDC, Atlanta, GA, USA

Background: Influenza seasonality in tropics is diverse ranging from annual monsoon peaks to year-round circulation.Improved understanding of temporal circulation of influenza virus types and subtypes is essential for development of effective prevention and control strategies. We present four years of community based active surveillance data from three villages in Ballabgarh, North India. **Methods:** weekly active household Surveillance for febrile acute respiratory illness (FARI) was conducted in a dynamic cohort of >18,000 individuals of all ages as part of phase IV clinical trial of trivalent inactivated influenza vaccine (IIV) given to children 6 months through 10 years of age. Combined nasal and oropharangeal samples were collected from FARI cases and tested for influenza viruses using real time RT-PCR assays. **Results:** Between November 2009 to October 2013, 4,971(11.7%) of 42,358FARI samples were influenza positive. Twenty-five percent of influenza A positive cases and 24.5% of influenza B positive cases were among children aged under five years; 5.3% and 4.2% of influenza A and B positive cases respectively were aged 60years and above. Among the 3,119 influenza A viruses, 1,348 (27.1%) were A/H1N1pdm09, 1,771 (35.6%) were A/H3N2; 1,793 (36.1%) wereinfluenza B viruses. The prevalence of influenza types and subtypes varied substantially over the study period. Predominant strains were A/H1N1pdm09 in 2009, 2010, 2012 and A/H3N2 in 2011 and 2013. Influenza A showed distinct peaks during monsoon season with 75% of total Influenza A positives occurring between July and September. Influenza B tended to have a later peak from August to October and 65% of all detections were in this period but was also detected in non-monsoon months. **Conclusion:** Influenza viruses are a common cause of febrile illness in this rural Indian community. Influenza vaccination with the most recent formulation of vaccine should precede the seasonal peak. This may necessitate use of Southern Hemisphere (SH) formulations despite this community being situated in the Northern Hemisphere (NH). Studies are underway to assess protection afforded by SH influenza vaccination in April-May in this population.

Board 514. The Impact of Seasonal Influenza Vaccination Among Persons 60 Years and Older on Rates of Influenza-associated Mortality and Hospitalization from 1994 to 2009 in São Paulo State, Brazil

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Background: Annual influenza vaccination is the most effective method for preventing hospitalization and death due to influenza. However, clear impact on these outcomes has been difficult to demonstrate in countries with longstanding vaccination programs in part because of slow incremental coverage. In Brazil, influenza vaccination was initiated in 1999-2000 for persons ages ≥60 and reached a coverage of >80% in São Paulo. We conducted an ecological study on the impact of the introduction of seasonal influenza vaccination in São Paulo on influenza-associated mortality and hospitalizations among persons ages ≥60 years. **Methods:** Weekly ICD9-1994-1998 and ICD10-1999-2009 coded respiratory-R (ICD-9- 460-519, ICD-10-category J) and circulatory-C (ICD-9 390-459, ICD-10-category I) deaths and hospitalizations from 1994 to 2009 among persons of >60 years and a control (unvaccinated) group of persons 40-59 years, were extracted from the state database. A Serfling model of pneumonia and influenza each of deaths and hospitalizations (J10-19) defined the epidemic period and a separate Serfling model of R and C coded deaths and hospitalizations established a baseline. Observed R and C deaths or hospitalizations occurring in excess of the baseline during epidemic period were deemed influenza-associated. A t-test was performed to compare differences in annual influenza-associated rates, before and after introduction of influenza vaccine. **Results:** Influenza-associated mortality and hospitalization rates in those ≥60 years dropped by 57% and 70%, respectively, in the post vaccination period(1999-2009) compared with the prevaccination period(1994-1998) ($p<0.001$). However, persons

aged 40-59 years who were not routinely vaccinated also demonstrated a drop in influenza-associated mortality and hospitalization rates (41% and 48%, respectively p<0.01), but the drop was less than in the elderly. All cause respiratory-coded deaths or hospitalizations did not decrease significantly in the post-vaccination era. **Conclusion:** We show significant reductions in influenza-associated mortality and hospitalization rate among the elderly ≥60 years, following vaccine introduction in Brazil. The unexpected reductions among unvaccinated persons aged 40-59 years may be due better health care or to indirect effects.

Board 515. Immunity to Influenza A (H3N2v) Virus in Semirural Communities in Peru

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Background: More than 320 human infections with influenza A (H3N2) variant (H3N2v) have been reported in the United States since 2011, mostly among children. Limited serologic studies conducted to date indicate that young children have minimal preexisting immunity. More data are needed to assess immunity to H3N2v in the general population from semirural communities to assess the pandemic potential of H3N2v. **Methods:** We assessed age-specific presence of serum cross-reactive antibody to H3N2v in population-based cohorts (children and adults) in Peru, using stored serum specimens collected in July 2011. Antibody to H3N2v was assessed by hemagglutination inhibition assay. Seroprevalence was defined as an HI titer of ≥40. Data on 2011 trivalent influenza vaccination (TIV) status, direct contact with swine or its secretions, age and sex were recorded. **Results:** 1534 sera samples were tested. The overall prevalence of HI titers against H3N2v was 19%. The highest prevalence was observed in the 20-29 year-old group (44%, 121/278) followed by 26% (56/216) in the 30-39 year-old group, 9% (30/332) in the 40-59 year-old group and 16% in people older than 60 years. Children under 10 years had 1.4% (4/288) of prevalence. The prevalence among vaccinated participants was 29% (20/68) compared to non-vaccinated (18%, 269/1466). Immunization with the 2011 TIV had no impact on cross-reactive antibody levels in those aged <10 years. In overall, people vaccinated with 2011 TIV had 2 times more probabilities of developing cross-reactive antibodies against H3N2v (OR: 2, 95% CI: 1.1-3.7) after adjusting by age, sex, site and swine contact. **Conclusions:** People aged from 20 to 39 years have cross reactive antibodies against H3N2v, while children <10 years are susceptible to infection due to minimal preexisting immunity and apparent no cross-protective effect from TIV vaccine. We found that TIV favored the presence of cross reactive antibodies in adults probably due to previous infections with seasonal influenza viruses however in case an epidemic arises specific H3N2v vaccine would be necessary in conjunction with an increase in vaccine coverage particularly in children.

Bacterial/Viral Co-Infections

Wednesday, August 26, 12:30 PM - 1:45 PM
Grand Hall

Board 516. Potential Impact of Co-infections and Co-morbidities Prevalent in Africa on Influenza Severity and Frequency: A Systematic Review

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Background: Influenza is increasingly recognized as an important cause of disease in Africa. Infectious diseases and underlying medical conditions common to this region may affect influenza burden, clinical presentation, severity, and vaccine response. Other than HIV, little is known about the interaction between influenza and many co-infections and co-morbidities prevalent in Africa. **Methods:** We conducted seven separate systematic reviews of published studies on influenza and the following co-infections or co-morbidities: dengue, malaria, measles, meningococcus, *Pneumocystis jirovecii* pneumonia (PCP), hemoglobinopathies, and malnutrition. **Results:** Each literature review yielded from 327 to 3,902 potential articles. Relevant articles were included in all of the systematic reviews except PCP, though very few studies were found on the potential interaction between influenza and dengue (2 studies), malaria (6 studies), and measles (1 study). More studies were included on the interaction of influenza and meningococcus (16 studies), hemoglobinopathies (29 studies), and malnutrition (19 studies). Except for studies of influenza and malaria, very few studies were from Africa. Underlying medical conditions such as sickle cell disease and malnutrition were found to increase severity of and incidence of hospitalization for influenza disease. Few studies evaluated influenza vaccine response except among those with sickle cell disease and nutrient deficiencies. Vaccination against influenza was found to be effective among those with sickle cell disease (70-100% seroprotection based on 7 studies); vaccine response was impaired with nutritional deficiencies, including iron and vitamins D and E. The few published studies found that influenza co-infection increased severity among patients with dengue, malaria, and measles. Influenza was also found to increase the risk of meningococcal disease (relative risk from 4 studies, range 1.5-2.0). **Conclusions:** Morbidity and mortality from influenza may be more common in Africa because certain infections and diseases common in the region lead to more severe outcomes, increase the propensity to contract influenza and impair vaccine response. However, gaps exist in our knowledge about these interactions.

Board 517. Investigation of Other Respiratory Viruses in Influenza Negative Samples in Sentinel Sites, Burkina Faso, 2010-2012

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Background: Although the influenza surveillance is established by 2010 in Burkina Faso, only data on influenza viruses are available. No data are found concerning other respiratory viruses circulating in the country. The aim of the present study was to detect respiratory viruses in negative to influenza viruses samples collected according to WHO/CDC influenza-like illness case definition. **Methods:** From May 2010 to June 2012, throat swabs were collected from outpatients who presented

influenza-like illness (ILI) symptoms in public hospital in Ouagadougou and Bobo-Dioulasso. Case of ILI was defined as temperature ≥38°C with either cough or sore throat and no alternative diagnosis. We performed rRT-PCR using primers, probes and CDC protocol, to detect influenza viruses. Then 796 negative specimens for influenza viruses were sent to Luxembourg for further investigation on six respiratory viruses by nested RT-PCR. **Results:** Overall, 116/796 (14.6%) respiratory viruses were detected: 53/116 (45.7%) were positive for respiratory syntictial virus, 25/116 (21.5%) for human metapneumovirus, 38/116 (32.7%) for parainfluenza viruses. Of the parainfluenza virus isolates, 7/116 (18. 42%) were parainfluenza viruses type 1, 10 (26. 31%) were type 2 and 21 (55. 26%) were type 3. **Conclusion:** In our study, we found that respiratory viruses play an important role in ILI in Burkina community. These data provide a better understanding of the viral etiology of outpatients with ILI symptoms.

Board 518. Prevalence of Respiratory Viruses Among Hospitalized Children Under 5 Years with Severe Acute Lower Respiratory Infection in Kashmir, North India

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Background: Data on the contribution of respiratory viruses to severe acute lower respiratory infection (SARI) among hospitalized children in India are limited. The present study was designed to determine the prevalence of various respiratory viruses among children <5 years hospitalized with ALRI. **Methods:** Children <5 years of age admitted to the GB Pant Hospital, a 200-bed pediatric facility in Srinagar, Kashmir (north India) were screened for SARI and 2 randomly selected eligible cases were enrolled per day over one year and clinical, epidemiological, and demographic data collected. Nasopharyngeal swabs or aspirates were collected, and tested by real-time PCR for influenza viruses, human rhinovirus, adenovirus, respiratory syncytial (RSV), and other common respiratory viruses. **Results:** During October 2013 to September 2014, a total of 426 patients were enrolled, of whom 57.5% (n=245) were males and 72.3% (n=308) were aged <2 years. The common presenting symptoms included fever (n=410, 96%), cough (n=418, 98.1%), nasal discharge (n=326, 76.5%), breathlessness (n=359, 84.3%), lethargy (n=266, 62.4%), refusal to feed (n=191, 44.8%). Diagnosis at admission included acute bronchiolitis (n=141, 33.1%), wheeze with ARI (n=103, 24.1%), bronchopneumonia (n=129, 30.3%), exacerbation of asthma (n=25, 5.9%), acute bronchitis (n=25, 5.9%) and croup like illness (n=3, 0.7%). Influenza viruses were detected in 17 (4.0%) patients including 12 (2.8%) for influenza A (H3N2) and 5 (1.2%) for influenza B. Of the 426 samples, 314 (73.7%) collected till April 2013 were further tested for other respiratory viruses; 171 (54.5%) tested positive including 24 (7.6%) with co-infections. The commonly detected viruses were RSV B (28.3%), RSV A (7.0%) and rhinoviruses (16.6%). Of the RSV positive cases, 41.4% were in infants aged 0-6 months, and 28.8% were among 6-12 months. Other viruses detected included coronaviruses (3.2%), bocavirus (2.9%), human metapneumovirus (1.9%), adenovirus (1%) and para-influenza viruses(1.6%). Among the co-infections, RSV-B (18/24) and rhinovirus (15/24) are commonly detected pathogens. **Conclusions:** Our data reveal that RSV is an important cause of ALRI requiring hospitalization of children especially infants aged 0-6 months in Srinagar, North India.

Novel Agents of Public Health Importance

Wednesday, August 26, 12:30 PM - 1:45 PM

Grand Hall

Board 519. Salivirus in Children and Its Association with Childhood Acute Gastroenteritis: A Paired Case-control Study

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Background: Salivirus was recently discovered in children with gastroenteritis and in sewage. Though a causative role for salivirus in childhood gastroenteritis was suggested in the previous study, the relationship between salivirus and acute gastroenteritis has not yet been clearly clarified. The sewage strain, although represented by incomplete genome sequencing data, was distinct from previously reported saliviruses, and had not previously been detected in humans. **Methods:** A case-control study examining 461 paired stool samples from children with diarrhea and healthy controls (1:1) was conducted. Common diarrheal viruses were detected using real-time polymerase chain reaction (PCR) and saliviruses were detected using nested PCR. Real-time PCR was used to quantify viral loads. PCR and rapid-amplification of cDNA ends were employed to obtain the full-length genome of the virus. **Results:** Salivirus was detected in 16 (3.5%) and 13 (2.8%) of the case and control samples, respectively; no differences in detection rates (p=0.571) or mean values of viral loads (p=0.400) were observed between the groups. Multivariate Cox regression revealed no association between salivirus and gastroenteritis (p=0.774). The data also demonstrated that salivirus infection did not exacerbate clinical symptoms of gastroenteritis in children. Furthermore, complete genome sequence of a salivirus recovered from the feces of a child with diarrhea (i.e., SaliV-FHB) shared a 99% nucleotide identity with the sewage strain. **Conclusions:** A paired case-control study did not support a causative role for salivirus in pediatric gastroenteritis. This study also demonstrated that all known saliviruses can be detected in the feces of children with or without gastroenteritis.

Board 520. Clinical and Pathological Evaluation of a Large Outbreak of *Mycobacterium marinum* Skin Infections Associated with Fish Markets in New York City

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Background: In March 2014, public health officials began investigating an outbreak of *Mycobacterium marinum* associated skin and soft tissue infections (SSTI) in patients who handled fish from Chinese markets in New York City (NYC). Clinicopathologic and laboratory investigations were performed on a series of patients. **Methods:** Medical records were reviewed for 29 patients. Culture results were available for 27 patients and 24 biopsy specimens were evaluated by histopathology, immunohistochemical (IHC) staining, Acid Fast Bacillus (AFB) staining, and mycobacterial polymerase-chain-reaction (PCR) assays. **Results:** All patients received antibiotic

treatment. The most commonly prescribed antibiotic treatment regimen was a combination of clarithromycin and ethambutol. Of the 29 patients in this case series, 16 (55%) received surgical treatment, and of these, 7 (44%) had deep tissue or tendon involvement. Surgical procedures included incision and drainage, mass excision, and synovectomy. All patients showed improvement by these treatment modalities. For those with culture results, 11 out of 27 (41%) were positive for *M. marinum;* the remainder showed no growth. Poorly formed granulomas (96%), neutrophils (76%), and necrosis (80%) were found in the 24 biopsies examined. Of 15 cases that were culture-negative and analyzed by other methods 9 were PCR positive, 8 were IHC positive, and 3 were positive by AFB stains. **Conclusions:** A multidisciplinary approach was used to identify cases in a large outbreak of *M. marinum* infections associated with handling fish purchased from NYC markets. The use of histopathological study and IHC plus PCR from full thickness skin biopsy or surgical specimens can lead to improved diagnosis and treatment of *M. marinum* SSTIs compared to relying solely on mycobacterial culture, the current gold standard.

Board 521. Chikungunya Surveillance in New York City, 2014

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Background: Chikungunya is a mosquito-borne virus; humans are the primary reservoir. Local transmission of chikungunya virus in North America was first identified in December 2013 in the Caribbean and has spread to parts of Central and South America and Florida. While not geographically close to these regions, New York City (NYC) has a large immigrant population that travels frequently. In addition, the mosquito vector, *Aedes albopictus,* is present throughout the city. A sudden influx of case reports occurred in 2014 in NYC. Protocols, data collection methods, and staff training were rapidly developed to accommodate surveillance needs. The primary goals were to describe the affected population, identify possible autochthonous cases, and direct educational outreach. **Methods:** After receiving laboratory reports for positive serology or PCR results, patient interviews were conducted to obtain clinical and travel history and risk factors and to determine whether patients were viremic in NYC. Weekly reports of viremic cases were shared with the mosquito control authorities. From June through October, weekly mosquito surveillance was conducted to monitor mosquito populations, including *A. albopictus*. **Results:** Since May 2014, NYC has had 339 travel-associated chikungunya cases; 218 were viremic in NYC. Several potentially locally acquired cases were investigated, although none were identified. Cases peaked in September, and patients most commonly reported travel to the Dominican Republic (78%) followed by Guyana (8%) and Puerto Rico (6%). Cases predominantly resided in the Bronx (38%) and Manhattan (32%). The median age was 49 years (range 0-88 years), and 69% percent of cases were female. No deaths were reported, and 16% of cases were hospitalized. *A albopictus* was identified in NYC, though the decision was made not to test pools for chikungunya virus. **Conclusions:** Over 20% of all chikungunya cases reported in the U.S. in 2014 were in NYC residents. This sudden outbreak posed many challenges from rapid development of surveillance activities requiring hundreds of patient interviews, to investigation of potential autochthonous cases. Surveillance information aided monitoring for autochthonous transmission and development of targeted outreach and education to providers and residents in Dominican communities.

Board 522. Serial RNA Detections of Middle Eastern Respiratory Syndrome Coronavirus (MERS-CoV) Among Laboratory Confirmed Cases — Abu Dhabi, United Arab Emirates, 2013-2014

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Background: In March 2013, the first case of Middle East Respiratory Syndrome Coronavirus (MERS-CoV) in Abu Dhabi, United Arab Emirates was identified. A total of 65 cases of MERS-CoV have been reported in Abu Dhabi based upon RNA detection in upper and lower tract respiratory specimens via real-time reverse transcription polymerase chain reaction (rRT-PCR). To guide ongoing surveillance and control efforts, we sought to describe the natural history of MERS-CoV infection through analysis of serial RNA detections. **Methods:** Data collected through 3 Abu Dhabi surveillance systems and subsequent contact-tracing were merged into a single database containing demographic, clinical, epidemiologic, and laboratory information. Upper and lower respiratory tract samples were tested via rRT-PCR upE and ORF1a assays. Length of positivity was defined as duration between date of symptom onset for symptomatic case-patients or date of collection of first positive sample for asymptomatic case-patients and the first negative sample for both symptomatic and asymptomatic case-patients. **Results:** Of 65 laboratory confirmed MERS-CoV case-patients, including 44 that were symptomatic and 21 that were asymptomatic, a total of 473 respiratory samples (median=5, Interquartile Range=3-9 samples per case-patient) were included. The majority of respiratory samples were collected from the lower respiratory tract among both symptomatic (252 [82%] of 308) and asymptomatic (150 [91%] of 165) case-patients. A higher proportion of lower respiratory tract samples (82 [53%] of 155) were positive >2 weeks compared to upper respiratory tract samples (7 [37%] of 19). Of the 250 positive lower respiratory tract samples, 25 (10%) were positive for >3 weeks, including 4 from asymptomatic cases. Twenty-two (34%) of the 65 case-patients had at least one follow up negative PCR result followed by a positive result within 48 hours. **Conclusion:** These results demonstrate that persons infected with MERS-CoV may have rRT-PCR positive detections for multiple weeks after onset of illness, although it is unclear whether these detections represent viable virus. This investigation raises important issues regarding use of rRT-PCR for MERS-CoV diagnosis of mildly ill and severely ill patients, and may help inform infection control recommendations.

Board 523. The Epidemiology of Invasive *Haemophilus influenzae* (nontype b) Disease—Ontario, Canada: 2004–2013

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Background: Since the widespread use of *Haemophilus influenzae* (Hi) type b (Hib) vaccines among children aged <5 years, an increase in invasive non-Hib disease incidence has been reported internationally. We sought to describe the epidemiology of invasive non-Hib disease in Ontario, Canada (population ~12 million). **Methods:** Confirmed invasive non-Hib cases (nontypeable [NT] and serotypes a, c, d, e, and f) were obtained from the provincial laboratory data system for 2004-2013. Data was then deterministically linked to the provincial reportable disease system to provide further case information. Non-Hib cases are not reportable but are often included as cases under investigation until

serotype b is confirmed. Descriptive analyses included incidence rates by year, age group, serotype and site of specimen collection; ethnicity data were not available. Temporal trends were evaluated by Poisson regression and p-values <0.05 were considered significant. Analyses were conducted using SAS v9.3 and Mircosoft Excel 2010. **Results:** During the study period in Ontario 1307 cases of invasive non-Hib disease occurred, increasing from 0.67 cases to 1.60 cases /100,000 from 2004 to 2013. Between 2004 and 2013 significant increases in the incidence of NT (0.50 to 1.28 cases/100 000 population), as well as Hia (0.02 to 0.08 cases/100 000) and Hif (0.13 to 0.18 cases/100 000 population) were seen. No cases of Hic and Hid were identified. The increase over time was especially prominent in adults aged 40+ years; among persons aged 40-64 years, 3 Hi types significantly increased over time; NT (0.22 to 0.99 cases/100 000), Hia (0.00 to 0.06 cases/100 000) and Hif (0.05 to 0.21 cases/100 000). Among persons aged 65-84 years, there was also a significant increase of NT (1.62 to 3.14 cases/100 000,) and Hia (0.00 to 0.34 cases/100 000). Among persons aged 85+ years, NT significantly increased from 4.89 to 10.28 cases/100 000). **Conclusions:** The incidence of invasive non-Hib disease has increased over time; NT and Hia are emerging pathogens, and should be monitored in Ontario, Canada. Further research to develop a non-Hib vaccine should be considered. Abstract Category: Ecology of infectious diseases

Tuberculosis

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Board 524. Evaluating Cell-mediated Immune Response and the Role of Transfer Factor in Immunotherapy of Tuberculosis

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Background: Tuberculosis is a chronic zoonotic disease that causes major health problems on a global scale. To evaluate the potential protective efficacy of transfer factor as an immunotherapy option, cell-mediated immune response was evaluated in guinea pigs inoculated with prepared transfer factor and then infected with virulent *Mycobacterium bovis*. **Methods:** When *M. bovis* was isolated from the lymph node of a tubercular cow and cultured on stonebrink media, colonies appeared within 58-72 days. Heat was used to kill bacterial antigens and new tuberculin was prepared. The heat killed *M. bovis* antigen was then used to immunize ten healthy animals. Ten days after immunization, transfer factor was prepared from the immunized animals according to protocol developed by Rozzo and Kirkpatrick (1992). This transfer factor was used to inoculate Group A of 12 test animals, while Group B of 12 test animals served as the control. Both groups were exposed to virulent *M. bovis*. Transfer factor activity was evaluated and delayed-type hypersensitivity skin reactions were determined in both groups. **Results:** The first group exhibited delayed-type hypersensitivity after 48 hours in the form of a skin reaction; erythrocytes rosette formations increased in Group A with significant differences [p<0.01] between Group A and B. The migration inhibitory factor was determined and showed significant differences [p<0.01] between Group A and Group B. The transfer factor recipient group remained healthy, while the non-recipient group appeared weak with weight loss, loss of appetite, difficult respiration, as well as showed different sizes of tubercles in the liver, spleen and lungs. **Conclusions:** The health of the transfer factor recipient group demonstrates that the cellular immunity of tuberculosis can be activated and transferred by transfer factor, a specific mediator to tuberculosis. This study concludes that transfer factor can be used as immunotherapy within a protective program against tuberculosis in animals.

Board 525. Tuberculosis Contact Investigation at an Island Resort in Michigan, 2014

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Background: During August 2014, a foreign-born hotel employee on an island in Michigan, with smear-positive, drug-susceptible, tuberculosis (TB), was reported to public health authorities and offered treatment. The resort island has a predominantly seasonal workforce, often foreign-born persons visiting on temporary work visas without TB-screening requirements. We investigated contacts at risk for *Mycobacterium tuberculosis* infection to prevent further cases. **Methods:** We interviewed the index patient and employer to find contacts. Contacts at highest risk for disease (defined as employees who worked the same shift as the index patient, visited the patient 1 time/week in their dormitory, or had TB predisposing medical conditions) were screened by using an interferon-gamma release assay (IGRA). Persons with positive results were examined by chest radiograph. **Results:** Among 102 contacts identified, 26 (25%) met 1 criterion for IGRA screening. Of those persons screened, 17 (65%) were female; median age was 24 (range: 21-63) years. Twenty-three (88%) of screened contacts were foreign-born. Of 14/26 (54%) persons with positive results, 11 (79%) were from South Africa; 2 (14%) were U.S.-born; and 1 (7%) was from Jamaica. Five/14 (36%) contacts reported having received a prior TB test, all with negative results, and 3 (21%) reported prior TB exposure. Chest radiographs did not reveal signs of active disease, and all 14 IGRA-positive contacts started treatment for latent TB infection (LTBI). **Conclusions:** We identified 14 contacts with LTBI; however, we cannot distinguish between recent transmission and prior infection because the majority of infected contacts were from the high-TB-incidence country of South Africa. We recommended that island employers implement preemployment TB screening to prevent importation of TB disease among foreign-born seasonal employees.

Infectious Causes of Chronic Diseases

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Board 526. Hantavirus Infection in Ho Chi Minh City, Vietnam: A Case Report, 2013

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Background: Hantaviruses cause two human zoonosis: hemorrhagic fever with renal syndrome (HFRS) and Hantavirus pulmonary syndrome (HPS). At Ho Chi Minh City in 2012, there was a case of HFRS confirm by seropositive. At the end of April and May 2013, there was a case hospitalized because of hantavirus infection. To gain a detailed understanding of Hantavirus epidemiology and it associated hosts we do a case report here. **Methods:** Epidemiological, rodent captured. The serum sample, lung, liver, spleens of rodent were taken. The patient and contact person were also take serum sample. The serum was test by RAC-ELISA-Hantavirus. **Results:** Patient is a male with symptom onset of a HFRS case and the case-patient was confirmed by seropositive. Patient not direct contact with rodents. There are 3 contact persons and they were seronegative. Before onset, patient was stay in the two different places is HCM City and Can Tho City. Of 78 rodents were

captured at Ho Chi Minh City, 65.38% was *Rattus norvegicus,* 34.61% was *Rattus exulans*. No rodents were captured at the patient's house. The percent of seropositive was 20% and only positive on *Rattus norvegicus.* At Can Tho City, the number of rodent captured was 35 include: *Rattus exulan* (7 con), *Suncus murinus* (17 con), *Rattus norvegicus* (4), *Rattus losea* (1), *Rattus argentiventer* (6). The number of seropositive was 4: 01 *Rattus exulan,* 01 *Rattus argentiventer*, 02 *Suncus murinus.* **Conclusions:** This case was HFRS case. *Rattus exulans* was predominant in density and high percent of Hantavirus infected. Further teststudies are needed to confirm the patient infected by virus on infected rodent around his house.

Board 527. Mutational Analysis of Hepatitis E Virus ORF1 "X-Domain" Identifies an Evolutionary Conserved Macrodomain Protein/Appr-1"-pase Active-site, Critical for Virus Replication

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Background: HEV is primarily a water/foodborne human pathogen that has recently emerged to cause chronic hepatitis and neuropathic symptoms. Of the four recognized human HEV genotypes (1, 2, 3 and 4), genotypes 3 and 4 are potentially zoonotic. HEV ORF1 gene encodes the nonstructural polyprotein wherein the "X-domain" still remains poorly defined. Cellular X-domain associated macrodomain protein/ADP-ribose-1"-monophosphatase (Appr-1"-pase) activities are already reported in CoVs, including its homologs in alpha and rubella viruses. The present study therefore, investigated the regulatory role(s) of X-domain in HEV life cycle. **Methods:** GenBank (NCBI) a.a. sequences of ORF1 X-domain of HEV strains representing the four genotypes, including genetically-related viruses, prokaryotic and eukaryotic sequences were analyzed (ClustalW 1.83). The evolutionary conservation of X-domain residues positions (ConSurf) and the secondary structure (PROFSec) were predicted. ORF1 X-domain mutants (N806A, N809A, H812L, G815A, G816A and 817A), were constructed by site-directed mutagenesis in SAR55 replicon (pSK-GFP). The mutant-replicon RNA were tested in hepatoma S10-3 cells, and analyzed by flow cytometry (FACS). **Results:** In silico analysis showed a high degree of evolutionary conservation of X-domain a.a. positions wherein the N-terminus residues 'N806, N809, H812, G815, G816 and G817' formed a potential catalytic-site homolog of CoV Appr-1"-pase. The structure prediction further revealed formation of β-3/α-2 elements by active-site residues, similar to published structures. FACS analysis showed complete abrogation of HEV replication by G816A and G817A constructs compared to G815A mutant that replicated very poorly. Furthermore, while the N806A mutant retained RNA replication, N809A and H812L showed nonviability. The sequential mutation analysis revealed indispensability of X-domain nucleotides on virus replication. Taken together, our data strongly argue for an essential role of X-domain residues at post-translational level, indicating for its Appr-1"-pase activity. **Conclusions:** the regulatory/catalytic role of ORF1 X-domain in HEV life cycle critically depends on the N-terminal 'NNHGGG' segment/secondary-structure. Nevertheless, further biochemical or biophysical characterizations of HEV X-domain's Appr-1"-pase activity would only confirm its significance in virus biology or pathogenesis.

Viral Hepatitis

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Board 528. Burden and Factors Associated with Sero-positivity to Hepatitis C Virus Among Hospital Attendees in Plateau State, Nigeria

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Background: Chronic hepatitis C virus have been implicated as the most common cause of death associated with liver failure, cirrhosis and cancer globally. We determined the burden and assessed factors associated with Sero-positivity to hepatitis C virus (HCV) among hospital attendees in Plateau State Specialist Hospital Jos, Nigeria. **Methods:** We reviewed the virology laboratory records of January 2011 to December 2013. A case of HCV was defined as a patient with complete laboratory data entry and a positive test result using serology through detection of anti-HCV in the blood using HCV-AB kits and interpretation of results was according to manufacturer's protocol. **Results:** Of the 3580 patients screened for anti-HCV antibodies 1916 (54%) were males. A total of 403(11.3%) 95% CI:10.25-12.32% were positive for HCV. Of these 243 (60%) 95% CI: 55.45-64.99% were males. The median was 43.5 years (range of 7 - 95) and 40.0 years (range 5 - 85) for males and females respectively. The age group of > 35 (35-95) had infection rate of 265(66%) CI: 61.02-70.27.Chi square analysis revealed significant association between age and gender to HCV Seropositivity at 40.022 and 8.3872 respectively with P< 0.05. **Conclusions:** Our findings demonstrated that the burden of HCV is more prevalent in the older age group therefore the need for closer monitoring and health education on prevention practices.

Emerging Aspects of HIV

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Board 529. HIV Molecular Epidemiology: How Much Have We Missed?

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Background: A rapid growth of HIV strains identified worldwide has imposed great challenges on HIV genotyping that lays the foundation for HIV basic science and global surveillance. HIV genotyping information, however, has frequently proven inconsistent, even erroneous, from public genome repositories (such as, GenBank), mostly due to the fact that genotyping methods are utilized at the users' discretion. **Methods:** Motivated by our pilot study that demonstrated inadequate genotyping in several epidemiologically important areas, we performed a systematic genotyping investigation on worldwide publicly available HIV-1 sequences. The evaluation pipeline included phylogenetics, genetic distance measure, and subtype profile comparison. Genotyping difference between evaluation pipeline results and the literature genotyping assignment defines mis-genotyped cases. All analyzed sequences were normalized to avoid sampling bias and redundancy. **Results:** Overall, 5.28% of global HIV-1 sequences have been identified as mis-genotyped cases, the majority of which are recombinant strains. An uneven distribution of mis-genotyped cases was discovered among four risk groups (IDU, MSM, heterosexual, and MTCT) sampled from various geographic regions. Across the viral genome, overall mis-genotyped cases were 3-6%, with various degrees of

mis-genotyping among individual risk groups. The results also suggested a closer monitoring of genotyping quality is needed for the heterosexual group in West Central Africa, IDU group in South America, and IDU and mother-to-child groups in China. **Conclusions:** This is the first systematic investigation of genotyping quality of worldwide publicly available HIV-1 sequences. Our study not only demonstrated an uneven distribution of mis-genotyped cases, across the viral genome, geographic regions, and risk groups, but also indicated unknown viral diversities that can't be genotyped using extant methods. Genotyping results obtained from this study can be used as references for global and regional HIV molecular surveillance and antiviral therapy development.

Board 530. Determinants of Infant-feeding Choices of HIV-positive Women Attending Prevention of Mother-to-child Transmission Clinics in Oyo State, Southwestern Nigeria, 2013

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Background: The Nigerian National HIV Guidelines recommends avoidance of all breastfeeding when replacement feeding is acceptable, feasible, affordable, sustainable and safe. Otherwise, exclusive breastfeeding is recommended during the first six months of life. This study determined factors influencing the infant-feeding choices of HIV-positive women enrolled in Prevention of Mother-to-Child Transmission (PMTCT) of HIV clinics in Oyo State, Nigeria. **Methodology:** A cross-sectional survey of 450 HIV-positive women who had received infant-feeding counselling prior to delivery using a two-stage sampling technique. A semi-structured questionnaire was administered to obtain data on socio-demographics, infant feeding choice and factors influencing these choices. We defined mixed feeding as addition of other food or water to breast milk in the first six months of life. Four Focus Group Discussions (FGD) were conducted. Data was analyzed using Epi-info software version7.Detailed content analyses of the FGDs were done. **Results:** The mean age of the mothers is 31 ± 3.5years. Exclusive breastfeeding (EBF), exclusive replacement feeding (ERF) and mixed feeding (MF) were 62.0%, 25.0%, and 13.0% respectively. Determinants of ERF were mode of delivery (AOR 2.3, 95%CI 0.8-4.3) and the desire to reduce the risk of transmission (AOR 5.4, 95%CI 2.8-6.4). For EBF, household income (AOR 3.6, 95%CI 1.8-5.4) and health workers influence (AOR 2.5, 95%CI 1.2-3.8), while for MF, non-disclosure of HIV status to spouse (AOR= 4.3,95%CI 1.5-12.8), Neighbours' advice ((AOR 1.8,95%CI 1.5-4.7) and infant illnesses (AOR= 2.9, 95%CI2.3-7.8) were the predictors. FGDs revealed pressure from family members as the major determinant of mixed feeding practice. **Conclusion:** Pressure from family/neighbours to practice mixed feeding should be discouraged. Incorporation of family members into programs promoting safer infant feeding options in mothers living with HIV/AIDS and male involvement is imperative. **Keywords:** infant food, HIV, Women, Nigeria

Board 531. Risk Perception for HIV Infection Using Multi-stage Stratified Random Cross-sectional Survey, South Africa, 2012

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Background: South Africa (SA) has a high HIV prevalence. In 2012 the HIV prevalence in South Africa was 12.2%. Incidence of HIV among male and females aged 15-49 years has been decreasing: from 1.9% during 2005 - 2008 to 1.7% during 2008-2012. However, prevention efforts must focus on high risk groups and assess their risk perception. We describe identified factors associated with perceived risk of HIV infection in an SA population using a national representative survey. **Methods:** To assess factors associated with perceived risk of HIV infection we used data from a multi-stage stratified random cross-sectional survey conducted in 2012 with South Africans aged 16-55 years. Multivariable logistic regression was used to determine factors associated with perceived risk of HIV infection. Forward selection, variables with p-value <0.05 and improved fit model were retained in the final model. Analyses were adjusted for clustering and done using STATA. Results were summarized using Adjusted Odds Ratios (AOR) with their corresponding 95% confidence intervals. **Results:** Of the 8,756 respondents 19.9% (1,743) perceived themselves to be at high risk of HIV infection. Female gender (AOR 1.76, 95% CI: 1.53-2.04), living in Mpumalanga compared to Western Cape Province (AOR 3.53, 95% CI: 2.33-5.36), low socio-economic status (SES) (AOR 1.28, 95%CI: 1.05-1.57), having multiple sexual partners (AOR 2.58, 95%CI: 2.11 - 3.13), and low self-esteem (AOR 1.67, 95% CI: 1.23-2.27) were significant predictors of high risk of HIV perception. **Conclusion:** Heightened risk perception of HIV infection in SA is associated with specific gender, geographic, economic, behavioural and self-esteem factors. To expand on HIV prevention efforts, initiatives targeted at groups linked to these identified risk factor should be developed.

Sexually Transmitted Diseases

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Board 532. Epidemiology of *Chlamydia trachomatis* and *Neisseria gonorrhoeae* in Air Force and Navy Beneficiaries

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Background: *Chlamydia trachomatis* (CT) infection is the most commonly reported notifiable disease in the U.S.*; Neisseria gonorrhoeae* (GC) is the second. Centers for Disease Control and Prevention (CDC) data show that 1,412,791 CT and 321,849 GC cases were reported in the U.S. in 2011. During the same year, Air Force (AF) Medical Treatment Facilities (MTFs) reported 5,024 CT and 359 GC cases and Navy MTFs reported 10,289 CT and 973 GC cases. In addition to acute illness, the disease burden of these sexually-transmitted infections includes pelvic inflammatory disease, ectopic pregnancy, and infertility. CDC recommends screening sexually active women under age 26; however, screening programs differ between and within services. A recent, thorough evaluation of screening practices has not been accomplished, indicating the need for this particular study. **Methods:** The U.S. Air Force School of Aerospace Medicine (USAFSAM) Epidemiology Laboratory receives specimens from AF and Navy MTFs and performs nucleic acid amplification testing. Reason for testing was added to lab orders May 2012. Results from AF and Navy beneficiaries from May-December 2012 were analyzed based on provider's reason for testing, gender, service, and other demographic variables. Percent

of specimens positive for CT and GC were calculated. **Results:** Of 140,967 specimens, 6,987 were CT positive (5.0%) and 698 GC positive (0.5%); 209 were positive for both. Over half of the tests were requested for asymptomatic screening. Asymptomatic individuals who were case contacts or indicated high risk behavior had the highest percent CT positive (16.1%) while symptomatic individuals had the highest percent GC positive (2.4%). Females contributed 71.9% of the total specimens. Results of screening asymptomatic females under age 26 were 4.5% CT and 0.2% GC positive while specimens outside of this targeted group were 2.8% CT positive and GC 0.2%. **Conclusions:** We provide the first comprehensive analysis of CT/GC testing results from the USAFSAM laboratory. Screening recommendations focus on young women. This analysis provides further information on epidemiology of CT/GC and can inform screening recommendations within our population to expand beyond CDC recommendations for examining other populations with high risk behaviors.

Board 533. Antimicrobial Susceptibility Pattern and Molecular Characterization of Resistance Genes of *Neisseria gonorrhoeae* Isolates in Bhutan

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Background: Antimicrobial resistance *N. gonorrhoeae* is an emerging public health problem worldwide. Rapid development of resistance to a variety of antimicrobial agents has made treatment options very limited. Recently, reports of declining susceptibility to cefixime and resistance to ceftriaxone have raised major concerns which resulted in the amending of the CDC treatment guidelines to dual therapy. **Methods:** *N. gonorrhoeae* isolated from patients with genitourethral discharge in Bhutan was included in this study. MICs were determined for penicillin, tetracycline, ciprofloxacin, ceftriaxone, cefixime, azithromycin, and spectinomycin using E-test. MIC breakpoint was interpreted as per CLSI guideline. Selected isolates with different MICs were submitted for molecular characterization of resistance genes. **Results:** A total of 132 *N. gonorrhoeae* isolates were tested for antimicrobial susceptibility after confirmation**.** MIC results showed that none of the isolates were resistant to ceftriaxone, cefixime, spectinomycin and azithromycin. Resistance and intermediate susceptibility to penicillin, ciprofloxacin and tetracycline were observed among 59% and 35%; 82% and 17%; 69% and 11% of the isolates, respectively. Eighty seven isolates (66%) were positive for beta lactamase. Among these, 68% were encoded with the plasmid mediated beta-lactamase gene, TEM-1. Isolates with different levels of resistance to penicillin and ciprofloxacin were submitted for molecular characterization of resistance genes (*penA, gyrA and parC*). Point mutations and amino acid substitutions were observed on *penA* allele of an isolate resistant to penicillin with MIC =24 ug/mL. Two point mutations of *gyrA* gene and 1 - 2 mutations of *parC* were detected among isolates with a MIC for ciprofloxacin >=0.19 ug/mL and >=3 ug/mL, respectively. **Conclusions:** *N. gonorrhoeae* isolates in Bhutan are still highly susceptible to cephalosporin, azithromycin and spectinomycin. However, resistance to penicillin and ciprofloxacin with mutations of *penA, gyrA and parC* genes have been observed. Continuous monitoring of antibiotic resistance to detect decreasing susceptibility and a more robust understanding of resistant mechanisms are urgently required for effective control and treatment of *N. gonorrhoeae* infections.

Board 534. Seroprevalence and Seroincidence of Herpes Simplex Virus (2006-2010) and Vaccine-preventable Human Papilloma Virus Subtypes (2000-2010) Among United States Military Personnel

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Background: Sexually transmitted infections (STI) have historically been burdensome in military populations. We describe the seroprevalence and seroincidence of vaccine-preventable human papillomavirus subtypes in a sample of 200 servicemen along with the seroprevalence and seroincidence of herpes simplex virus (HSV-1/2) in a sample of 200 males and 200 females. **Methods:** Sera from 200 males along with associated demographic data were obtained and tested for HPV types 6, 11, 16, and 18 at entry to service and ten years later. Similarly, 200 active duty males and 200 active duty females were tested for HSV-1/2 at entry to service and four years later. **Results:** The cumulative seroincidence of new infection with HPV was 34% over a 10-year period (n=68); with 63% (n=43) wart-type, 18% (n=12) oncogenic-type, and 19% (n=13) mixed. At entry to military service, 33.5% of males were seropositive for HSV-1 and 1.5% positive for HSV-2; seroincidence was 3.4 and 1.1 per 100 person-years, respectively. Among females, 39% were seropositive for HSV-1 and 4.0% for HSV-2; seroincidence was 5.5 and 3.3. per 100 person-years, respectively. **Conclusions:** STIs in military populations are highly prevalent, incident, and epidemiologically distinct. Our data show rates of HPV and HSV-1/2 acquisition that are higher than those seen in the general public, again highlighting the need for continued preventive efforts. Consideration of universal HPV vaccination among males is warranted.

Board 535. Antibiotic Resistance in *Neisseria gonorrhoeae* Isolates from Five Clinics in Accra and the Western Region of Ghana

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Background: The emergence and transmission of multi-drug resistant *Neisseria gonorrhoeae*, necessitates monitoring of antibiotic resistance trends across the globe with a focus on resource-limited regions such as the West African nation of Ghana. In Ghana, syndromic management is the standard of care for treating sexually transmitted infections (STIs). Knowledge on prevalence of resistance patterns will help to guide clinicians on proper medications to treat drug resistant *N. gonorrhoeae* and provide data support for public health control programs. The objective of this study was to determine the prevalence and antibiotic resistance profile of *N. gonorrhoeae* cases among individuals presenting at five healthcare facilities located in the Greater Accra and Western Regions of Ghana between October 2012 and July 2014. **Methods:** Urethral or endocervical swabs were obtained from consenting patients presenting with symptoms of STI at five clinics in Accra and Sekondi/Takoradi, Ghana. Swabs were cultured on Modified Thayer-Martin agar and

growing colonies were subcultured on chocolate agar. *N. gonorrhoeae* isolates were identified by gram staining, catalase, as well as oxidase tests purified colonies were confirmed using the API-NH. Antibiograms were determined by Antibiotic Susceptibility Testing (AST) with the disc diffusion method. The Minimum Inhibitory Concentration of resistant and intermediate isolates was recorded using the E-test. **Results:** Twenty-six *N. gonorrhoeae isolates* were obtained from a total of 578 STI clinically diagnosed cases. One isolate, representing 4%, was resistant to both cefixime and ceftriaxone. Spectinomycin resistance was 13%, azithromycin 25%, ciprofloxacin 85%, and 100% resistance was detected for both tetracycline and penicillin. **Conclusions:** This investigation provides data on *N. gonorrhoeae* prevalence and resistance in Ghana hitherto poorly characterized. We note significant resistance to fluoroquinolones (FQ), mirroring global trends, and identified the first known case of resistance to the extended-spectrum cephalosporins in Ghana. Our surveillance efforts, if adopted and sustained in Ghana can help fill the gap in knowledge on the prevalence of *N. gonorrhoeae* and their antimicrobial resistance profile.

Board 536. Occupational Factors and Their Influence on Sexually Transmitted Infections in Active Duty Air Force Members

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Background: Ever since General David Grant, Air Surgeon of Army Air Forces in World War II, linked clandestine use of sulfanilamide to a flying officer's death, there has been greater recognition of the value of reporting of sexually transmitted infections (STIs). New opportunities to identify occupational factors in STI burden have developed with the recent construction of the Occupational and Environmental Air Force Health Study. This database connects approximately 33.7 million records containing 221 unique variables from six health and personnel databases consisting of 519,000 subjects from 2006 through 2010. **Methods:** Inpatient, outpatient, and reportable event surveillance data were queried for STIs utilizing a coding algorithm derived from The International Classification of Diseases, 9th Revision, Clinical Modification. Annual burden of STIs was counted in an ever/never method as to whether a service member had an STI code each year. These data were linked to Air Force demographic data to evaluate risk factors for STI burden. **Results:** Overall higher rates of STIs were identified in Air Force members who were enlisted, younger, female, non-married, and those with lower education. Organizationally, Air Force members belonging to mission support, security forces, and logistics readiness units had the highest rates of STIs. Occupationally, those with a Duty Air Force Specialty Code (DAFSC) involving support and medical specialties had the highest rates of STIs among enlisted personnel, while officers show little difference by DAFSC categories. As compared with reported civilian cases, Air Force members had higher crude rates of reported chlamydia (857-995 cases versus 344-426 per 100,000 population), but lower crude rates of reported gonorrhea (63-83 cases versus 98-120 per 100,000 population) and syphilis (4.2-5.0 cases versus 12.3-15.2 per 100,000 population) over the study timeframe. Temporal trends in type of STI were comparable between Air Force and civilian populations as chlamydia trended upward while gonorrhea and syphilis rates remained stable over the five year study. **Conclusions:** We identify actionable associations between STI burden and demographic, organizational, and occupational risk factors. Future studies can utilize this data to model the value of proposed interventions.

Late Breakers II

Wednesday, August 26, 12:30 PM - 1:45 PM

Grand Hall

See page 259.

M6. Tropical and Zoonotic Infections

Wednesday, August 26, 1:45 PM - 3:15 PM

International Ballroom North

First Outbreak of Locally Acquired Hepatitis E Virus Infection in Australia

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Background: Foodborne transmission of hepatitis E virus (HEV) has been previously reported in developed countries but not in Australia, where laboratory testing for HEV is generally performed in persons with a history of overseas travel. In March 2014, two HEV infected patients who had not recently travelled overseas, but who were part of a larger group that dined at a single restaurant, were reported. We initiated aninvestigation to determine the source and extent of the outbreak. **Methods:** In Australia, laboratory diagnoses of HEV infection (by IgG seroconversion, detection of HEV-specific IgM or nucleic acid, or isolation in culture), are notifiable to the public health authority. We interviewed notified HEV-infected cases about potential risk factors such as overseas travel, foods consumed and occupational history in their incubation period. Further cases were identified by serological testing and interviewing co-diners of cases, and by testing patients in whom viral hepatitis screening was requested at a major private and public reference laboratory, where hepatitis A, B, C, Epstein-Barr virus and cytomegalovirus infection had been excluded. Reported foods eaten by cases were compared with those reported by uninfected co-diners. Serum isolates collected from restaurant cases were genotyped and sequenced. Implicated foods were traced back to the source. **Results:** Thirty-five cases were notified from October 2013 to June 2014, of whom eighteen reported eating at the implicated restaurant in their incubation periods. Pork liver pâté was the only food consumed by all 16 cases with complete food histories, compared with seven uninfected co-diners (RR 3.0, CI 0.3 - 33.5). Cases reported no other common food exposures. HEV was detected by nucleic acid testing in 11 of 18 cases - all were genotype 3. Viral sequencing showed greater than 99% sequence homology between cases. Pork livers were traced back to a single farm. **Conclusions:** This is the first HEV outbreak in Australia and one of the largest associated with consumption of contaminated pork products. We recommend that clinicians in Australia consider the diagnosis of HEV in patients presenting with a compatible illness in the absence of overseas travel history. Further, the food service industry should ensure that pork liver products are thoroughly cooked.

Epidemiology of Ebola Virus Disease and Impact of Isolation and Treatment in Remote Outbreaks in Liberia

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Background: Prospective investigations of Ebola outbreaks in remote areas of Liberia provided an opportunity to characterize Ebola transmission and measure the impact of response interventions. **Methods:** We conducted epidemiologic investigations and constructed complete transmission chains for nine outbreaks in seven counties between August and December, 2014. After the initial alert for each outbreak was received by the county health teams, interventions were initiated that included isolation and treatment of case-patients, contact tracing, and safe burials. The basic and effective reproduction numbers were calculated as the average number of secondary infections before and after response interventions began, respectively. The impact of admission to an Ebola treatment unit (ETU) on survival was evaluated with a Cox proportional-hazards model. **Results:** There were 165 Ebola cases identified, of which 70% were laboratory-confirmed and 61% were isolated and treated in an ETU. The overall case-fatality rate (CFR) was 67%, but higher (94%) for those not admitted to an ETU compared to those admitted (51%). The average number of secondary cases, R_0, across the different outbreaks was 1.66 (95% confidence interval [CI], 1.0 to 2.76) in the periods before interventions began while the average number of secondary cases after interventions began, R_c was 0.11 (95% CI, 0.05 to 0.25). The risk of generating a secondary case was significantly greater among cases not isolated in an ETU compared to those admitted within four days of symptom onset (risk ratio [RR], 9.32; 95% CI, 2.24 to 38.84), but isolation after four days of symptom onset did not significantly increase the risk of transmission compared to isolation within four days (RR, 3.95; 95% CI, 0.32 to 48.3). Admission to an ETU was associated with a 46% reduction in mortality (hazard ratio 0.54, 95% CI 0.35 to 0.84). **Conclusion:** Rapid isolation and treatment of cases had the dual benefit of contributing to interruption of community transmission and improving survival of Ebola patients.

Ebola Virus Disease Outbreak in Nigeria: Investigation and Epidemiological Profile of Affected Persons, July-September 2014

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Background: Ebola virus disease (EVD) is a complex zoonotic disease, highly virulent in humans. The current epidemic of EVD was first reported in March 2014 in West Africa and is the largest ever reported globally. Nigeria had its first imported case on the 23rd of July 2014; we investigated and described the epidemiological profile of this outbreak that affected two megacities in Nigeria in terms of person, place and time characteristics of the cases. **Methods:** Cases were identified through contact tracing, line-listed and described. We adopted the WHO case definitions for EVD. A suspected case was defined as any person with axillary temperature ≥38oC, who had visited an affected area within 21days or had contact with a confirmed or probable case and with two or more cardinal symptoms of EVD. A confirmed case was a suspected case with positive reverse transcription (RT)-PCR laboratory result and a probable case was a suspected case evaluated by a clinician or any deceased suspected case with an epidemiological link with a confirmed EVD case. **Result:** Twenty cases were identified (19 laboratory-confirmed Ebola cases and one probable case); mean age of cases was 39.5±12.4years with over 75% within the age-group 20-39years. Majority (11 or 55%) were females. The most frequent (14 or 73.7%) exposure type was direct physical contact and median incubation period was 11days. Overall case-fatality ratio (CFR) was 40%; CFR was higher among healthcare workers (46%) compared with non-healthcare workers (22%). The duration of epidemics was 43 days with typical propagated pattern **Conclusion:** Investigation revealed the size and spread of the outbreak. Enhanced surveillance measures, including contact tracing and daily follow-up were useful in early case detection and containment of the outbreak.

The Epidemiology and Clinical Features of *Balamuthia mandrillaris* Disease in the United States, 1974–June 2014

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Background: *Balamuthia mandrillaris* is a free-living ameba that causes rare, nearly always fatal disease, in humans and animals worldwide. *Balamuthia* causes three known diseases: granulomatous amebic encephalitis (GAE), disseminated Balamuthiasis, and cutaneous Balamuthiasis. *B. mandrillaris* has been isolated from soil, dust, and water and likely spreads hematogenously via the lungs or skin. To date, only individual case reports and small case series have been published on this rare disease. We present the first national case series of *Balamuthia* disease in the United States. **Methods:** The Centers for Disease Control and Prevention (CDC) maintains a Free-living Ameba (FLA) laboratory and registry. To be entered into the registry, a *Balamuthia* case must be laboratory-confirmed. Several sources were used to complete entries in the registry, including case report forms, CDC laboratory results, published case reports, and media information. Case reports were included in this analysis if the final diagnosis was GAE, disseminated Balamuthiasis, or cutaneous Balamuthiasis. SAS© version 9.3 software was used to calculate descriptive statistics and frequencies. **Results:** There were a total of 89 case reports of *Balamuthia* disease between 1974 and June 2014. Most (85.4%) had solely GAE. Case-patients' median age was 33 years (range 3 months to 89 years) with 34.5% of case-patients being children (≤ 13 years). Males accounted for 68.2% of the case-patients. California had the highest number of case reports followed by Texas and Arizona. Hispanics accounted for 71.4% when ethnicity was documented. Almost one-third (30.3%) of case-patients had a documented soil-related exposure. Among those with a known outcome, 91.7% of case-patients died. **Conclusion:** This description of *Balamuthia* disease in the U.S. is the largest case series reported to date. Our results indicate that *Balamuthia* disease in the U.S. is mostly characterized by a highly fatal encephalitis that affects patients of all ages. Hispanics were disproportionately affected. The southern and western regions of the U.S. have reported the most cases. This case series further characterizes this rare but nearly always fatal disease.

Comparing the Natural History of Human Nipah Infection in Bangladesh by Route of Exposure

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Background: Nipah virus (NiV) is an emerging, bat-borne paramyxovirus that causes encephalitis in humans and can be transmitted from person-to-person, posing a global pandemic threat. Almost all Nipah cases in Bangladesh acquired infection following drinking raw date palm sap, likely contaminated with bat-saliva, or contact with other Nipah cases. These two routes of transmission likely expose people to different doses of virus, which could affect the natural history of disease. The objective of the analysis was to assess whether the incubation period, viral shedding, and clinical outcomes differed between patients infected through each route. **Methods:** We compared viral shedding and clinical outcomes of Nipah cases identified between 2005-2013 by route of exposure. We compared the incubation period between the two exposure groups using Kaplan Meier estimates with the sub-set of patients for which the exact date of exposure was known. **Results:** Among 150 Nipah cases, 87 (58%) drank raw date palm sap and 33 (22%) had contact with other Nipah cases during preceding month of onset of illness. Of these, 77 (64%) cases were exposed on a single day with reasonable certainty. The median incubation period of Nipah cases who drank raw date palm sap was 5 days shorter than those who had contact with other Nipah cases (6 days vs. 11 days; p value <0.001). Nipah cases who drank raw date palm sap were more likely to die than the Nipah cases who acquired NiV infection after contact with other Nipah cases [91% vs. 55%; risk ratio=1.7, CI (1.2-2.3), p value <0.001]; Kaplan Meier estimate log rank p value <0.001. There was no significant difference in viral shedding in oral secretions between the two exposure groups [risk ratio=1.2, CI (0.8-1.9), p value =0.4]. **Conclusions:** Compared with persons who contracted Nipah infection from another person, Nipah cases who drank raw date palm sap were more likely to have a shorter incubation period and die. Drinking raw date palm sap may result in NiV contact with gastro-intestinal mucosa in a higher dose compared to cases acquiring infection from contact with other Nipah case's oral secretion. These data suggest that, there may be a window of opportunity for targeted interventions with personal protective equipments and/or post exposure prophylaxis for persons who contact Nipah patients.

Severe Fever with Thrombocytopenia Syndrome Has Long Been Circulating in South Korea: A 6-year Study

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Background: Severe fever with thrombocytopenia syndrome (SFTS) is an emerging tick-borne disease caused by a novel bunyavirus called SFTS virus (SFTSV). Major clinical manifestations of SFTS are fever, thrombocytopenia and diarrhea. SFTS cases were first reported in China in 2009 and subsequently from Japan and Korea in 2012. After the first cases were reported in each countries, retrospective studies discovered the previous undiagnosed cases in China and Japan: the earliest cases dated back to 2005 in Japan and 2006 in China. However, such past cases have not been reported in Korea yet. The aim of this study was to investigate whether SFTS patients existed in Korea before 2012. **Methods:** A retrospective study was conducted on patients who came to a university hospital between 2008 and 2013 and underwent bone marrow examination due to fever and thrombocytopenia with no clear hematologic or microbiologic causes at that time. RNA was extracted from stored blood samples, and real-time reverse transcription PCRs were performed to amplify L, M and S segments of SFTSV; sample was considered positive for SFTSV if 2 or more segments were detected. Morphologic findings of the bone marrow were reviewed. **Results:** A total of 35 patients were included in this study. Of these, 4 patients were positive for SFTSV (11.4%). Median age of the 4 SFTS patients was 54.5 years (range 24-62), and all of them were male. All the SFTS patients were living in southeastern Korea, and three of them had outdoor activities before the illness. The earliest case was in 2008. All the SFTS patients were also diagnosed as having hemophagocytic lymphohistiocytosis: 2 patients were treated with cytotoxic and immunosuppressive agents. One of the cases treated for HLH was fatal. **Conclusions:** SFTS has long been circulating in southeastern Korea since 2008. In Korea, SFTS should be considered as one of the differential diagnoses in patients with fever and thrombocytopenia.

N1. Healthcare-Associated Infections

Wednesday, August 26, 3:30 PM - 5:00 PM

Centennial Ballroom I

Treatment and 12-month Outcomes Among Patients with Fungal Meningitis (FM) and Epidural Abscess (EA) Due to Contaminated Epidural Methylprednisolone Acetate (MPA) Injections—United States, 2012-2013

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Background: In September 2012, CDC and others responded to an outbreak of invasive fungal infections associated with contaminated MPA injections. This outbreak represents the largest cohort of fungal infections reported with this emerging infectious pathogen. We present 12-mo data on the treatment and outcomes for a subset of pts with documented FM or EA. **Methods:** Pts with documented case definitions were enrolled in a follow-up study to assess treatment and outcomes. Data from medical records were extracted at baseline, 6 and 12 wks, 6, 9, and 12 months entered into standardized case report form. **Results:** Of the 752 pts who met the original CDC outbreak case definition, 395 (52.5%) have been enrolled, 347 have 6-mo follow-up, and 286 have 12-mo follow-up. For this preliminary analysis, 153 pts had a diagnosis, FM in 81 cases (52.9%), EA in 95 (62.1%), and both sites in 23 (8.0%). All pts received some antifungal therapy (AFTx) by 12-mo follow-up (100%, n=153). In line with CDC recommendations, voriconazole was the first line AFTx for all pts. Combination Amphotericin B therapy was noted in 109 (71.2%) of these cases: among those with FM 56 (69.1%) and among those with EA without FM 39 (67.2%). AF related adverse events (AEs) were common with 140 (91.5%) of pts experiencing at least one. Voriconazole related AEs were reported in 139 patients and most commonly involved hepatic complications (73.6%), hallucinations

(39.3%) visual disturbance (37.9%), difficulty thinking (37.1%), and gastrointestinal complaints (65.0%). At 12-mos, the proportion of pts who achieved cure or partial response to AFTx overall was 86.2%. Pts with a single site infection had a higher proportion that had achieved a cure or partial response than multiple site infections (FM: 88.8%; EA: 79.5%; both: 69.6%). **Conclusions:** The findings from this investigation will increase understanding of clinical, therapeutic, and outcome data from guidelines that were created real time in this outbreak response. Although this was the first outbreak with this emerging infection, at 12-mos, the majority of case pts in this cohort had either a complete or partial response to treatment.

Geographic Distribution of CRE Cases in Tennessee Informs a Regional Strategy to Strengthen Prevention Practices and Control Measures in Healthcare Facilities

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Background: Carbapenem-resistant Enterobacteriaceae (CRE) are an important public health threat and are reportable to the Tennessee Department of Health (TDH). Recently, TDH was successful in extracting antimicrobial susceptibility results from the electronic reportable disease surveillance system. **Methods:** Data from CRE cases reported in 2014 were analyzed using the 2015 National Healthcare Safety Network (NHSN) case definition. Each person was counted once per organism for the calendar year. SAS 9.3 was used to summarize cases by demographics, organism, public health and Emergency Medical Services (EMS) region, and testing healthcare facility/laboratory. ArcGIS 10.2.2 was used to map the cases according to the case residential address and corresponding county, public health, and EMS region. Cases were also mapped based on the testing healthcare facility/laboratory. **Results:** Marked geographic differences were noted for the distribution of organism genera and species by residential public health and EMS region, and testing healthcare facility/laboratory. *Enterobacter* spp. cases were distributed throughout the state, with a concentration of *Enterobacter cloacae* in the metropolitan area of southwestern Tennessee. A similar distribution was noted for *Escherichia coli* cases. In contrast, cases caused by *Klebsiella pneumoniae* were highly concentrated in northeastern Tennessee. A regional CRE workgroup comprised of regional epidemiologists, healthcare facility infection preventionists, infectious diseases physicians, and laboratorians was organized to represent geographic areas with both high and low incidence of CRE. Laboratory surveys are in development to assess current laboratory practices, including carbapenem CLSI breakpoints and resistance mechanisms tests. Facility level surveys are in development to assess the implementation of CDC prevention and control measures guidance. **Conclusions:** The marked geographic variation in CRE incidence in Tennessee suggests a regional approach will be the most successful strategy for controlling the transmission of CRE within and between healthcare facilities. The regional collaborative is moving forward to improve the implementation of the tiered recommendations described in the CDC CRE toolkit for facilities, including providing up-to-date situational awareness.

Shedding of Nipah Virus and Contamination of Hospital Surfaces During an Outbreak in Bangladesh, 2013-2014

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Background: Nipah virus (NiV) is an emerging, bat-borne paramyxovirus that has been transmitted in hospital settings from patients to family caregivers presumably through oral secretions. In 2004, NiV RNA was identified on a hospital wall during an outbreak with person-to-person transmission in Bangladesh. It is unknown whether patients with NiV infection contaminate the hospital environment posing a risk for disease transmission. The objective of this study was to detect whether hospital surfaces adjacent to Nipah patients were contaminated with NiV. **Methods:** From December 2013 to March 2014, the NiV outbreak period in Bangladesh, research assistants collected surface swabs near the beds of all suspected Nipah patients in 3 surveillance hospitals in Bangladesh. They collected swabs from walls, bed rails, bed sheets, clinical record files, and local towels used by family caregivers for cleaning patient secretions, hand drying, and other caregiving purposes. We tested suspected cases for NiV-IgM antibodies in serum to confirm NiV infection. We tested confirmed cases for NiV RNA in oral swabs and in surface swabs by real-time RT-PCR. We summarized the data using frequency and percentages. **Results:** Among 11 laboratory-confirmed Nipah cases, 6 had NiV RNA in their oral swabs and 5 of these had evidence of NiV RNA on at least one surface near them including 2 patients that contaminated multiple surfaces. Three patients contaminated their towels, 3 contaminated their bed sheets and one patient contaminated the bed rail. Of the 6 cases shedding NiV RNA in oral secretions, 4 were involved in person-to-person transmission chains and 3 of these had contaminated hospital surfaces. Of the 6 cases shedding NiV RNA, 3 transmitted the virus to their caregivers and 2 of these contaminated hospital surfaces. Half of the 6 NiV shedding cases had difficulty breathing and all died. Of the 5 patients who had no evidence of NiV RNA in oral swabs, all were isolated cases and 4 survived their illness. **Conclusion:** This study demonstrates that NiV patients who shed virus in their respiratory secretions frequently contaminate their immediate environment and are more likely to transmit NiV to their caregivers. To reduce the risk of fomite transmission, infection control should target hospital surfaces, particularly the towels used by caregivers.

Validation of Risk Score to Identify Future *Clostridium difficile* Infection Following Hospital Discharge in a Cohort of Hospitals Submitting Data to a Hospital Drug Database

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Background: *Clostridium difficile* is an urgent U.S. antimicrobial resistant threat. Identification of patients at risk for future CDI is critical to inform upcoming *C. difficile* vaccine trials. We have previously developed a risk score using two academic hospitals in the Emerging Infections Program to identify patients at high risk of CDI ≥ 28 days after hospital discharge, and now our goal was to validate this risk score in a cohort of US hospitals. **Methods:** Adult drug use and hospitalization data was obtained from the Truven Health MarketScan® Hospital Drug Database (HDD), a representative sample of U.S. hospitals, for the years 2006-2010. Retrospectively, we randomly selected one index visit per patient from a cohort of all adult patients with at least one inpatient stay from 2007-2009 without previous CDI, CDI during the index visit, or death during the index visit. We then determined the occurrence of hospitalized CDI ≥ 28 days after discharge using ICD-9-CM discharge codes. Risk score was calculated for each patient using the same predictors and model used in the previous study, including index visit length of stay, age, past hospital visits within 90 days, and exposure to 3rd/4th generation cephalosporin, clindamycin, or fluoroquinolones during the index visit. We then evaluated the utility of the risk score to identify a population

at greater risk of CDI ≥ 28 days after discharge. **Results:** Among 451 hospitals, we identified 8,674,351 randomly selected index visits. Of those, 7,807 (0.09%) developed CDI ≥ 28 days after discharge. From a logistic model, the c-statistic for the risk score was 0.8. When divided into high and low risk cohorts, using the previously established score of 14 or higher as high risk, 3,789,020 (44%) index visits were identified as high risk, and 6,805 (87%) of the cases occurred in that high risk cohort (RR=8.77, p<0.0001). **Conclusions:** Our study validated a previously developed risk score using a large representative sample of US hospitals. This score can be applied at discharge to identify a population at risk for CDI that can be targeted for *C. difficile* intervention at the time of hospital discharge.

Importance of Adherence to Targeted Screening for *Strongyloides stercoralis* Infection in Solid Organ Transplantation

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Background: Donor-derived *Strongyloides stercoralis* infection is a public health concern among solid-organ transplant (SOT) recipients. Donor-derived infection may lead to hyperinfection syndrome and disseminated disease. To prevent these infections American Society of Transplantation (AST) recommends that evaluation for strongyloidiasis be strongly considered in donors with epidemiologic risk factors or unexplained eosinophilia. Positive donor test results reported to transplant centers allow for treatment and prevention of strongyloidiasis. **Methods:** We describe three recent investigations of donor-derived strongyloidiasis and assess the outcome of each investigation based on adherence to the current AST guidelines and reporting of donor testing results to recipient's transplant centers. We highlight the New York Organ Donor Network's (NYODN) experience with targeted donor screening. **Results:** All three donors were from *Strongyloides*-endemic areas. In one investigation, 5 recipients received organs from an untested donor. Disseminated strongyloidiasis was confirmed in at least one recipient. Testing performed on donor serum after diagnosis of the index case was positive. In a second investigation, 5 recipients received organs from a donor who tested positive shortly after organ procurement. Test results were submitted to an internet-based system, but not directly reported to the transplant centers. Two recipients developed fulminant strongyloidiasis and died. In the third investigation, 4 recipients received organs from a donor who tested positive prior to organ procurement. All transplant centers were notified of the donor's status and preemptive therapy was provided to all recipients; none had evidence of strongyloidiasis. Targeted donor screening by the NYODN since 2010 has identified 10 positive donors of 355 screened; preemptive therapy offered to recipients likely prevented donor-derived strongyloidiasis in these cases. **Conclusions:** Donor-derived strongyloidiasis is preventable with strict adherence to screening guidelines and effective communication between organ procurement and transplant centers. The NYODN's experience suggests that targeted donor screening performed prior to SOT may ensure preemptive treatment and prevent donor-derived strongyloidiasis.

Healthcare-associated Outbreak of Legionnaires' Disease in a Leukemia Unit—Alabama, 2014

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Background: In May 2014, the Alabama Department of Public Health detected an outbreak of Legionnaires' disease (LD) associated with a recently-opened leukemia unit at Hospital A. Healthcare-associated LD has a mortality rate up to 30%, and immunocompromised patients are particularly susceptible. We characterized the outbreak and evaluated contributing factors to stop transmission. **Methods:** A case of LD was defined as radiographically-confirmed pneumonia with a positive urinary antigen test and/or respiratory culture for *Legionella* in a person with exposure to the leukemia unit at Hospital A after February 20, 2014 (date of unit opening) and during the incubation period of 2-10 days prior to symptom onset. Clinical and epidemiological characteristics of confirmed cases were captured by chart review. We conducted an environmental assessment at Hospital A and collected water samples for *Legionella* culture. Clinical and environmental isolates were compared by molecular subtyping. Short-and long-term prevention strategies, including water restrictions for inpatients, were implemented. **Results:** We identified ten cases of LD in nine leukemia inpatients and one visitor. Six (60%) patients were admitted to the unit for their entire incubation periods; five (50%) had diagnostic testing performed >1 week after symptom onset. Environmental sampling revealed growth of *Legionella pneumophila* serogroup 1 in the potable water at nine sites (90%) sampled on the leukemia unit; all three clinical isolates were identical to environmental isolates from the unit (subtype ST36). No cases resulted from exposure to the unit after implementation of water restrictions and remediation of the water supply. **Conclusions:** Contamination of the hospital's potable water system, possibly due to stagnant water in the piping during the two-month period between completion of construction and the unit opening, was the likely source of this outbreak. Clinicians caring for immunocompromised patients should maintain a high index of suspicion for healthcare-associated LD; clinical surveillance to detect healthcare-associated LD cases, including timely and appropriate diagnostic testing, is recommended. Implementation of water restrictions and prompt intervention may help protect highly susceptible patients.

N2. Respiratory Diseases

Wednesday, August 26, 3:30 PM - 5:00 PM

International Ballroom North

Direct and Indirect Benefits of Pediatric Influenza Immunization on US Hospitalizations

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Introduction: Between 2006 - 2007 and 2010-2011, the US Advisory Committee of Immunization Practices (ACIP) gradually broadened its recommendations for annual influenza vaccination to include healthy children from 6-23 mo, 24 - 59 months, 5 to 18 years, and eventually everyone over the age of 6 months. We analyzed the population-level effects of this policy on influenza-related hospitalizations. **Methods:** Age-specific annual vaccination rates were derived from the National Immunization Survey (NIS) and Behavioral Risk Factor Surveillance

System (BRFSS). We estimated age-specific rates of influenza-associated hospitalizations each season during 1989 - 2012 by modeling weekly pneumonia and influenza and respiratory and circulatory outcomes from the State Inpatient Databases of the Agency for Health Care Research & Quality (AHRQ). Models were stratified by age and state and included covariates for temporal and seasonal trends, and proxies of virus activity. Vaccine benefits were evaluated by modeling seasonal influenza-associated hospitalization rates as a function of vaccine coverage and dominant influenza subtype each season. **Results:** Influenza vaccination coverage in children under 5 yrs increased from ~5% to ~70% during 1990-2012, while coverage increased more slowly over the same period among seniors over 65 years from 42 to 67%. Direct vaccine effects in children under 5 yrs were significant and protective in models adjusted for state, but not for season. Vaccine effects were significant in children 5-19yrs (P=0.01). Pediatric influenza-related hospitalization rates did not systematically differ between high and low vaccination states in individual seasons. Over the study period, influenza-related hospitalization rates declined in all adult age groups, coinciding with the onset of pediatric vaccination (P<0.0008). **Discussion:** There was weak evidence of a direct protective effect of pediatric influenza vaccination in population-level hospitalization time series. The recent decline in adult hospitalization rates is intriguing; further research should evaluate whether this may be due to herd immunity or declining influenza activity. Mathematical models of influenza transmission suggest that an indirect protective effect would be expected with pediatric vaccine coverage above 70%.

Use of Disease Clusters to Estimate Severity of H7N9 Infection in China

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Background: Almost 90% of reported cases of avian influenza A (H7N9) infection (H7N9) have been classified as severe. The true risk of hospitalization and death after infection, however, is unclear, since severe cases are more likely to seek care and be tested than mild cases. To provide a less biased assessment of the spectrum of illness caused by H7N9, we used data on H7N9 infections identified via active surveillance and monitoring of contacts of confirmed (index) cases of H7N9 infection. **Methods:** Fourteen clusters of laboratory-confirmed H7N9 illness, defined as one index case and ≥1 epidemiologically linked contact-case, have been reported to China Center for Disease Control and Prevention. We assigned cases to one of two groups: non-severe or severe. According to the National Protocol for H7N9 Human Diagnosis and Treatment, a case of H7N9 disease was classified as severe if at least one of following criteria was met: 1) chest radiography displays multiple pulmonary lobes affected or lesions progress> 50% within 48 hours; 2) difficulty breathing with breathing rate > 24 times per minute (≥5 years); 3) severe hypoxemia with SpO2 ≤ 92% under a condition of oxygenation at 5 liters per minute; and 4) shock, ARDS, or Multiple Organ Dysfunction Syndrome. We calculated the proportion of contact-case H7N9 illnesses that were severe, with a confidence interval estimated using the Wilson score interval method with continuity correction. We compared the severity proportion among adult and child contact-cases using Fisher's Exact test. **Results:** All fourteen index cases (9 male; median age= 39.5 years) were severe and seven died. Of the 15 contact-cases from the 14 index cases, 4 were severe (including 3 deaths) and 11 were mild for a severity proportion of 27% (4/15; 95% confidence interval [95%CI]= 11%-52%). Eight adult contacts developed H7N9 infection; of these, 4 were classified as mild and 4 as severe (3 died), for a severity proportion of 50% (4/8; 95%CI= 22%-78%). In contrast, none of the 7 child contacts who developed H7N9 illness were severely ill (0/7; 0%, 95%CI=0%-35%); this proportion was statistically significantly different from adults (p=0.03). **Conclusions:** Surveillance data from China may be missing milder cases especially among children, but likely correctly indicates a high severity of H7N9 illness in adults.

Viral Identification in Children with Previously Undiagnosed Pneumonia

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Background: Viral respiratory infections are a significant cause of morbidity and mortality, especially in cases where they lead to pneumonia. A diverse array of viruses and bacteria can be associated with community-acquired pneumonia (CAP); however no pathogen is identified in 15-25% of pediatric CAP even when systematic and comprehensive diagnostic testing is conducted. Therefore, further discovery of pathogens among otherwise negative CAP cases enhances the understanding of CAP epidemiology and etiology. **Methods:** As 1 of 3 sites participating in the CDC Etiology of Pneumonia in the Community (EPIC) study, children <18 years old with clinical and radiographic CAP admitted to Primary Children's Hospital (Salt Lake City, UT) were enrolled; pediatric controls who were undergoing elective outpatient surgery and had no fever or respiratory symptoms were also enrolled. We randomly choose a subset of children <5 years old with no known viral or bacterial pathogen detected for further testing of NP/OP swabs using a pan viral family/genus conventional PCR assay for broad yet sensitive detection of viruses across numerous viral families . In parallel, total RNA was also subjected to metagenomics and viral sequences identified with a custom data analysis pipeline. **Results:** We selected a total of 236 NP/OP swabs for this study. A subset of 20 swabs was first selected as a pilot study. They included 13 from children with CAP with no pathogen detected, 2 from children with CAP with hMPV detected (blinded to investigators), and 5 controls. Of the 15 CAP NP/OP swabs, 2 were positive for hMPV, 2 for human bocavirus (HBoV) and anellovirus, 1 for EBV and HBoV, 1 for PIV4 and anellovirus, 1 for HBoV and 2 for anellovirus. Of the 5 asymptomatic controls, 3 were positive for anellovirus. **Conclusions:** We detected viral pathogens using two broad pathogen discovery approaches in 7 out of 13 of NP/OP swabs among children with CAP with no pathogen previously detected. Anellovirus and HBoV were most commonly detected. Their role in human disease remains undefined. Additional samples have been tested and results will be presented. With a broad diagnostic viral assay, we were able to identify viral agents for a proportion of children with CAP for which there was no previous pathogen identified. Further analysis on a larger sample set is underway.

Human Adenovirus Infections Associated with Severe Respiratory Disease, Oregon, 2013-2014

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Background: Human adenoviruses (HAdVs) cause a range of clinical symptoms and are associated with sporadic infections and outbreaks. HAdV-7 is associated with severe respiratory illness and death, but has rarely been identified among HAdV submissions to CDC in the last 10 years. Although HAdVs are not reportable in Oregon, clinician reports

of increased HAdV detections in 2014 prompted the Oregon Public Health Division (OPHD) to implement active laboratory surveillance for HAdV to better understand the epidemiology of these infections. **Methods:** OPHD contacted Oregon's major hospital systems to determine whether they conducted testing for HAdVs and, if so, to ascertain demographic and clinical information for HAdV+ respiratory cases and collect available HAdV+ specimens for typing at CDC. CDC typed HAdV+ specimens either by polymerase chain reaction (PCR) and sequencing of HAdV hexon gene or by HAdV type-specific real-time PCR assays. We described demographic and clinical characteristics of the cases and used X^2 tests to examine associations between age, type, and disease severity [defined as admission to the intensive care unit (ICU)]. **Results:** We identified 198 HAdV+ infections in Oregon with onsets between October 9, 2013 and July 7, 2014. Cases ranged in age from 3 weeks to 80 years (median 8 years) and were 60% male. Among 136 (69%) hospitalized cases, 58% received supplemental oxygen, 31% were admitted to the ICU, and 18% required ventilation. Five cases (4%) died. Viral co-infections were reported in 11% of hospitalized cases. Of 109 HAdV+ specimens typed at CDC, the most common types identified were HAdV-7 (64, 59%), HAdV-2 (14, 13%), HAdV-21 (10, 9%), HAdV-1 (10, 9%), and HAdV-3 (6, 6%). Among 85 hospitalized cases with type results, adults ≥18 years were more likely to be HAdV-7+ than children (82% vs. 44%, p<0.01), and HAdV-7 cases were more likely to be admitted to the ICU (46% vs. 23%, p=0.03). Of those HAdV-7 cases admitted to the ICU, 80% (20) were adults and 20% (5) were children. **Conclusions:** We identified severe respiratory disease associated with HAdV-7 infections in Oregon primarily in adults. Without national HAdV surveillance we do not know whether HAdV-7 is circulating elsewhere in the US; physicians are advised to keep HAdVs in their differential diagnosis for patients presenting with severe pneumonia.

Enhanced Transmission of *Streptococcus pneumoniae* Serotype 5 Among Unaccompanied Children with Severe Respiratory Infections

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Background: In 2014, over 60,000 unaccompanied children (UC) from Central America crossed the US-Mexico border, prompting the opening of temporary shelters. After apprehension, UC often transit through border patrol processing centers and remain in shelters until placed with sponsors. In June-July 2014, 16 UC aged 13-17 years in four shelters and one processing center (center A) located in four US states were hospitalized with acute respiratory illness. Six had *S. pneumoniae* serotype 5 infection, which rarely causes disease among US adolescents and infrequently colonizes the nasopharynx (NP). A multistate investigation evaluated pneumococcal transmission and disease among UC. **Methods:** Medical charts were abstracted for all hospitalized UC. NP swabs were collected from all assenting UC at two shelters and a sample of UC at two other shelters during July 2014. *S. pneumoniae* was identified by optochin susceptibility and bile solubility. Travel histories were collected from facility records. Available pneumococcal blood isolates and a sample from NP swabs were characterized by serotyping (Quellung), multi-locus sequence typing (MLST), and whole-genome sequencing (WGS). **Results:** Among 16 UC hospitalized for respiratory infections, 14 had blood cultures and six were positive for *S. pneumoniae* (43%). All pneumococcal blood isolates were characterized as serotype 5 MLST Colombia[5] ST289. Among 991 UC (aged 9-18 years) approached, 812 (82%) assented to NP swab collection and 774 (78%) had adequate culture growth. Of these, 181 (23%) yielded pneumococcus; 68 (38%) were serotype 5. UC with serotype 5 carriage were from El Salvador (41%), Guatemala (28%), and Honduras (28%). UC who transferred through center A had higher odds of serotype 5 colonization (OR 5.1; 95% CI: 2.6-9.8). WGS identified two clusters based on key differences in the *folA* gene. **Conclusions:** An outbreak of severe serotype 5 pneumococcal disease occurred among UC entering the US in summer 2014. UC experienced high prevalence of carriage, suggesting increased transmission. WGS data suggest the outbreak had multiple sources. Future efforts to prevent outbreaks will require use of pneumococcal conjugate vaccines—both in countries of origin and among unvaccinated UC entering the US—and infection control efforts in processing centers and shelters.

Synthesizing Data and Models for the Spread of MERS-CoV, 2013: Key Role of Index Cases and Hospital Transmission

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Background: The outbreak of Middle East respiratory syndrome coronavirus (MERS-CoV) has caused 209 deaths and 699 laboratory-confirmed cases in the Arabian Peninsula as of June 11, 2014. Preparedness efforts are hampered by considerable uncertainty about the nature and intensity of human-to-human transmission, with previous reproduction number estimates ranging from 0.4 to 1.5. **Methods:** Here we synthesize epidemiological data and transmission models for the MERS-CoV outbreak during April-October 2013 to resolve uncertainties in epidemic risk, while considering the impact of observation bias. We match the progression of MERS-CoV cases in 2013 to a dynamic transmission model that incorporates community and hospital compartments, and distinguishes transmission by zoonotic (index) cases and secondary cases. **Results:** When observation bias is assumed to account for the fact that all reported zoonotic cases are severe, but only ~57% of secondary cases are symptomatic, the average reproduction number of MERS-CoV is estimated to be 0.45 (95% CI:0.29-0.61). Alternatively, if these epidemiological observations are taken at face value, index cases are estimated to transmit substantially more effectively than secondary cases, (Ri = 0.84 (0.58-1.20) vs Rs = 0.36 (0.24-0.51)). In both scenarios the relative contribution of hospital-based transmission is over four times higher than that of community transmission, indicating that disease control should be focused on hospitalized patients. **Conclusions:** Adjusting previously published estimates for observation bias confirms a strong support for the average R < 1 in the first stage of the outbreak in 2013 and thus, transmissibility of secondary cases of MERS-CoV remained well below the epidemic threshold. More information on the observation process is needed to clarify whether MERS-CoV is intrinsically weakly transmissible between people or whether existing control measures have contributed meaningfully to reducing the transmissibility of secondary cases. Our results could help evaluate the progression of MERS-CoV in recent months in response to changes in disease surveillance, control interventions, or viral adaptation.

N3. Advances in Microbial Detection and Characterization

Wednesday, August 26, 3:30 PM - 5:00 PM
Centennial Ballroom II

Quality Laboratory Systems in an Era of Emerging Technologies and Infectious Disease Threats

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Background: As part of the public health system, it is imperative that public health laboratories (PHLs) lead the way in implementing new technologies while considering biosafety and other quality implications. The use of Matrix Assisted Laser Desorption Ionization Time-of-Flight (MALDI-TOF) in both PHLs and clinical labs has initiated discussions about biosafety of these new technologies. Emerging threats such as Ebola lead to the deployment of the Department of Defense Ebola Zaire real-time polymerase chain reaction assay through the Laboratory Response Network for Biological Threats Preparedness (LRN-B). Deployment of this assay and others is only the first step in providing capability for laboratories; proper biosafety measures must be established as well. This session will describe a safety evaluation of the MALDI-TOF platform, the implementation of an assay for Ebola in PHLs and the necessary communication tools to link clinical and PHLs to ensure a robust public health system capable of responding to emerging threats. **Methods:** The Association of Public Health Laboratories (APHL) led a MALDI-TOF safety study to determine if the established standard operating procedures (SOPs) inactivated organisms during sample processing. Since clinical labs are also using this technology, data from this comprehensive study will be used to provide guidance to sentinel lab. APHL also developed a comprehensive risk assessment template to be used to assess risk for the implementation of the Department of Defense Ebola-Zaire assay. The Minnesota Laboratory System (MLS), established in 2000, is a robust network of sentinel labs and is the cornerstone of our outreach and communication to sentinel labs in Minnesota. **Results:** The data collected on the safety of sample processing by MALDI-TOF suggested that current SOPs don't render samples inactive. The risk assessment developed by APHL was utilized across the country to establish local procedures for handling potential Ebola samples. The MLS provided the infrastructure to rapidly provide guidance to MLS labs. **Conclusion:** Importance of quality laboratory systems continues to become increasingly more important as technologies advance and public health threats evolve.

Simultaneous Detection and Identification of Thirty-one Enteric Bacteria, Viruses and Parasites Associated with Gastroenteritis Using PCR Assay: Five Real-time Multiplex Reactions and Its Clinical Application

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Background: Enteric infectious disease is a major concern of public health problem worldwide. Rapid and accurate detection methods play an essential role in acute diarrhea and foodborne disease outbreaks response and patients management. **Methods:** We developed modified molecular beacons based multiplex real-time PCR(rt-PCR) assay and multiplex ligation dependent reaction based probe melting curves assay (MLMA) for the simultaneous detection of 31 enteric pathogens including 22 pathogenic bacteria, five enteric viruses and four parasites in five reactions. The specificity of the target genes selected was confirmed by detecting 986 intestinal pathogenic strains. Then detection limits of the assay were tested. Lastly, the assay was applied to detect clinical samples for evaluating the specificity and sensitivity by comparing with the conventional PCR or traditional culture methods. **Results:** Cross-reactivity of the assay was not observed. For reaction - one and two, detection limits of the assay were 10 copies/μL for each virus or parasite. Amplification efficiency ranged from 87.6% to 99.2% with strong correlation coefficients ($r^2 \geq 0.98$). The assay was applied to detect five viruses in 812 stool samples. Compared with monoplex real time PCR, the multiplex rt-PCR showed more than 75% sensitivity and 99% specificity for each virus, and the kappa correlation for detection of all viruses ranged from 0.85 to 1.00. For reaction - three, detection limits of the assay were 10^3 CFU/ml for each bacterium. For reaction- four and five, detection limits ranged from 1.36×10^6CFU/mL to 1.5×10^8CFU/mL for each diarrheagenic *E.coli* or each *vibrio*. To further validate the developed assay, 136 stool samples were detected using multiplex rt-PCR and MLMA assay with the PCR and traditional culture methods as control. A total of 62 samples were tested positive for virus (n=37) or/and bacteria (n=33), and no parasites was observed. The result of the developed assay is consistent with the conventional method. **Conclusions:** Compared to the existing methods, the multiplex rt-PCR and MLMA assays were simple, fast, highthrought and more cost effective, while exhibiting high sensitivity and specificity. It is capable of meeting the pressing needs for both laboratory and clinical detection of multiple pathogens.

Next Generation Molecular Epidemiology for Pathogenic Fungal Outbreaks

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Background: Fungi present a number of problems for molecular epidemiology due to their reproductive, morphologic, ecologic, and genomic complexities. While current methods of genotyping can infer genetic relationships among isolates, they provide limited empirical estimates of genetic relatedness among strains. Here we describe investigations of outbreaks of *Coccidioides immitis, Cryptococcus gattii, Apophysomyces sp., Exserohilum rostratum* and *Sarocladium kiliense* using advanced, increasingly accessible, and highly sensitive whole genome sequence (WGS) analyses. **Methods:** Isolates from health-care associated outbreaks of *C. immitis* (n=9), *E. rostratum* (n=35), and *S. kiliense* (n=45), and environment-associated outbreaks of *C. immitis* (n=11), *C. gattii* (n=115) and *Apophysomyces* (n=23) were collected by CDC, local public health officials and other partners for WGS-based analyses to support ongoing investigations. Multiple WGS platforms and bioinformatic tools were employed. **Results:** In each case, WGS-based analysis was able to confirm outbreak sources and/or elucidate the population structure of the fungal etiologies. The investigation results include: a) a suspected cluster of transplant-associated *C. immitis* infections was confirmed; b) a nationwide outbreak of fungal meningitis from an injectable steroid was shown to be caused by a single clone of *E. rostratum*; c) an outbreak of mycoses in pediatric cancer patients was confirmed to be caused by a single source of *S. kiliense*; d) *C. immitis* infection in non-endemic Washington was proven to be autochthonous; e) *C. gattii* in the Pacific Northwest was shown to have emerged multiple times, likely from South America; and f) a never

before seen outbreak of *Apophysomyces* was due to exposures to multiple distinct local populations of the fungus following the 2011 Joplin MO tornado. **Conclusions:** The next generation of molecular epidemiology of fungal diseases must include WGS analyses. The rapid employment of WGS enables highly informed investigations of fungal outbreaks without previous knowledge of the pathogen's genome or population structure. Additionally, the continued use of WGS in epidemiology allows for the creation of a public archive of sequence data to be used in future investigations, further improving overall public health response.

Advanced Molecular Detection of Waterborne and Zoonotic Pathogen *Cryptosporidium*

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Background: Genotyping and subtyping tools are frequently used in molecular epidemiologic studies of *Cryptosporidium hominis* and *C. parvum.* The recent development in next generation sequencing techniques has facilitated advanced molecular detection of *Cryptosporidium* spp. **Methods:** We developed procedures for the isolation and enrichment of *Cryptosporidium* genomic DNA from fecal specimens, using a combination of oocyst purification and whole genome amplification. Using this strategy and next generation sequencing, we sequenced the genome of various *Cryptosporidium* species. The sequences obtained were used in development of typing tools for emerging Zoonotic *Cryptosporidium* spp. and comparative genomic analysis of species and isolates with various host ranges and virulence. **Results:** The genomes of >30 isolates of six *Cryptosporidium* species were sequenced, generating sequence data covering 94.5-99.7% genomes. This led to the development of subtyping tools for emerging human pathogens *C. ubiquitum* and chipmunk genotype I and assessment of the role of various animals in transmission of these species in humans. Comparative genomic analyses have identified significant differences among species in copy numbers of several telomeric gene families such as the MEDLE family of secreted proteins and insulinase-like proteases, suggesting that gene duplications could be responsible for host expansion in some zoonotic species such as *C. parvum*. The comparative genomics also demonstrated the occurrence of genetic recombination in virulent *C. hominis* subtypes in the United States. **Conclusions:** Advanced molecular tools have been developed for genetic characterizations of emerging zoonotic *Cryptosporidium* spp. and identification of genetic determinants for the emergence and dispersal of virulent *C. hominis* subtypes in the United States. Efforts are needed to develop a user-friendly bioinformatic pipeline for analyzing sequence data and guidelines on interpretations of pathogen variants in the context of surveillance andepidemiologic data, and adopt whole genome sequencing in molecular surveillance and outbreak investigations of cryptosporidiosis.

Employing Short Read Pneumococcal Whole Genome Sequence Data for Routine Extraction of Invasive Strain Parameters and for Fine Resolution of a Disease Cluster

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Background: Whole genome sequencing (WGS) may provide more efficient bacterial characterization than performing conventional assays, but how well results correlate is unknown for pneumococci. We performed conventional lab testing and concurrent WGS analysis for invasive pneumococcal disease (IPD) isolates. We compared data from the two approaches to determine if results were similar. We also employed WGS-based approaches for resolution and characterization of pneumococcal isolates from a disease cluster. **Methods:** For approximate 1500 diverse IPD isolates, including 700 national IPD surveillance isolates from children aged <5 years recovered during 2008-2013 from CDC's Active Bacterial Core surveillance, we used automated algorithms to predict capsular serotypes, antimicrobial susceptibility testing (AST) values, pilus types, and multilocus sequence types (MLSTs) from short read Illumina MiSeq WGS data. We employed deeper analysis on 37 serotype 5 isolates from carriage nd IPD associated with a disease cluster. Quellung serotyping and broth dilution AST was performed on all isolates. **Results:** For nearly all isolates, one of 47 different serotypes and an AST profile for 18 antimicrobials were accurately predicted by the automated WGS analysis. Several serotype switch events were identified through automated WGS, where routine pipeline features often revealed both recipients and donors in these switch events. Adhesion determinants had strong clonal associations. Deeper analysis of the serotype 5 disease cluster-associated isolates revealed two independent but closely related substrains, one of which had undergone a mutational antibiotic resistance-conferring event involving interspecies recombination. **Conclusions:** We now know that WGS-based analysis is effective and economical for capturing key IPD isolate information that is critical for routine surveillance and specialized resolution of IPD clusters. This first version of WGS-based typing yielded more strain information than what we obtain using standard testing approaches, and this expanded analysis costs less to perform. WGS-based surveillance will become even more useful as we extract additional strain features.

Rapid Identification of Mycobacteria from Paraffin-embedded Pulmonary and Extrapulmonary Tissue Biopsies of Patients by Multigene Targeted PCR and Sequencing: Implications for Diagnostic Pathology

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Background: Early detection and differentiation of *Mycobacterium tuberculosis*-complex (MTBC) spp. from nontuberculous mycobacteria (NTM) is critical for patient management and appropriate public health response. However, diagnosis of mycobacteriosis is challenging due to diverse clinical presentations and fastidious culture identification that requires several weeks. Also, culture is frequently negative for small tissue biopsies due to inadequate bacterial load. Furthermore, because of clinical similarities with non-infectious conditions, specimens are often not processed for culture and formalin-fixed, paraffin-embedded (FFPE) tissues are the only specimens available. Acid-fast bacilli (AFB) stains and immunohistochemistry (IHC) can be performed on FFPE tissue, but cannot identify species. Sensitive and specific molecular assays are needed for identification of *Mycobacterium* spp. in FFPE tissues. **Methods:** DNA was extracted from FFPE tissue biopsies of 310 patients with clinical and histopathological suspicion of mycobacterial infection (received from 2013 to 2015) and evaluated by multistage *Mycobacterium*-genus, complexes-and species-specific PCR assays targeting *16S rRNA, hsp65*, *IS6110* and *rpoB* genes, and amplicon sequencing. Tissues were also examined by AFB stains and mycobacteria IHC. **Results:** A *Mycobacterium* species was detected in 151 (49%) cases by PCR analysis. Of these, 130 (86%) were positive by IHC and 70 (46%) were AFB-positive. A MTBC spp. was identified in 38% (58/151) of cases while NTM was identified in 62% (93/151), including: *M. avium* complex (n=27), *M. marinum* group (n=23), *M. kansasii*

(n=7), *M. haemophilum* and *M. chelonae-abscessus* group (n=6, each), *M. leprae* (n=3), *M. genavense* (n=2). Mycobacteria were detected in various pulmonary and extrapulmonary tissues from patients with diverse disease presentations, including granulomatous pneumonia, lymphadenitis, and dermatitis. **Conclusions:** FFPE tissue analysis by multigene targeted PCR assays greatly expands diagnostic opportunities, allows differentiation of MTBC from NTM, and provides rapid identification of *Mycobacterium* species that can aid in the selection of appropriate antimicrobial therapy. Combination of histopathological and molecular analysis improves accuracy of identification.

N4. Surveillance II

Wednesday, August 26, 3:30 PM - 5:00 PM
International Ballroom South

The EpiCore Project: Improving Non-traditional Outbreak Detection Through Collaboration with Field Epidemiology Training Programs (FETPs)

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Background: Innovative surveillance of non-traditional sources (e.g., news and Internet media, field reports) can cost-effectively inform quick responses to emerging disease outbreaks. The EpiCore project seeks to address the unmet need for field-based validation of these sources by creating a cadre of FETP epidemiologists trained to detect outbreaks faster. **Methods:** The EpiCore project brings together experts from HealthMap, ProMED, the Skoll Global Threats Fund, and TEPHINET to: *Train*: Pilot in-person training was developed by ProMED and conducted at TEPHINET regional conferences in Asia, Africa, the Middle East, and Latin America. *Connect*: The EpiCore platform, developed by HealthMap, supports information exchange from trained field epidemiologists in the vicinity of a possible outbreak. *Mentor*: FETP trainees receive a mentor (initially, an experienced ProMED moderator) based on shared scientific interests, language, and learning styles. *Fund*: Competitive funding supports FETP resident and graduate development of innovative surveillance tools, use of non-traditional sources, and national-level analysis of time to detect disease. **Results:** *Training:* 104 people attended the regional workshops and provided feedback through surveys, interviews, and focus groups. Given the global FETP audience, an online module was deemed the best training mechanism. *Connecting*: ProMED moderators develop and direct requests for information to trained individuals in the EpiCore platform who may know of the situation or able obtain the needed information rapidly. *Mentoring*: Mentors receive formal training and will meet virtually with mentees regularly to establish a long-term working relationship, assist in use of the EpiCore system, and foster trust and transparency. *Mini-grants*: Five awards to date: Pakistani FETP - study on outbreak detection through astute observer report; four national-level baseline analyses of time to disease detection (Kenya, Pakistan, Taiwan, and Zimbabwe). Initial findings anticipated November 2014. **Conclusion:** The EpiCore project's training and online platform will create a cadre of trained field epidemiologists to validate reports of potential outbreaks from non-traditional sources, complimenting traditional surveillance, and contributing to finding outbreaks faster.

Identification of Potential Source Cases for Young Children with Tuberculosis Infection—New York City, 2006-2012

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Background: Young children with tuberculosis infection (TBI) are indicative of recent TB transmission. Young children are also at increased risk for rapid progression to TB disease. Consequently, the New York City (NYC) Health Code mandates the reporting of any child <5 years who has TB, is suspected of disease, is a contact to an infectious TB case or has a positive TBI test to the NYC Bureau of TB Control (BTBC). We reviewed these surveillance reports to assess whether more active follow-up is needed to prevent and control TB among this vulnerable population. **Methods:** All children <5 years who were reported to BTBC between 2006-2012 were abstracted from the TB Registry to identify those with TBI. Potential source cases were identified for children; these were defined as any infectious TB case diagnosed in the two years before a child was reported and whose residence was within 0.5 miles of the child. Neighborhood risk factors for TB transmission were examined among children with a source case identified. **Results:** Among 3511 children reported to BTBC from 2006-2012, 1795 (51%) had TBI. The number of children with TBI reported decreased from 396 in 2006 to 133 in 2012. Children with TBI were 2.4 years of age on average, and most were female (53%) and US-born (64%). The majority of children initiated TBI treatment (86%), and among these, 743 (48%) completed treatment. A potential source case was identified for 1461 (91%) of the 1604 children who had a valid address and were not a contact to a TB case; 26 children lived in the same building as a TB case (2%), 1256 children matched to a case diagnosed <6 months before their report (86%), and 484 had >10 cases within 0.5 miles (33%). Children with a potential source case tended to live in neighborhoods with high TB incidence (61%) and ≥25,000 persons per square mile (79%). **Conclusions:** The high proportion of children with TBI born in the US and the young average age imply that undetected TB transmission may be occurring in NYC. This notion is also strongly supported by the 26 children who lived in the same building as a TB case. Transmission may be associated with residence in areas with exposure risk factors such as high TB incidence and population density. Therefore, monitoring reports of TBI in young children could be used as a method for BTBC to identify transmission and prevent future disease.

Analysis of Surveillance Data: Trends of Priority Health Problems in Afghanistan from 2007 to 2012

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Background: The Afghanistan National Public Health Institute's Disease Early Warning System (DEWS) was established in 2006 to provide sentinel-based surveillance of diseases. DEWS conducts daily and weekly reporting and outbreak investigations and is a National Focal Point for International Health Regulations (IHR2005). Since 2007 sentinel sites have expanded from 8 provinces to cover all 34 provinces. In 2012 there were 330 sites. This study aimed to analyze six years of data to better understand patterns of morbidity and mortality in Afghanistan. **Methods:** Data was collected daily and weekly in addition to outbreak-specific reporting on priority diseases including acute respiratory infections (ARI), diarrheal diseases and vaccine-prevented diseases. All data was synthesized into graphs and maps using MS Access, Excel and GIS tables. **Results:** From 2007 to 2012 more than 300 integrated weekly

and 1500 outbreak reports were analyzed and shared with stakeholders. 30% of consultations at sentinel sites were for priority diseases: 20% of consultations were for ARI, 10% were for acute diarrheal diseases. The top killers were pneumonia, meningitis, and diarrheal diseases but the case fatality rates were higher for meningitis, tetanus and hemorrhagic fevers. Malaria, typhoid fever and meningitis/severely ill children (SIC) were also a problem but were not as frequently recorded at sentinel sites. **Conclusions:** Surveillance data has the potential to inform national health policy if wisely used by program managers and stakeholders. Since the establishment of DEWS, Afghanistan has had a better understanding of what diseases cause morbidity and mortality. To better analyze these patterns in the future, surveillance of communicable diseases should be integrated with surveillance of non-communicable diseases, as well as surveillance of chemical and environmental hazards. Improved coordination between stakeholders and continuous enhancement of the culture of evidenced-based decision making are key strategic goals of DEWS.

Results from the Centers for Disease Control and Prevention's "Predict the 2013-2014 Influenza Season Challenge," United States

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Background: Early insights into the timing of the start, the peak, and the intensity of the influenza season could be useful in planning influenza prevention and control activities, but incorporation of forecasts into public health decision making requires a quantification of the accuracy of different forecasting approaches. In response, the Centers for Disease Control and Prevention organized a challenge to predict the 2013-14 influenza season in the United States. **Methods:** Challenge contestants were asked to forecast the start, the peak, and the duration of the 2013-2014 influenza season at the national level and at any or all Health and Human Services (HHS) region level(s). The challenge period ran from December 1, 2013-March 27, 2014, and contestants were required to submit a total of 9 biweekly forecasts at the national level to be eligible for judging. The selection of the winner for this challenge was based on an evaluation of the methodology used to make the prediction and the accuracy of the prediction. **Results:** Sixteen individuals or teams initially registered for the challenge, 15 entered at least one prediction, and 9 teams submitted 13 forecasts for all required milestones. The submission of the first contestant forecast occurred on December 2, 2013; 3/13 (23%) forecasts received correctly predicted the start of the influenza season within one week, 1/13 (7.7%) forecasts predicted the peak within 1 week, 3/13 (23%) predicted the peak ILINet percentage within 1%, and 4/13 (31%) predicted the season duration within 1 week. By the next prediction made on December 19, 2013, the competitors adjusted their models based on updated data and the number of forecasts that correctly forecasted the peak week increased to 2/13 (15%), the peak percentage to 6/13 (46%), and the duration of the season to 6/13 (46%). As the season progressed, the forecasts for peak week, peak percentage, and peak duration for the United States became more stable and reflected the season milestones. **Conclusion:** Further work is required before the results of influenza forecasting can be widely used by policy makers to inform the selection and implementation of prevention and control measures. CDC and Challenge participants plan to build upon the methods developed during this contest to improve the accuracy and lead time of influenza forecasts.

Integrated Food Safety Centers of Excellence (CoEs): Strengthening State and Local Capacity for Foodborne Illness Surveillance and Outbreak Response

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Background: As required by the Food Safety Modernization Act (FSMA), CDC designated five CoEs (Colorado, Florida, Minnesota, Oregon and Tennessee) through a competitive grant process in August 2012. CoEs, located at state health departments in partnership with an academic center, serve as resources for other local, state, and federal public health professionals to respond to outbreaks of foodborne illness. **Methods:** CoE activities included in FSMA: Collaboration with frontline public health professionals to strengthen routine foodborne illness surveillance and outbreak investigations Evaluation and analysis of the timeliness and effectiveness of foodborne illness surveillance and outbreak response Training local and state public health personnel in epidemiological and environmental investigation of foodborne illness, including timeliness, coordination, and standardization of the investigation process Establishment of fellowships, stipends and scholarships to train future food safety leaders in foodborne disease surveillance and outbreak investigation and to address critical workforce shortages Strengthening capacity to participate in foodborne illness surveillance and environmental assessment information systems Conducting program evaluation and outreach activities focused on increasing prevention, communication, and education regarding food safety **Results:** CoEs have begun work under several of the FSMA activity areas. Through their unique health department/academic institution partnerships, CoEs provide technical assistance, online and in-person training, and various tools to other local, state, and federal public health professionals to improve capacity for foodborne illness surveillance and outbreak response. Examples of these will be presented. **Conclusion:** In 2012, CDC responded to Congress's mandate to designate five CoEs. Since their establishment, CoEs have begun to address the required activities. Many products developed by the CoEs are available online for immediate use by other local, state, and federal public health professionals. Additionally, CoEs are available for support and guidance for those looking to improve their foodborne illness surveillance and response capacity.

The Global Landscape of Participatory Disease Surveillance

A. W. Crawley, **M. S. Smolinski**, J. M. Olsen, A. DeBelloy; Skoll Global Threats Fund, San Francisco, CA, USA

Background: Digital, participatory disease surveillance systems have been implemented in several countries throughout the world. This approach to crowdsourcing disease detection has shown promise for both routine and mass-gathering scenarios and can supplement traditional surveillance systems such as provider reporting and laboratory data. Following similar approaches to participatory systems

in Europe and Australia, the Skoll Global Threats Fund has supported the development of *Flu Near You* in North America, *Salud Boricua* in Puerto Rico, *SickSense* in Thailand, and *Saude na Copa* in Brazil. **Methods:** While each system is unique in its design, all participatory systems offer digital mechanisms through which volunteers can report symptoms on a daily or weekly basis. These data can be analyzed for clusters meeting certain syndrome profiles in time and space. This approach also allows for messaging to an engaged audience for health promotion and, potentially, emergency communications. Partnerships between government, NGOs, academia and technology groups have been vital to the success of each project. **Results:** *Flu Near You* has registered over 140,000 participants and received upwards of 1.3 million weekly reports since its launch in 2011. As of February 2015, nearly 18,000 users had submitted a total of over 81,000 reports to the *SickSense* system in Thailand during the first five months of operation. *Saude na Copa*, designed for mass gathering surveillance during the 2014 World Cup in Brazil, engaged over 4,700 active users and obtained over 47,000 symptom reports. Analyses to compare the syndromic reporting from these systems with established surveillance sources are ongoing. **Conclusions:** Participatory surveillance systems offer a low-cost, scalable method for supplementing existing surveillance systems while engaging the public in this vital activity. This presentation will discuss the latest data from each system and explore the opportunities and challenges presented by this approach.

N5. Foodborne Diseases II

Wednesday, August 26, 3:30 PM - 5:00 PM

Centennial Ballroom III

Emergence of *Salmonella* Typhimurium in Australia, 2000-2013

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Background: Internationally, salmonellosis is a leading cause of foodborne gastroenteritis. In Australia, the most common serotype is *Salmonella* Typhimurium, which has dramatically increased as a cause of outbreaks in recent years. We analyzed *S.* Typhimurium notifications to quantify the increase and determine trends in age and sex. **Methods:** We analyzed national notification data for 2000-2013 in a negative binomial regression model to estimate an incidence rate ratio (IRR) for the trend in *S.* Typhimurium, adjusted for age and sex. We excluded all *Salmonella* cases where no serotype, age, or gender was listed. Australian Bureau of Statistics population numbers by age and sex were used to standardise the incidence rates to the population. **Results:** There were 53,148 notifications of S. Typhimurium during this surveillance period, representing 43% of all *Salmonella* notifications. The proportion of notifications that were S. Typhimurium ranged from 38% in 2004 to 49% in 2011 and from 10% to 63% across Australia's eight states and territories. There was an increasing trend of *S.* Typhimurium notifications (IRR 1.06; 95%CI 1.06-1.06). This corresponds to a 211% increase in the rate of *S.* Typhimurium notifications in 2013 compared to 2000. During this period, there was a slightly lower incidence of *S.* Typhimurium notifications in males than in females (IRR 0.93; 95%CI 0.90-0.96) and the highest incidence rate was in children aged 12-23 months old (IRR of 1.30; 95%CI 1.17-1.44) compared to children 0-11 months. **Conclusions:** In Australia, *S.* Typhimurium is the dominant serovar and we observed significant increases in notifications during the period of surveillance. This is consistent with an increase in *S.* Typhimurium outbreaks associated with eggs from 2000 to 2011. As *S.* Typhimurium is such an important serotype in Australia, it is essential to have good subtyping for outbreak detection. However, recent shifts from phenotypic to genotypic testing of *Salmonella* has made surveillance complex and necessitates routine national trend analysis.

Traceback and Intensified *Salmonella* Testing Approach—a Regional Investigation of Multidrug Resistant *Salmonella* Heidelberg Illnesses Associated with Consumption of Company A Brand Chicken

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Background: A recent study estimated the cost of *Salmonella* illnesses associated with poultry at $693 million per year; the 2012 Food Safety and Inspection Service (FSIS) chicken parts baseline study estimated the prevalence of *Salmonella* in raw chicken parts at 26.3%. **Methods:** In June 2013, the Centers for Disease Control and Prevention (CDC) notified FSIS of a cluster of *Salmonella* Heidelberg illnesses with a single, rare Pulsed-field Gel Electrophoresis (PFGE) pattern. The PFGE cluster included 18 case-patients in CA, AZ, NV, and WA, as well as *Salmonella* isolated from a retail sample of Company A brand chicken collected through the National Antimicrobial Resistance Monitoring System. In mid-July, based on the geographic distribution of illnesses and high frequency of exposure to Company A brand chicken among case-patients, CDC added four *Salmonella* Heidelberg PFGE patterns to the case definition. The California Department of Public Health began gathering shopper card numbers from case-patients and requested that FSIS obtain details on the food purchases and perform traceback to the source establishments. In early August, a probability-based approach was applied to retail chain shopper history chicken purchases to determine which companies, establishments, and products to target for intensified sampling. On September 3, CDC added two more *Salmonella* Heidelberg PFGE patterns to the case definition. On September 9, intensified sampling began at four Company A establishments in California and Washington. When *Salmonella* was identified, FSIS analyses included serotyping, PFGE, and antimicrobial susceptibility testing. **Results:** A high percentage of case-patients recalled consumption of Company A chicken in the week prior to illness onset, with multiple establishments and production dates linked to this company. The multi-establishment intensified testing approach documented six of the seven outbreak patterns of *Salmonella* Heidelberg in four Company A slaughter and processing establishments. **Conclusions:** Shopper histories were a key element in designing a probability-based sampling protocol. As part of the strategy to stop the outbreak and prevent future illnesses, Company A was able to lower the frequency of isolation of *Salmonella* from raw chicken parts to 5%.

Giardiasis and Subsequent Irritable Bowel Syndrome: A Longitudinal Study Using Health Insurance Billing Data

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Background: *Giardia intestinalis* is the most commonly reported human intestinal parasite in the United States with approximately 20,000 cases reported per year. Post-infectious irritable bowel syndrome (IBS) has been documented for bacterial diarrheal illnesses. While giardiasis is generally self-limited in healthy individuals, increased incidence of chronic gastrointestinal complaints has been reported after some outbreaks. Here,

we assess the longitudinal relationship between giardiasis diagnosis and IBS diagnosis using a large health insurance database. **Methods:** We used the 2006-2010 Marketscan insurance database, which allows longitudinal observation of insured persons. Persons with at least one giardiasis diagnosis (ICD-9-CM code 007.1) were individually matched on age group, sex, and enrollment length in months to five persons without a giardiasis diagnosis. Persons diagnosed with the primary outcome of IBS (ICD-9-CM 564.1) prior to the index date (date of giardiasis diagnosis or date of study entry for matched controls) were excluded. We calculated one-year incidence rates (IR) and developed stratified Cox models to examine the association between giardia diagnosis and IBS diagnosis. **Results:** The matched cohort included 4,899 persons with a giardiasis diagnosis and 24,488 persons without a giardiasis diagnosis. Persons with giardiasis had higher pre-diagnosis healthcare utilization and a higher prevalence of anxiety, depression, and smoking than persons without giardiasis. One-year incidence of IBS was higher in persons with giardiasis than in persons without giardiasis (IR = 37.1/1,000 person-years vs. 4.4/1,000 person-years). The unadjusted hazard ratio was 6.6 (95% confidence interval [CI] 5.3-8.2); this was attenuated slightly after adjusting for anxiety, depression, and healthcare utilization, to 5.7 (95% CI 4.5-7.1). **Conclusion:** In a large insurance database, individuals diagnosed with giardiasis were more likely than those without giardiasis to have a subsequent IBS diagnosis. These findings are consistent with reports from outbreak follow-up studies using self-reported symptom data. Longitudinal analysis of billing data includes sporadic cases and can help address concerns with recall bias when studying chronic sequelae of infections.

A Multi-district *Streptococcus suis* Outbreak Associated with Undercooked Pork Consuming in Chiang Mai Province, Thailand, During July–August 2013

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Background: *Streptococcus suis* causes disease in pig and human and can be found in healthy pig and wild boar. The infection is disease burden in human with symptoms of meningitis, septicemia, loss of hearing and death. The disease situation in Thailand is under-reported regarding to lack of laboratory capacity. In August 2013, excess number of *S. suis* among human cases in Chiang Mai province were reported to Bureau of Epidemiology. The investigation team conducted a study to describe source of infection and potential risk factors. **Methods:** National passive surveillance system, medical records, and laboratory records from four hospitals in Chiang Mai were reviewed. Person-to-person interview with structured questionnaire were implemented to all cases. Matching neighborhood case-control study was performed to identify possible risk factors. Food supply chains including pig slaughterhouses and wet markets that were related to the cases were surveyed to examine the existence of pathogen. **Results:** Morbidity rate of *S. suis* infection in Chiang Mai in 2013 was 1.26 per 100,000 populations. The morbidity rates were three times higher compared to the occurrence in 2012. There were 21 confirmed cases started onset from July to August 2013. A pattern of distribution was sporadic in 10 districts. A case-fatality rate was 9.5% (two deaths) and seven cases have permanent deafness. Median age was 53 years (range 26-85 years). A male-to-female ratio was 2:1. First diagnoses of most cases (86%) were sepsis and meningitis. Consuming undercooked pork was significantly associated with *S. suis* infection (adjusted OR = 31.4, p value < 0.004). Six cases exposed to pigs, which had poor conditions and culled those pigs however this factor was not significant associated with the infection. There were correlated finding of S. *suis* in tonsil specimen collected from slaughterhouse at the same period of the outbreak in human. **Conclusions:** Consuming undercooked pork product especially raw blood-enriched minced pork salad attributed risk to *S.suis* outbreak. Health education should be emphasized and awareness of disease severity should be raised in the community. Collaboration between veterinary sector and public health sector is needed for early detection when any abnormalities at pig farm, slaughterhouse, and market were detected.

Knowledge, Attitude and Practices Regarding Brucellosis Infection Among Smallholder Farming and Pastoral Populations in Kenya, 2012

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Background: Brucellosis is a zoonosis of public health importance worldwide with an annual incidence of more than 500,000 human cases. Knowledge, perceptions, attitude and practices among communities are key in understanding the transmission dynamics and determinants of infection, thereby informing control policies. The aim of the current study was to describe and compare the community knowledge, attitude and practices with regard to brucellosis in households within the small-scale farming as well as pastoral eco-systems. **Methods:** Data on knowledge, attitude and practices (KAP) was obtained through a semi-structured questionnaire surveys administered to household heads involved in a brucellosis prevalence cross-sectional survey in three counties. The survey was done in Kiambu, Kajiado and Marsabit counties between 2012 and 2013. A multistage sampling involving sub-location and households was employed. Households were randomly selected using random geographic coordinates method. **Results:** A total of 1088 household heads were enrolled and interviewed. Majority of the respondents (79.2%) had heard about brucellosis and of these, 91.5% knew brucellosis affects humans but only a third (38.7%) knew that brucellosis affects animals. Two thirds of the households (66.6%) in all the three counties obtained milk for domestic use from their own animals. Only 26.6% of respondents from Marsabit reported that they boil the milk before drinking while most respondents from Kiambu (90.4%) and Kajiado (92.8%) reported doing the same. The proportions of respondents who assisted animals during deliveries were 38.2%, 59.9% and 86.3% for Kiambu, Kajiado and Marsabit respectively. However, most of them (89.1%, 92.2% and 95.3% for Kiambu, Kajiado and Marsabit respectively) did not use gloves at the time of assistance. Most pastoralists (60.8% from Marsabit and 62.9% from Kajiado counties) disposed of the fetal membranes by giving to their dogs. **Conclusions:** Public health education on practices to minimize exposure to brucella infected animals and products including consumption of heat-treated milk, safety precautions following abortions and observance of hygiene and protection during slaughtering of animals and practices to reduce environmental contamination are critical especially among pastoral communities.

A National Outbreak of Shiga-toxin producing *E. Coli* in England, August to September 2014

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Background: Since 1st May 2012, multi-locus variable number tandem repeat analysis (MLVA) has been undertaken on all human isolates of shiga-toxin producing *Escherichia Coli* (STEC) in England. This led to increased recognition of clusters of STEC and reduced apparently sporadic STEC cases from approximately 60% to 40%. Next Generation Sequencing (NGS) has also been used to inform outbreak investigations through; providing phylogenetic context for outbreak strains; insights into strain severity; and clarity where MLVA appears less stable. The increased sensitivity and specificity of molecular techniques have impacted on outbreak investigations, and we find ourselves operating in a new paradigm of outbreak management. We report an outbreak in September 2014 where these molecular techniques were employed. **Methods:** Cases were defined as UK residents with STEC O157 Phage Type (PT)1 *stx2* infection of the MLVA outbreak profile. Exposure data collected via the National Enhanced Surveillance System for STEC database was analysed to identify potential links. Cases were re-interviewed using a hypothesis generation questionnaire, supplemented by menus where available. A complex trace-back investigation was undertaken as was sampling at implicated restaurants and suppliers. Isolates from outbreak cases underwent NGS. **Results:** Twenty confirmed cases were reported with onset dates between 30th August and 13th September 2014. The majority (19/20) were adults with a median age of 35 years. All cases reported bloody diarrhoea, 10 were hospitalised and one developed HUS. Cases shared a history of eating meals at different chain restaurants. Analysis of menu items indicated shared consumption of 'slaw' garnishes. Records showed that the restaurants were supplied with "slaw" vegetables from two producers. Ingredients were sourced from within the UK and elsewhere. STEC was not recovered from sampling of product. **Conclusions:** The severity of disease appeared unusual amongst this adult cohort. Furthermore, in England, these strains are usually detected as *stx* negative or as *stx1+2* in travellers returning from Europe, and are not usually associated with severe disease. Analyses of information from restaurants demonstrated higher levels of exposure to suspect stealth vehicles than food histories taken from cases.

N6. Late Breakers II

Wednesday, August 26, 3:30 PM - 5:00 PM

Centennial Ballroom IV

See page 263.

Late-Breaker Poster and Oral Presentation Abstracts

Late Breakers I (Posters)

Monday, August 24, 12:30 PM - 1:45 PM

Grand Hall

Board LB-1. Empiric Antibiotic Usage in Mild Respiratory Illness Among Outpatients in Bangladesh: National Hospital-based Influenza Surveillance Findings (2007–2014)

M. A. Aleem[1], K. Sturm-Ramirez[2,1], M. A. Islam[1], A. S. M. Alamgir[3], S. Haider[4,5], S. P. Luby[6,1], M. Rahman[4], E. S. Gurley[1], J. D. Heffelfinger[2,1]; [1]Intl. Ctr. for Diarrhoeal Dis. Res., Bangladesh (ICDDR,B), Dhaka, Bangladesh, [2]CDC, Atlanta, GA, USA, [3]World Hlth. Organization (WHO), Dhaka, Bangladesh, [4]Inst. of Epidemiology, Disease Control and Res. (IEDCR), Dhaka, Bangladesh, [5]Hlth. Economics Unit, Ministry of Hlth. and Family Welfare (MOHFW), Dhaka, Bangladesh, [6]Stanford Univ., Stanford, CA, USA

Background: Antibiotic use has the potential to contribute to antibiotic resistance. Empiric prescription rates for mild respiratory illness range from 40-60% in developed countries. We reviewed ICDDR,B-IEDCR's collaborative hospital-based influenza surveillance data collected from May 2007 to August 2014 to assess antibiotic prescriptions for mild respiratory illness. **Methods:** Staff collected clinical data at presentation for outpatients with influenza like illness (ILI) defined by WHO, at 12 sentinel hospitals using a structured questionnaire. We determined prescription rates for mild respiratory illness, defined as absence of signs of severe illness (e.g., difficulty breathing, abnormal breath sounds) and no co-morbidities (e.g., chronic lung or heart conditions) among outpatients with ILI. We performed bivariate analysis followed by stepwise multivariate logistic regression and trend analyses to identify factors associated ($p \leq 0.05$) with prescriptions. **Results:** Antibiotics were prescribed for 80% (4648/5842) of subjects. On bivariate analysis prescriptions were significantly more likely in government vs. non-government hospitals (odds ratio [OR]: 3.1), in urban vs. rural settings (OR: 1.4), among persons with positive influenza test results (OR: 1.3) and during the winter (OR: 1.1). Treatment in government hospitals (adjusted odds ratio [aOR]: 3.1; 95% confidence interval [CI]: 2.8-3.6), influenza infection (aOR: 1.4; CI: 1.2-1.7) and illness in winter (aOR: 1.2; CI: 1.1-1.4) were independently associated with antibiotic prescriptions. During 2010-2014 vs. 2007-2009 and adjusted for age, the likelihood of antibiotic prescription increased for all antibiotics (aOR: 2.0; CI: 1.9-2.4), penicillin (aOR: 2.2; CI: 1.9-2.5) and macrolides (aOR: 2.1; CI: 1.9-2.4); it decreased for quinolones (aOR: 0.5; CI: 0.4-0.6), tetracyclines (aOR: 0.3; CI: 0.1-0.3) and sulfamethoxazole (aOR: 0.2; CI: 0.1-0.3). **Conclusions:** Antibiotic prescription frequencies for mild respiratory illness among outpatients were most likely higher in Bangladesh than that in developed countries. Such prescriptions increased and types of antibiotics prescribed changed over the study period. Further evaluation of antibiotic prescribing practices is warranted to characterize inappropriate antibiotic use.

Board LB-2. A Prospective Clinicomicrobiological Study of Tuberculous Meningitis in a Neurocare Centre: An Indian Perspective

R. Ravikumar, J. E. Kaviyil; Neuromicrobiology, Natl. Inst. of Mental Hlth. Neuroscience, Bangalore, India

Background: Tuberculous meningitis (TBM) is a condition that is caused by *Mycobacterium tuberculosis* complex and is difficult to diagnose due to the nonspecificity of the presentations. The study analyzed the different modes of diagnosis available in a developing country set up over a period of five years to understand the diagnostic values of the current conventional and automated methods of diagnosis of TBM among the cases suspected with chronic meningitis. **Methods:** A total of 10281 cerebrospinal fluid samples (CSF) were collected from suspected chronic meningitis cases presented in a Neurocare centre through aseptic techniques. Of these, 790 CSF samples were from individuals who had clinically suspected TBM based on the clinical findings. The samples were subjected to CSF cytology and staining, automated and conventional culturing, immunological tests like enzyme-linked immunosorbent assay (ELISA), molecular techniques like polymerase chain reaction (PCR) using IS6110 probes and methods for detection of drug resistance like the line probe assay (LPA). The isolated strains were also checked for drug resistance by Mycobacterium Growth Indicator Tube (MGIT) system. Identification was also attempted using mass spectrometry. **Results:** The TBM cases were predominantly male, within a mean age of 21-40 years. CSF pleocytosis and lymphocytic predominance are the predominant features observed in cases of TBM. CSF cytospin and staining could suggest a diagnosis of TBM in 20.40% of cases of chronic meningitis. Culture had 40.13% positivity among clinically suspected TBM cases. The multidrug resistant *M. tuberculosis* (MDR-TB) isolates constituted 3.14% of the total clinical isolates. With the IS6110 PCR, a specificity of 92.86% and sensitivity of 100% is seen with diagnostic accuracy of 95.24% ($P < 0.001$). Assay has a threshold of 30pg of *M. tuberculosis* complex DNA per milliliter. Line probe assay using culture samples had a sensitivity of 97.67% and a specificity of 100%. Direct CSF LPA showed a sensitivity of 96.15% and a specificity of 100% were observed. **Conclusions:** A combination of techniques that involved culture, cytology and DNA amplification methods was found to be promising in specific, accurate and rapid detection of *M. tuberculosis* in the CSF samples from patients.

Board LB-3. Findings of the Disease-specific Surveillance Program

W. M. Kyaw, A. Chow, D. W. Lim, Y. S. Leo; Tan Tock Seng Hosp., Singapore, Singapore

Background: Singapore has set up a surveillance system to monitor the entry of the MERS-CoV since Sept 2012 after the report of this emerging infection in the Middle East. **Methods:** We conducted a retrospective review study on all cases screened at Emergency Department of Tan Tock Seng hospital, the national referral centre for outbreak response in Singapore, between September 2012 and Feb 2015. **Results**: There were 443 cases screened during the study period. 88% aged ≤65 years, and half were male. 162 (37%) of patients were admitted, only 39% of them met the Ministry of Health criteria of a suspect case; a person with clinical signs and symptoms suggestive of pneumonia and have a travel history to the countries where MERS-CoV cases have been reported. All hospitalized patients had combined nasal and throat samples tested for MERS-CoV by RT-PCR except 7 whom clinicians ruled out based on clinical ground. All were tested negative. 141 (87%) were tested for influenza virus by RT-PCR. Of these, 39 (28%) tested positive for influenza (18 A/H3, 12

A/H1N1 and 9 B). There were no difference in length of stay (LOS) between influenza (median 4 days, range 3-5) and non-influenza cases (median 3 days, range 3-4) among admitted patients (p=0.664). 51 patients (31% of total admission) had clinical and/or radiological evidence of pneumonia. Of these, 11 (22%) tested positive for influenza (6 A/H1N1, 4 A/H3, 1 B). Median LOS among patients diagnosed with pneumonia was 4 (range 2-23 days) with 25% had LOS ≥ 4 days. Two patients needed ICU care and both were positive for influenza (1 A/H1N1, 1 A/H3), however mortality has not been reported among these cases. There was no statistically difference in LOS between influenza (median 4 days, range 3-23) and non-influenza cases (median 4 days, range 2-15) (p=0.161) among patients diagnosed with pneumonia. There was also no statistically difference in LOS between pneumonia (median 4 days, range 2-23) and non-pneumonia cases (median 3 days, range 1-32) (p= 0.932). Six cases had pneumococcal disease. **Conclusions:** This study highlighted high proportion of vaccine preventable infections among returning travelers to the Middle East. In addition to mandatory vaccine, it is imperative to include influenza and pneumococcal vaccine, particularly to the individuals at risk of complication from such infections.

Board LB-4. Factors Influencing the Duration of Immunity in Poultry Vaccinated Against Highly Pathogenic Avian Influenza H5N1 in the Mekong River Delta of Vietnam, 2008–2010

L. V. Nguyen[1], M. A. Stevenson[2], D. T. Nguyen[1]; [1]Dept. of Animal Hlth. of Vietnam, Hanoi, Vietnam, [2]The Univ. of Melbourne, Melbourne, Australia

Background: A prospective cohort study was carried out to document factors influencing the duration of immunity in poultry vaccinated against highly pathogenic avian influenza H5N1 in the Mekong River Delta of Vietnam between December 2008 and April 2010 to (1) determine the median time taken for a H5N1 vaccinated, seropositive birds to become seronegative (that is, quantify the duration of immunity in vaccinated poultry), and (2) quantify the effect of flock-level factors influencing the duration of immunity. **Methods**: A total of 12,536 serum samples from 5,104 birds in 157 poultry flocks were tested using the haemagluttination inhibition test. Survival analyses were used to quantify the timing of seronegative events relative to the date of the last H5N1 vaccination. Because birds were tested at set time intervals thoughout the follow-up period the data were treated as interval censored. The effect of the identified putative explanatory variables on time to event was quantified using an Weibull acceleration failure time model. A frailty term was included to account for multiple vaccination intervals per bird and clustering at the individual flock level. **Results**: The overall time taken for H5 seropositive birds to become seronegative to HPAI H5N1 following a vaccination event was 56 (95% CI 51 - 61) days. The time taken for H5 seropositive birds aged less than 90 days, aged between 91 and 356 days and aged more than 365 days to become seronegative was 46 (95% CI 39 - 54), 69 (95% CI 49 - 97) and 96 (95% CI 72 - 132) days, respectively. The time taken for H5 seropositive birds vaccinated during the two dry seasons (from December to March 2009 and from December to March 2010) was 40 (95% CI 29 - 55) and 39 (95% CI 28 - 54) days, respectively. These are shorter than the 46 (95% CI 39 - 54) days recorded for birds vaccinated during the rainy season (from April to November 2009). **Conclusions**: Under field conditions the overall duration of immunity in vaccinated poultries was considerably shorter than documented in laboratory-based studies. Age of poultry at the time of vaccination and time of the year when vaccination was carried out significantly influenced duration of immunity in vaccinated birds. These two factors should be taken into account if the current vaccination strategy is to be continuously practiced in Vietnam.

Board LB-5. Prevalence of Middle East Respiratory Syndrome Coronavirus (MERS-CoV)-like Antibodies in Dromedary Camels in Israel

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Background: Middle East Respiratory Syndrome Coronavirus, MERS-CoV, was first identified in Saudi Arabia in 2012. As of February 16, 2015, the World Health Organization reports 983 laboratory confirmed cases of MERS-CoV, including at least 360 related deaths. MERS-CoV infection causes severe respiratory disease in humans. MERS-CoV-specific antibodies have been detected in the serum of dromedary camels across Northern Africa and the Arabian Peninsula. The ability of dromedary-derived strains of MERS-CoV to replicate in human cell line cultures suggests that dromedary MERS-CoV strains are able to infect humans, and high similarity has been found in MERS-CoVs carried by humans and camels, but direct transmission from camels to humans had not been demonstrated. To date, MERS-CoV-associated disease has not been diagnosed in Israel. CDC-developed serologic assays were used to analyze 71 dromedary camel serum samples from Israel for the presence of MERS-CoV antibodies. **Methods:** Sera collected in 2013 from 71 camels across three sites in Israel were gamma irradiated to inactivate potential pathogens. The presence of MERS-CoV antibodies was determined by microneutralization assay with additional confirmation by MERS-CoV immunofluorescence assay (IFA). Cross-reactivity against bovine coronavirus (BCoV) was assessed by using a BCoV- specific IFA. **Results:** Fifty-one of the 71 (71.8%) camels had MERS-CoV neutralizing antibodies. Thirty-five camels had MERS-CoV serum neutralizing titers ≥ 80, with MERS-CoV IFA titers ≥ 1:100 in 34 of 35 of these camels. The MERS-CoV serum neutralizing titers of 16 camels was 20 - 40. Of these 16, the MERS-CoV IFA titer of 9 camels was ≤1:100, with indeterminate IFA results for 7 camels. Of the remaining 20 camels, MERS-CoV serum neutralizing titers were <20. There was no association of MERS-CoV neutralizing antibodies with age, location, or sex of the camels. There was no correlation between the presence or absence of BCoV antibodies and MERS-CoV neutralizing antibody titers. **Conclusions:** Our findings of high neutralizing antibody titers are suggestive that MERS-CoV or a similar virus has circulated through dromedary camels in Israel, extending the known range of MERS-CoV circulation in the Middle East region.

Board LB-6. Rates of Antimicrobial Resistant Organisms Under Surveillance in Canada: January 1, 2009, to December 31, 2014

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Background: Surveillance of antimicrobial resistant organisms (AROs) in hospitalized patients is vital to informing strategies to reduce the impact of antimicrobial resistance. **Methods:** The Public Health Agency of Canada collects national data on AROs in hospitalized patients through

the Canadian Nosocomial Infection Surveillance Program (CNISP). As of December 2014, CNISP conducted surveillance in 62 major acute-care hospitals in ten provinces across Canada. **Results:** Canadian healthcare-associated *Clostridium difficile* infection (HA-CDI) rates have decreased from 2009 to 2014 (5.8 to 4.3 per 10,000 patient days). HA-CDI attributable mortality has decreased by 38% from 6.4% in 2011 to 4.0% in 2014. Methicillin-resistant *Staphylococcus aureus* (MRSA) infection rates have decreased since 2009, most dramatically in healthcare-associated rates from 2.56 in 2009 to 1.70 per 10,000 patient days in 2014. Community-associated MRSA (CA-MRSA) rates have increased from 0.85 in 2009 to 0.96 per 10,000 patient days in 2014. MRSA bacteremia rates have remained stable over the six year surveillance period, with observed regional differences, and an all-cause mortality rate of 25% in 2014. Vancomycin-resistant Enterococci (VRE) infection rates in Canada remain low and have decreased in 2014 (0.45 per 10,000 patient-days) from their maximum of 0.61 in 2012. Rates in 2014 for carbapenemase-producing organism (CPO), 0.10, as well as carbapenem-resistant Enterobacteriaceae (CRE), 0.22, and carbapenem-resistant *Acinetobacter* (CRA), 0.01 per 10, 000 patient days, remain low. The central region of Canada reported the highest number of CPO and CRE cases, the majority of which are likely due to an outbreak at one hospital. **Conclusions:** In Canada, ARO rates among hospitalized patients have been relatively stable or have decreased over the six year surveillance period. Regional variations have been reported and may be partially explained by differences in the virulence of circulating strains, infection control practices, antimicrobial stewardship programs and surveillance and screening activities. This data highlights the importance of continuing to monitor trends to ensure the detection of new and re-emerging threats associated with antimicrobial resistance.

Board LB-7. Enhanced Chikungunya Surveillance—Florida, 2014

J. G. Jordan[1,2], S. Watkins[2], D. Stanek[2], A. Likos[2], C. Blackmore[2]; [1]CDC, Tallahassee, FL, USA, [2]Florida Dept. of Hlth., Tallahassee, FL, USA

Background: During 2014, Florida experienced an increase in the number of internationally acquired cases of chikungunya and the first confirmed case of local transmission in the continental United States. Given the extent of transmission in the Caribbean, we sought to determine whether additional cases of chikungunya were not being diagnosed or reported in Florida hospitals. **Methods:** Hospitals were selected on the basis of the number of chikungunya cases previously reported. Hospital admission records and Florida Electronic Surveillance System for Early Notification of Community-based Epidemics (ESSENCE-FL) data for May 1-August 10 were reviewed to identify patients whose clinical presentations were consistent with chikungunya (i.e. travel to Caribbean country or fever and joint pain). We attempted to contact these patients and offered additional testing if illness was consistent with chikungunya. **Results:** We selected 2 hospitals to review; these hospitals had a total of 7 previously reported cases. Seven additional patients were identified for follow-up (2 from ESSENCE-FL and 5 from hospital records). One patient was no longer in the United States; 3 were unwilling to participate; and a fifth patient was excluded after additional history was obtained. Of the remaining 2 who were tested, both were positive for chikungunya. Both were male, with high fever, arthralgia, myalgia, mosquito bites history and recent travel to Hispaniola. No diagnosed cases were found that had not been reported. **Conclusions:** Hospital admission records and ESSENCE-FL can be used to identify symptom constellations consistent with chikungunya. This investigation resulted in confirmation of 2 previously undiagnosed cases that were not captured by routine testing or surveillance efforts in south Florida after review of only 2 hospitals. Enhanced surveillance activities are being considered for this emerging disease.

Board LB-8. Analyzing Influenza Pandemic Preparedness in Nepal: Simulation Modeling and Surveillance Mapping

A. S. Lambrou[1], D. Bajracharya[2], K. P. Baral[3], A. Thapa[2], D. Boyd[1]; [1]Duke Global Hlth. Inst., Durham, NC, USA, [2]Group for Technical Assistance, Lalitpur, Nepal, [3]Patan Academy of Hlth. Sci., Lalitpur, Nepal

Background: The complex issue of influenza pandemic preparedness in developing countries was examined through a case-study lens of Nepal. Nepal has recently developed into an emerging infectious disease hotspot due to its geography, epidemiology, potential for animal-to-human crossover and lack of resources. Pandemic preparedness was assessed by examining hospital resources and analyzing Nepal's disease surveillance system. **Methods:** Pandemic simulation modeling and surveillance system mapping were conducted using data from field visits. The CDC's FluSurge 2.0 was used to examine hospital surge capacity in the Kathmandu Valley with a 35% attack rate and pandemic durations of 6 and 12 weeks. The outcome of preparedness was measured by percent of current capacity utilized during a simulated pandemic. Nepal's influenza surveillance system was also mapped to identify strengths and areas of improvement. **Results:** FluSurge 2.0 outputs suggest the hospitals of the Kathmandu Valley, comprised of Kathmandu, Lalitpur and Bhaktapur, were prepared to handle the simulated influenza pandemics. The individual hospitals in the Kathmandu and Lalitpur Districts were prepared. However, the Bhaktapur District would require over 100% of its ICU and ventilator capacities. Public hospitals are more accessible as compared to private hospitals during emergencies. Forty of Nepal's 75 health districts had an active respiratory disease surveillance system, an Early Warning and Reporting System. Possible reporting gaps were identified between rural SARI/ILI cases and urban sites. **Conclusions:** Case-study outcomes suggest that FluSurge 2.0 can assist resource-poor hotspots in analyzing potential surge capacities and in determining areas in need of increased hospital infrastructure. Nepal's influenza surveillance system could be strengthened through sustainable mechanisms utilizing existing platforms such as mHealth, One Health and community-based interventions like Female Community Health Volunteers.

Board LB-9. Tuberculosis and Cryptococcosis Co-infection: A New Challenge for Global HIV/AIDS and TB Control

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Background: Tuberculosis (TB) remains a major global health problem and is the second leading cause of death from infectious diseases after HIV/AIDS. Since the first report in 1894, cryptococcosis has emerged as one of the most important fungal infections in AIDS-associated deaths worldwide. Current, TB/cryptococcosis co-infections in HIV/AIDS or TB patients are not receiving sufficient attention. **Methods:** In this study, we systematically reviewed all studies published until the end of 2014. Additionally, we collected laboratory examination data on clinical CSF

samples from 69 tubercular meningitis (TBM) and 111 cryptococcal meningitis (CM) patients in our hospitals, then conducted a comparative analysis of CSF characteristics. **Results:** A majority of the 47 co-infection cases (72.3%, 34/47) were reported since 2000. Approximately 68 % of cases (32/47) were collected from the Western Pacific region. The most frequent profile was TBM combined with CM (31.9%, 15/47). Fever (78.7%, 37/47), headache (55.3%, 26/47), and meningeal irritation (51.6%, 24/47) were the most common clinical features. The case fatality rate of TBM/CM co-infection (20%, 5/25) was significantly higher than that of TBM (P = 0.019). Among the examined parameters, the ICP was significantly higher in the TBM/CM co-infected patients than in the TBM patients (P<0.05). **Conclusions:** Although TB/cryptococcosis co-infection appears to be uncommon at present, these cases have been increasingly reported in recent years. Physicians should consider the possiblility of TB/cryptococcosis co-infections in HIV-positive patients who have received regular but unsuccessful antibacterial, antibacterial, and/or antifungal, and/or anti-TB treatments, particularly in the African and the Western Pacific regions. Our findings regarding the unique characteristics of clinical CSF samples from TBM/CM-co-infected patients, such as the ICP, show great potential for clinical applications in differential diagnosis between TBM/CM co-infection, TBM and CM, particularly in resource-limited settings.

Board LB-10. Estimating the MERS-associated Risk of Death in the Republic of Korea, 2015

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Background: An outbreak of the Middle East respiratory syndrome (MERS) has been observed in the Republic of Korea, 2015, involving more than 180 cases. As the transmission is seen at healthcare settings, it is pressing to understand the epidemiological determinants of MERS death so that one can predict heterogeneous risk of death at clinical settings. **Methods:** Here we device a novel statistical model that identifies the risk of MERS death in real time. While accounting for the time delay from illness onset to death, risk factors of death are identified using a linear predictor of logit model. Using the proposed model, not only the risks of death were explored but also the time dependence of the case fatality ratio (CFR) was examined, as the case ascertainment was greatly improved during the course of an epidemic. **Results:** Elderly aged 60 years or over appeared to be 9.1 times (95% confidence interval (CI): 3.2, 32.4) more likely to die compared to younger cases. Patients under treatment was 5.2 times (95% CI: 1.7, 21.6) more lethal than others. CFR among patients aged 60 years or older under treatment was estimated as high as 47.5% (95%CI: 32.8, 63.0) as of 23 June 2015, while the CFR among others was below 10%. From 6 June 2015, the CFR was shown to have declined 0.3 times (95% CI: 0.1, 0.6) of that in earlier period, perhaps due to increased ascertainment of cases through contact tracing practice. **Conclusions:** The risk of MERS death was significantly associated with not only treatment for underlying disease but also older age after explicitly adjusting for the time delay from illness onset to death. Besides, MERS outbreaks are greatly amplified in the healthcare setting, enhanced infection control practices in medical facilities should strive to eliminate potential exposure of risk groups to the MERS virus.

I6. Late Breakers I (Oral Presentations)

Tuesday, August 25, 3:30 PM - 5:00 PM

Centennial Ballroom IV

Cross-sectional Study of Influenza Viruses at Swine Slaughterhouses in Vietnam, 2013–2014

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Background: Avian influenza (AI) viruses, including highly pathogenic AI A/H5N1, have circulated in Vietnam since 2003, causing economic loss to the poultry industry and 127 human cases including 64 deaths (50% CFR). Novel AI viruses and H5N1 clade variants frequently have been introduced into Vietnam. Little is known of the influenza viruses circulating in swine in Vietnam. The majority of the 27 million pigs are raised at small-scale farms and processed at slaughterhouses with limited or no biosecurity. We proposed a study to identify influenza virus prevalence in swine in Vietnam. **Methods**: From September 2013 to June 2014, we conducted a cross-sectional study at 189 swine slaughterhouses located in 9 provinces in the North, Center and South of Vietnam using multi-criteria approach. At each slaughterhouse, 20 pigs (average weight of 107 kg) were selected at random to collect nasal swabs and blood samples. Four total sample collections occurred for a three month interval. Swab samples were tested for influenza A virus using real-time RT-PCR, with positives subtyped for H1, H3 and H5. All swab samples also were used for virus isolation with isolates sent to the U.S. Centers for Disease Control and Prevention (USCDC) in Atlanta, USA, for further molecular analyses. Serum samples were tested using IDEXX ELISA for antibodies against influenza virus and the positives subtyped by HI test. **Results**: A total of 7,489 swab samples and 7,560 serum samples were collected from 1,890 swine. Of the swab samples, 79 (1.05%) were positive with influenza A virus, and swine had the highest influenza virus prevalence in March 2014 (2.33%) followed by June 2014 (1.31%), compared with that recorded in September 2013 (0.42%) and December 2013 (0.11%). Of the serum samples, 591 (7.82%) were positive with influenza A virus, with 10 (1.75%) were H1 subtype and 21 (3.6%) H3 subtype. Swine had the highest seroprevalence in June 2014 (14.81%), followed by December 2013 (12.38%), March 2014 (12.22%) and September 2013 (6.67%). No samples were positive for H5. **Conclusions**: Swine had low to moderate prevalence of influenza A viruses at slaughterhouses in Vietnam. Influenza A/H3 virus was found to be the predominant influenza A subtype in this study. March and June 2014 had higher influenza virus prevalence.

Pregnancy as the Main Driver of Sex Disparities Among Adult Influenza Hospitalizations Across 14 FluSurv-NET Sites, 2010–2012

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Background: Previous studies from the Emerging Infections Program found that adult females were more likely to have influenza-related hospitalizations than males. To identify groups of women at higher risk than men, we used data from 14 FluSurv-NET (FSN) sites that conduct active population-based surveillance for laboratory-confirmed influenza-related hospitalizations among residents of 76 counties. **Methods:** We used 6,292 laboratory-confirmed adult (≥18 years) cases collected by the 14 FSN sites during the 2010-11 and 2011-12 influenza seasons, 2010 US Census (denominators), and 2008-2012 American Community Survey (percentage in a census tract below the federal poverty level) to calculate overall age-adjusted and age group-specific female:male incidence rate ratios (IRR) by race/ethnicity and socioeconomic status (SES). The percentage of US women 18-49 years with live births in 2010 applied to site denominators was used to calculate the number of pregnant women. **Results:** Overall, 55% of cases were female. Female IRRs were highest for 18-49 year-old women of low SES (IRR 1.50, 95% CI 1.30-1.74) and of Hispanic ethnicity (IRR 1.70, 95% CI 1.34-2.17). This difference disappeared after adjusting for pregnancy. Overall, 26% of 1,083 hospitalized 18-49 year olds were pregnant. Pregnant 18-49 year olds were more likely to have influenza-related hospitalizations than their non-pregnant counterparts (relative risk [RR] 5.23, 95% CI 4.57-5.99) but were no more likely to have been vaccinated (25.5% vs 27.8%). While the RR of influenza-related hospitalization of pregnant women was similar across the 14 FSN sites, the vaccination rates of pregnant cases varied widely (range: 9.1-57.1%, $p<0.01$). **Conclusions:** Pregnant 18-49 year-old women were at much higher risk of influenza-related hospitalization than other 18-49 year olds, with a similar level of risk across population-based surveillance sites in 14 states. Vaccination rates of pregnant women were low but highly variable between sites. Improving influenza vaccination rates in pregnant women should be emphasized given the higher risk and substantial burden of disease in this population.

Influenza Outbreak in Hematology/Oncology Unit of Pediatric Hospital in April 2015, Tbilisi, Georgia

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Background: Even before the emergence of the novel A/H1pdm09 strain, influenza disease was a serious complication in patients with hematologic malignancies receiving chemotherapy. On April 25, 2015 National Center for Disease Control and Public Health of Georgia was notified about two lethal outcomes of severe acute respiratory infections (SARI) in hematology/oncology unit of pediatric hospital in Tbilisi. Investigation was conducted to identify total number of cases, diagnose and develop recommendations to contain further transmission of infection. **Methods:** Nasopharyngeal specimens were collected, and demographic and clinical data was obtained from all patients in hematology/oncology unit. Laboratory diagnosis of influenza was performed by means of Real Time RT-PCR. Recommendations were developed. **Results:** 4 of 28 (14,3%)patients were confirmed as positive for A/H1pdm09 and 2 (7%) patients were positive for influenza B. All cases were male with mean age 7,5. 2 of 4 (2009 A/H1pdm09 positive) patients died on April 25, 2015 and others recovered in few days. As was found out lethal cases have received chemotherapy during 2 weeks prior SARI symptoms onset, while 2 others positive on A/H1pdm09 were relatively newly admitted patients. None of patients were vaccinated on influenza and none of them received antiviral treatment. No differences between influenza A/H1pdm09 or B -positive were noted in terms of demographic features. However, there was a high risk of infection because of no restrictions for visitors and doctors who received out-clinic patients inside hematology/oncology unit. All patients' influenza immunization were initiated after first lab confirmation and restrictions were implemented for unit visitors conjoined with outbreak investigation. **Conclusions:** Pediatric oncology patients, with pandemic influenza A/H1pdm09, had a similar demographic, but different clinical presentation with a fatal outcome in 2 cases. This was probably caused by duration of treatment course of chemotherapy which leads to immunosuppression among the patients. Additionally, the lack of herd immunity in this group should also be considered as an important factor for developing complications and lethal outcome. Hence, influenza immunization and antiviral treatment should be encouraged in these patients.

"Wash My Hands? Where and with What?!"—Water and Hygiene Conditions in Healthcare Facilities in Honduras, Rwanda, and Ghana

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Background: The World Health Organization (WHO) has identified universal access to drinking water, sanitation, and hygiene (WASH) in healthcare facilities (HCF) as an urgent priority for the post-2015 development agenda. Results from a recent WHO report on WASH conditions in HCF indicate that nearly 40% of HCF lack access to improved water sources, 19% lack access to improved sanitation, and 35% do not have soap and water for hand washing. In addition, many HCF in low-income countries suffer from water shortages, poor water quality, deteriorating water infrastructure, and rudimentary sanitation that may cause increased risks for preventable infections, including healthcare-associated infections. **Methods:** The Center for Global Safe Water, Sanitation & Hygiene conducted a multi-year, multi-country study to assess water access, use, and quality in 20 HCF in Honduras, Rwanda, and Ghana. A mixed-methods approach was used including surveys, observations, and water quality testing. **Results:** Water access, use, and quality differed by facility and country. Monitoring data for 10 HCF in Rwanda showed that HCF experienced water shortages for 367 of 664 days. Other data showed that water was unavailable once every 8 weeks in Honduras and once every week in Ghana on average. Water access, also defined by percentage of functioning taps, was higher (88%) at Honduran HCF compared to Rwanda (64%) and Ghana (63%). Honduran hospitals had a higher percentage of functioning taps with soap (62%) compared to Rwanda (47%) and Ghana (29%). However, in all countries, HCF patient access to hand washing stations was often limited due to locked, nonfunctioning, or nonexistent hygiene facilities. Assessment of water quality at the point of use in Honduras, Rwanda, and Ghana showed that 77%, 88%, and 61% of water samples met WHO guidelines for Total Coliforms and *E.coli*. (n=942). **Conclusion:** HCF in our study suffered from lack of access to water and soap, nonfunctioning water infrastructure, and poor water quality. Instead of being models of good WASH practices, these HCF demonstrate a neglected crisis in WASH services that affect the delivery of safe & effective health care. Further research is needed to measure the impact of poor WASH services on health care outcomes, health care seeking behavior, and medical staff satisfaction and retention.

Use of Supervised Machine Learning to Identify Subsets of WgMLST Loci Associated with Human *Listeria monocytogenes* Isolates from Different Food Sources

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Background: Whole genome sequencing has improved listeriosis outbreak detection and might also aid in estimating the food sources of sporadic illnesses. *Listeria monocytogenes* isolates from patients involved in an outbreak are more closely related to each other genetically than to isolates from patients who acquired infections from unrelated food sources. CDC has systematically sequenced *L. monocytogenes* isolates from patients and analyzed these genomes using whole genome multilocus sequence typing (wgMLST), which characterizes >5,000 loci (genes). We applied a supervised machine learning method called random forest to identify subsets of wgMLST loci that might be related to food sources. **Methods:** We linked wgMLST data to data on implicated foods for patients involved in listeriosis outbreaks from 2011-2014 reported to the Foodborne Disease Outbreak Surveillance System (FDOSS). Using the random forest package in R, we developed a random forest model of 1,000 trees to classify isolates into one of 4 categories of food exposure, i.e., dairy, produce, complex food (multiple ingredients), and unknown sources. We used repeated samples of the original data to build the random forest model and unsampled data from the same dataset to evaluate the model. **Results:** Among 1,347 patient isolates with wgMLST data, 84 were linked to outbreaks with an implicated food; 39 isolates were associated with outbreaks due to dairy products, 13 to produce, and 32 to foods containing multiple ingredients. The random forest model correctly classified 31 (80%) of 39 isolates linked to dairy, 6 (46%) of 13 isolates linked to produce. For isolates linked to foods with multiple ingredients, the model assigned 14 (44%) isolates linked to multiple ingredients. The model also ranked wgMLST loci by their influence on classification accuracy. **Conclusions:** Our preliminary results show that a random forest model is useful in identifying wgMLST loci associated with specific food sources among patient isolates. Random forest might aid in outbreak investigations by suggesting a possible food source based on wgMLST data and might also be used to estimate the sources of sporadic cases. Adding data from isolations from food sources might improve genomic profiling using this model.

Lessons Learned from a Time-limited Surveillance Pilot of Enterovirus D68 in Canada

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Background: In the Fall of 2014, outbreaks of Enterovirus D68 (EV-D68) were identified in Canada which prompted the Public Health Agency of Canada (PHAC), in collaboration with select federal and provincial/territorial partners (PT's), to develop a rapid-response surveillance tool for collecting data for national reporting. Within weeks of the outbreak, a time-limited surveillance pilot for hospitalized cases of EV-D68 was conducted in 7 Canadian jurisdictions. An evaluation of the pilot followed to determine the benefits of a rapid-response surveillance system for emerging/re-emerging pathogens (EPs). **Methods:** In the Spring of 2015, PHAC conducted a qualitative evaluation of the EV-D68 pilot. The survey was created using Fluid Surveys and administered via a secure online link. The number of questions varied based on the respondent's level of participation in the pilot or responses to previous questions. All PT's and all federal partners involved in the pilot, except those involved in the evaluation, were invited to complete one survey per jurisdiction. Proportions were calculated for responses to closed ended questions; recurring themes were identified for open ended questions. **Results:** 57% of PT's and 50% of the federal partners completed the survey. All respondents agreed that there is a need for rapid surveillance initiatives for EPs. However, the following were limitations to achieving this: non-notifiable disease; lengthy ethics approvals; restrictions to or lack of federal data sharing agreements; and lack of pre-existing protocols. Receiving timely case summaries (preferably weekly) was important for 88% of respondents; regular opportunities to discuss outbreak findings and any concerns would be preferred. The summaries that were provided were useful but were not representative of the national picture. The following were indicated as important in a surveillance data reporting platform: ease of functionality; data security; functionality for batch data uploads and jurisdictional control; web-based; and flexible to meet changing surveillance needs. **Conclusions:** Many valuable lessons were learned from the EV-D68 surveillance pilot that will assist with future rapid surveillance initiatives for EPs. It is important that barriers to surveillance be addressed prior to their emergence.

Late Breakers II (Posters)

Wednesday, August 26, 12:30 PM - 1:45 PM

Grand Hall

Board LB-11. Chromogenic Clinical Media to Quantify Antimicrobial Resistant Enteric Bacteria in Environmental Samples as an Indicator System for Environmental Surveillance

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Background: Methods to quantify antimicrobial resistant bacteria in environmental samples that are the same as those used in clinical settings are needed. Direct quantification of Extended Spectrum Beta Lactamase (ESBL) producing and *Klebsiella pneumoniae* Carbapenemase (KPC) producing gram-negative bacteria is proposed as an environmental indicator system. This research evaluated CHROMagar clinical media to quantify ESBL and KPC (carbapenem) resistant bacteria in environmental samples. **Methods:** Raw sewage samples of a major hospital and the municipal system and surface water samples upstream and downstream from the sewage effluent discharge were analyzed by standard membrane filter methods. **Results:** In hospital raw sewage 29.5% of all *E. coli* and 45.1 % of all total coliforms (TC) were ESBL resistant on CHROMagar ESBL compared to CHROMagar Orientation (base medium). Likewise, 21.6% of *E. coli* and 31.9% of TC were KPC resistant as detected on CHROMagar KPC medium. In municipal raw sewage 2.7 % of *E. coli* and 8.8% of TC were ESBL resistant and 1% of *E. coli* and 1.3% of TC were KPC resistant. In secondary treated effluent 1.2% of *E. coli* and 1.6% of TC were ESBL resistant and 0.4% of *E. coli* and 1% of TC were KCP resistant. In surface water samples above the wastewater effluent discharge, 1.4% of *E. coli* and 1.0% of TC were ESBL resistant and no *E. coli* but 0.2% of TC were KPC resistant. In surface water samples below the effluent discharge, 3.2% of *E.coli* and 3.1% of TC were resistant while 0.07% of *E. coli* and 0.5% of TC were KPC resistant. **Conclusions:** High levels of ESBL and KPC resistance were detected in E. coli and TC of hospital raw sewage, lower levels of such resistant bacteria were detected in municipal raw sewage and even lower but still detectable levels of such resistant bacteria were found in environmental surface waters, especially below sewage effluent discharges. From the results of this study, CHROMagar clinical media appear to be effective to directly quantify ESBL and KPC *E. coli* and coliform bacteria in environmental samples of

water and wastewater by standard membrane filter methods. These media and methods have promise as a candidate indicator system to detect and quantify ARB of great health concern in environmental media as a monitoring system to support environmental surveillance.

Board LB-12. Biomarkers on Patient T Cells Diagnose Active Tuberculosis and Monitor Treatment Response

T. Adekambi, C. C. Ibegbu, S. Cagle, A. S. Kalokhe, Y. F. Wang, Y. Hu, C. L. Day, S. M. Ray, J. Rengarajan; Emory Univ., Atlanta, GA, USA

Background: The identification and treatment of individuals with tuberculosis (TB) is a global public health priority. Accurate diagnosis of pulmonary active TB (ATB) disease remains challenging and relies on extensive medical evaluation and detection of Mycobacterium tuberculosis (Mtb) in the patient's sputum. Further, the response to treatment is monitored by sputum culture conversion, which takes several weeks for results. Here, we sought to identify blood-based host biomarkers associated with ATB and hypothesized that immune activation markers on Mtb-specific CD4+ T cells would be associated with Mtb load in vivo and could thus provide a gauge of Mtb infection. **Methods:** Using polychromatic flow cytometry, we evaluated the expression of immune activation markers on Mtb-specific CD4+ T cells from individuals with asymptomatic latent Mtb infection (LTBI) and ATB as well as from ATB patients undergoing anti-TB treatment. **Results:** Frequencies of Mtb-specific IFN-γ+CD4+ T cells that expressed immune activation markers CD38 and HLA-DR as well as intracellular proliferation marker Ki-67 were substantially higher in subjects with ATB compared with those with LTBI. These markers accurately classified ATB and LTBI status, with cutoff values of 18%, 60%, and 5% for CD38+IFN-γ+, HLA-DR+IFN-γ+, and Ki-67+IFN-γ+, respectively, with 100% specificity and greater than 96% sensitivity. These markers also distinguished individuals with untreated ATB from those who had successfully completed anti-TB treatment and correlated with decreasing mycobacterial loads during treatment. **Conclusions:** We have identified host blood-based biomarkers on Mtb-specific CD4+ T cells that discriminate between ATB and LTBI and provide a set of tools for monitoring treatment response and cure.

Board LB-13. The Tale of Two Neglected Tropical Infections: Using GIS to Assess the Spatial and Temporal Overlap of Schistosomiasis and Leprosy in a Region of Minas Gerais, Brazil

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Background: Despite multidrug therapy, leprosy remains a problem in highly endemic areas, with Brazil carrying the second highest burden of disease globally. Data suggest that helminth coinfection may increase the likelihood of the most infectious form of the disease. This is one potential avenue for sustained transmission in Brazil, where the incidence rate has remained stable or increased since 1979. This project presents the first-known analysis of the geospatial and temporal overlap of leprosy and *Schistosoma mansoni* infection in Brazil to assess the plausibility of a role of schistosomiasis in the transmission of *Mycobacterium leprae.* **Methods:** Data on new cases of leprosy and schistosomiasis were retrieved from the Brazilian national notifiable disease surveillance system (SINAN) for the years 2007-2014 for 7 contiguous municipalities near Vespasiano, Minas Gerais. Age, gender, date of diagnosis, and municipality of residence were tabulated and measurements of central tendency and frequencies compared using SAS (Carey, NC, v 9.4). Geospatial overlap was analyzed using ArcGIS (v. 10.3.1) with information down to a neighborhood level available for leprosy only at the time of submission. Temporal distribution was analyzed in aggregate and at the municipality level. **Results:** During the study period, 139 cases of leprosy (76% multibacillary) and 200 cases of schistosomiasis were reported. The same municipality, Confins, had the highest incidence of both leprosy and schistosomiasis (1.1 and 9.3 cases per 10,000 respectively). In the municipality with the most cases, the incidence of both diseases was highest for the period 2009-2011. This was true for the study area as a whole with a peak for both infections in 2011. Mapping of leprosy and schistosomiasis at the neighborhood level using GIS will further clarify the spatial relationship of these diseases and will be presented. **Conclusions:** Data analyzed thus far show both a spatial and temporal overlap of leprosy and schistosomiasis in 7 municipalities in Brazil. This spatial association provides an epidemiologic framework for the potential role of helminth coinfection in the transmission of leprosy. Furthermore, describing the geographic and temporal distribution of these co-endemic infections could provide the foundation for more integrated control efforts.

Board LB-14. Risk Assessment for Local Dengue Virus Transmission During a Binational Dengue Outbreak on the United States–Mexico Border—Yuma County, Arizona, October–December 2014

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Background: Dengue, an acute febrile illness caused by any of 4 dengue viruses (DENV) transmitted by *Aedes* species mosquitos, is endemic throughout the tropics and subtropics with 390 million infections worldwide in 2010. During September 2014-January 2015, while a dengue epidemic was ongoing in the Sonora state of Mexico, 95 travel-associated dengue cases were reported to the Arizona Department of Health Services. During 1997-2013, a total of 0-10 dengue cases were reported annually in Arizona. Because 71/95 (75%) cases were among Yuma County (bordering Sonora, Mexico) residents, we conducted a dengue risk assessment in Yuma County to evaluate potential local DENV transmission. **Methods:** Household (HH)-based cluster investigations were conducted December 15-19, 2014, and January 15-16, 2015, within a 50-meter radius of dengue patients' residences in Yuma County with reported illness onset during ≤90 previous days. All persons residing within the radius were offered participation, which included a questionnaire with demographic and medical information and testing a serum specimen for DENV by RT-PCR and anti-DENV IgM ELISA. Entomologic assessments were conducted by examining the house and yard for mosquito breeding sites and presence of *Aedes* species mosquitos. **Results:** Thirty-nine HH-based cluster investigations were conducted, including 194 participants in 113 HHs. Four persons were identified by detectable anti-DENV IgM antibody, but none reported a recent febrile

illness; all had travelled to Mexico during ≤3 past months. Among 194 participants, 152 (78%) reported travelling to Mexico at least monthly, 32 (16%) reported mosquito repellant use ≤3 past months, and 42 (37%) of 113 HHs reported mosquitoes in their home. Entomologic assessments in 105 HHs revealed 23.8 *Ae. aegypti* colonized containers/100 houses; 1.4% of total containers were colonized; and 11.4% of houses had ≥1 colonized container. **Conclusions**: Although no locally acquired dengue cases were detected, entomologic findings demonstrate potential for DENV transmission in Yuma County. Frequent travel to Mexico during future outbreaks might provide a method for DENV importation to Arizona. To reduce the risk for DENV transmission in Arizona, residents should cover, empty, or eliminate water containers and employ mosquito avoidance strategies.

Board LB-15. Introduction of Mosquito-borne Diseases into Non-endemic Locations: Infected Human Travelers Versus Mosquitoes

L. Mier-y-Teran-Romero, M. Johansson; CDC, San Juan, PR, USA

Background: Mosquito-borne diseases such as malaria and dengue are major causes of morbidity and mortality globally. Increased air travel to all regions of the world make the rapid importation and exportation of pathogens a concern for public health authorities. The factors necessary for pathogen transmission may be present in non-endemic areas, giving rise to the possibility of local outbreaks. In order to implement effective control measures, one would first have to know the answer to an important question: are infected people or infected mosquitoes more likely to introduce these pathogens to non-endemic areas? **Methods:** We developed a mathematical framework to characterize the exportation of mosquito-borne pathogens using branching process models. This framework allows us to estimate the probability of introduction by air travel from an endemic location via two alternative pathways: (i) an infected human, or (ii) an infected mosquito. The success of each introduction pathway relies on a chain of stochastic events that must each be satisfied sequentially for introduction to occur. **Results:** For the malaria parasite Plasmodium falciparum, the probability of a plane leaving a hyperendemic area with at least one infected person on board was approximately 100%. If that plane arrived in another highly suitable environment, the likelihood of transmission would also be high. In this situation, the median probability that at least one human is infected at the destination as a result of a human traveler was 0.999. In contrast, the probability that an infected mosquito on the plane would lead to a locally infected human was 0.0007. **Conclusions:** Our results have immediate policy implications. The International Health Regulations call for the disinsection of aircraft leaving areas affected by vector-borne diseases. Our results suggest that these vector-control measures, while potentially preventing the spread of mosquito species, would have little to no effect in impeding the spread of mosquito-borne pathogens.

Board LB-16. The U.S. Department of Defense Experience with Chikungunya Following Introduction of CHIKV into the Americas, January 2014–February 2015

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Background: The introduction and rapid spread of chikungunya virus (CHIKV) in the Western Hemisphere after December 2013 poses a potentially significant risk to DoD personnel, operations, and the military health care system from acute disease and any short and long term sequelae associated with CHIKV infection. In this study we describe the DoD experience with CHIKV during the 14-month period after introduction of the virus into the Western Hemisphere. **Methods:** The Defense Medical Surveillance System's (DMSS) Reportable Medical Events (RME) data and the Navy and Marine Corps Public Health Center's laboratory test results data were searched for laboratory confirmed cases of CHIKV fever among all DoD health beneficiaries diagnosed between 1 January 2014 and 28 February 2015. These cases were matched to personnel records to collect demographic data. We also searched for hospitalization and outpatient encounters recorded in the DMSS for diagnoses of joint pain or malaise/fatigue occurring more than three months after the CHIKV diagnosis date. **Results:** We found 157 confirmed cases (36 lab only, 57 RME only, and 64 lab and RME combined); of these 157, there were 50 (31.8%) Active Component, 68 (43.3%) Reserve Component, 15 (9.6%) dependents, 4 (2.5%) retirees, and 20 (12.7%) other/unknown. Exposure location was known for 117 (74.5%) cases and of these, 113 (96.6%) reported likely exposure in the Western Hemisphere; 85 (75.2%) of those occurring in Puerto Rico. We found that 51 (32.5%) of the cases had at least one outpatient visit with a diagnosis of joint pain or malaise/fatigue three months or more after the initial CHIKV diagnosis (range 91 to 288 days). **Conclusions:** Although historical data on CHIKV in DoD populations is scant, the number of cases associated with being in garrison or travelling to areas of the Western Hemisphere with ongoing CHIKV transmission appears to have resulted in a significant increase in the number of cases among DoD populations. Despite the emphasis on detecting and reporting CHIKV cases we expect some level of underreporting. Further study of the long term effects of CHIKV exposure seems warranted based on the number of outpatient visits reported here. The confirmed cases could form a registry for ongoing follow-up for long-term disease that is potentially associated with exposure to CHIKV.

Board LB-17. MERS-CoV: When Men Kiss Camels—An Anthropological Study About Human-Camel Relationships in Qatar

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Background: Qatar is one of the countries affected by the Middle East Respiratory Syndrome Corona-Virus (MERS-CoV). Qatar 15 reported cases of MERS. Dromedary camels are thought to play a central role in the epidemiology of MERS CoV as widespread evidence for antibodies and virus shedding was found in camels from the Arabian Peninsula (Aligaili et al., 2014). It remains unclear why MERS-CoV may have jumped from camels to humans; Mode of infection transmission is yet to be determined. This qualitative study sought to assess the potential exposures to the MERS-CoV among people dealing with camels in Qatar. **Methods:** Using ethnographic approach, semi-structured interviews were conducted; data was collected through focused group discussions and interviews with different camel stakeholders. **Results:** All cultural and social practices related to raising camels have been recognized and documented. Despite of the modernized life and the economic boom, raising camels remained an embedded traditional heritage and constitutes essential part of Qataris life. Fresh camel milk, boiled camel milk, camel meat, camel urine and camel skin are still drunk/eaten/ or used). Camels are not raised in the open areas anymore ,and although close contact with camels constantly occurs, it intensively increases during winter, where camel racing competitions organized, camels with their owners come from all neighboring countries, trade and breeding practices at its highest

rate, consistent with the disease seasonality. People do not believe transmission could be from camel to human. This is due to the high position of this animal in their domesticatory system. **Conclusions:** Highlighting these anthropological aspects pertaining to human-camel relationship might help narrow social practices required to understand the nature of the virus transmission. With the switch from a nomadic to sedentary lifestyle, and the recent zero grazing system, animals are now herded in much smaller areas (close to human), in farms, pens or barns (ezba),and camels and their owners movement , such determinants might facilitate the spillover of the virus from camel to Human . To conclude, we can say that in Qatar, "camel presence is more important than its diseases."

Board LB-18. An Investigation of a Potential Increase in Pertussis Cases Identified Through Sentinel Surveillance in South Africa, June 2012–December 2014

H. Ngobeni[1,2], F. Moosa[1], M. du Plessis[1], S. Walaza[1], E. Variava[3], H. Dawood[4], N. Wolter[1], A. Von Gottberg[1], C. Cohen[1]; [1]Natl. Inst. for Communicable Diseases, Johannesburg, South Africa, [2]South African Field Epidemiology Training Program, Johannesburg, South Africa, [3]Univ. of Witwatersrand, Johannesburg, South Africa, [4]Greys Hosp., KwaZulu-Natal, South Africa

Background: In 2009, the South African infant vaccination programme changed from whole-cell to acellular pertussis vaccine. Sentinel surveillance for severe respiratory illness (SRI) suggested an increase in pertussis cases from July-September 2014. We investigated, to establish whether this was a pseudo-outbreak due to environmental and/or laboratory contamination, or a true increase in disease. **Methods:** Respiratory specimens were collected from influenza-like illness (ILI) and SRI patients at four surveillance facilities and tested in duplicate for Bordetella pertussis using real-time PCR. We compared the characteristics of pertussis cases during baseline (June 2012-June 2014) and suspected outbreak (July-September 2014) periods. We interviewed 23 suspected outbreak cases. To identify potential contamination, laboratory instruments and reagents and environmental swabs from all facilities were tested. **Results:** We identified an average of 5 B. pertussis cases/month from July-September (the period of the annual observed winter seasonal increase) of baseline years compared to 14 cases/ month during the suspected outbreak period. Case numbers declined to 2 cases/ month from October-December 2014. Age distribution was similar during baseline (n=75) (9% <4 months, 11% 4-11 months, 11% 1-4 years, 19% 5-24 years, 35% 25-44 years and 16% ≥45 years) and outbreak (n=47) (6% <4 months, 4% 4 months-<1 years, 19% 1-4 years, 15% 5-24 years, 25% 25-44 years, 30% ≥45 years; p=0.138) periods. Among children <5 years 75% (12/16) during baseline and 36% (4/11) in suspected outbreak periods were fully vaccinated (p=0.045). No epidemiologic links were identified between cases. All laboratory controls were negative for B. pertussis. Of 32 environmental swabs, one (3%) surface swab tested positive. **Conclusions:** We describe a non-sustained increase in pertussis cases in South Africa in 2014, possibly related to disease periodicity or reduced vaccine coverage.

Board LB-19. Vaccination, Contact Precautions and Antivirals: What Best Controls Influenza Spread in a Hospital?

N. Blanco, M. Eisenberg, T. Stillwell, B. Foxman; Univ. of Michigan, Ann Arbor, MI, USA

Background: Influenza is a significant problem within hospitals, leading to extended hospital stays, excess morbidity and mortality, and economic loss. Prevention and control strategies are generally "bundled"; therefore, the individual effects and value of combined strategies cannot be determined directly, making it difficult to determine the optimal strategy. **Methods:** To quantify the individual and joint effectiveness of several known influenza infection control measures used in a general hospital, we simulated influenza transmission using an SEIR-type model. The hospital population was composed of patients and healthcare workers, interacting with its larger community population. We simulated the individual effects of five classes of interventions (influenza vaccination, handwashing, facemasks use, treatment with antivirals and patient isolation). Vaccination was implemented by altering the initial conditions of vaccinated and non-vaccinated classes, and all other interventions were implemented by altering the values of the appropriate transmission term based on data from the literature. In addition, we implemented each intervention (except vaccination) at levels of 25%, 50%, 75% and 100% of the reported effectiveness. These levels represent differences in compliance and appropriate implementation of each intervention in healthcare settings. We also modeled several multifaceted strategies that combined the effects of hospital-based interventions over baseline. **Results:** The most effective (% reduction of cases) individual strategies were: handwashing (11%-27%), antiviral treatment (7%-22%), HCW vaccination (6%-19%), prevaccination of patients (4%-17%), patient isolation (5%-16%), and facemask use (3%-10%). Using all strategies together with ideal levels of compliance could potentially halve the number of observed hospital cases; under a more realistic scenario a 40% reduction could be achieved. **Conclusions:** A multifaceted approach is imperative to control and prevent nosocomial influenza in healthcare settings.

Board LB-20. Lassa Fever and Contact Tracing in a Large Population

S. Semple[1], L. Hamilton[2], K. Cervantes[1], N. L. Mazur[1], D. B. Theriault[1], J. W. Wells[1], C. Tan[1]; [1]New Jersey Dept. of Hlth., Trenton, NJ, USA, [2]Council for State and Territorial Epidemiologists, Applied Epidemiology Fellow, Trenton, NJ, USA

Background: On May 25, 2015, the Centers for Disease Control and Prevention (CDC) confirmed the presence of Lassa virus in a New Jersey (NJ) resident with recent travel to Liberia. The individual had been under active monitoring (AM) for Ebola virus disease (EVD) but had not reported symptoms to the local health department (LHD); suspicion for Lassa fever (LF) was not reported until later in the illness course. LF is an acute viral illness caused by Lassa virus, an arenavirus endemic to West Africa, where persons primarily become infected by ingesting or inhaling excreta from multimammate rats. Symptoms present one to 21 days following exposure, and 1% of cases are fatal. Secondary cases may result from exposure to infected body fluids. **Methods:** Contact tracing was performed among community/family members and healthcare workers who were assigned to high or low risk classifications based on responses to a standardized questionnaire assessing contact with infected body fluids and use of personal protective equipment. Contacts were monitored for 21 days using the AM protocol implemented for EVD monitoring. **Results:** A total of 217 potentially exposed contacts were identified, of which 214 (98.6%) were interviewed. Of those interviewed, 181 (83.4%) reported possible exposures; of those exposed, 15 (8.3%) were classified as high risk and 166 (91.7%) as low risk. Daily symptom monitoring of contacts concluded on June 18, the end of the 21-day incubation period. Hospital A monitored 81 (44.8%) low risk contacts. Hospital B monitored 65 (35.9%) contacts, including one laboratory worker classified as high risk. LHDs monitored 35 (19.3%) contacts from the community, including 13 family members and a private physician classified as high risk. No secondary cases were identified. **Conclusions:** Although secondary transmission of LF is less likely to occur in the U.S., health care providers need to remain vigilant about Lassa and other viral

hemorrhagic fevers, to ensure timely identification, treatment and containment of disease. Also, stakeholders should address stigma that may be associated with travelers from EVD-affected countries, to minimize barriers to reporting symptoms and risk factors. Lastly, use of current EVD monitoring systems and protocols was valuable for rapid implementation of large-scale contact tracing.

N6. Late Breakers II (Oral Presentations)

Wednesday, August 26, 3:30 PM - 5:00 PM
Centennial Ballroom IV

Ebola Virus Disease Outbreak in Lagos State, Nigeria, July–September 2014: An Epidemiological Investigation

F. F. Osundina, A. M. Oladimeji, O. Ajumobi, S. O. Gidado, A. T. Olayinka, P. N. Nguku; Nigeria Field Epidemiology and Lab. Training Programme (NFELTP), Abuja, Nigeria

Background: The spread of Ebola Virus Disease (EVD) outbreak to Nigeria, Africa's most populous country, in July 2015 raised significant public health concern. We conducted this study to describe the socio-demographic characteristics of EVD patients and their contacts, magnitude of the outbreak and factors associated with outcome in patients. **Methods:** An outbreak investigation team was set up. Case and contact definitions were adapted from the World Health Organization (WHO) guidelines. Active case search in health facilities, communities, religious centers and various points of entry into the country was done. We traced EVD contacts by contact identification, listing and active follow-up; taking daily temperature measurements to identify suspected cases. Laboratory confirmation of cases was done. Data on socio-demographic characteristics, clinical symptoms and disease outcomes were gathered. Bivariate and multivariate analysis was done. **Results:** From the 16 confirmed cases, 293 contacts were identified. The mean age of cases was 39.1±11.9 years, while that of contacts was 33.2 ±13.9 years. Eight of the 16 cases (50.0%) were females while 10 (62.5%) were health workers, 150 (52.0%) of the contacts were females while 138 (47.0%) were health workers. Of the 15 cases traced to the index case, 13(86.7%) were primary cases while 2(13.3%) were secondary cases. The basic case reproduction number (R_0) for the outbreak was 13 and the secondary attack rate was 0.68%. The most reported symptom among the cases was fever (85.7%). Case fatality rate (CFR) among all the cases was 37.5% (6/16), while CFR among health workers was 40.0% (4/10). Average duration of illness from onset of symptoms to outcome of disease - survival or death was 16±4.8 days and 11.6±5.0 days respectively. There were no statistically significant associations between the average duration of illness and the outcome of disease (OR= 1.14, 95% CI = 0.08-16.95) and also between occupation of cases (health workers versus non-health workers) and outcome (OR = 0.75, 95% CI = 0.09-6.23). **Conclusion:** The EVD outbreak in Lagos was controlled via active case search, effective contact tracing and strict infection control. Duration of illness and occupation were not associated with outcome.

Emergence of Serogroup C *Neisseria meningitidis*, Niger—2015

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Background: To combat devastating *Neisseria meningitidis* serogroup A epidemics in the Meningitis Belt of Sub-Saharan Africa, a novel serogroup A conjugate meningococcal vaccine (MACV, MenAfriVac™) has been progressively rolled out since 2010 with the goal to eliminate epidemic meningitis. Monitoring for emergence of non-A serogroups is critical following MACV implementation. In March 2015, four years after nationwide MACV introduction, Niger reported its first meningitis epidemic. **Methods**: Epidemiologic data were collected through routine surveillance with aggregate case counts, the MenAfriNet-supported case-based surveillance system in eight districts, and an enhanced surveillance system during the epidemic. Cases were confirmed at the national meningitis reference laboratory by culture or detection of genetic material by direct real-time Polymerase Chain Reaction. Multi-locus sequence typing (MLST) was conducted on a subset of cerebrospinal fluid (CSF) specimens at a World Health Organization (WHO) Collaborating Centre. Information on vaccination campaigns was collected by the Ministry of Health and WHO. **Results**: From January 1 to June 30, 2015, a total of 8,500 suspected meningitis cases and 573 deaths (6.7%) were reported in Niger. Among 4,039 CSF specimens, 1,456 (36.0%) were positive: 1,087 (74.7%) were *N. meningitidis* serogroup C (NmC), 196 (13.5%) were NmW, and 65 (4.5%) were Nm with serogroup undetermined. MLST conducted on 10 CSF specimens revealed ST-10217, a novel strain detected in 2 smaller outbreaks in Nigeria in 2013-2014. Due to a global vaccine shortage, half of the 1.4 million vaccine doses procured for outbreak response became available after the epidemic had largely subsided. **Conclusions**: The epidemic in Niger due to NmC, a rare cause of epidemics in Africa, demonstrates the continued threat of *N. meningitidis* in the region. The risk of further regional expansion highlights the need for continued strengthening of case-based surveillance, monitoring of emerging strains, and an adequate global supply of multivalent vaccine for epidemic response. This unprecedented NmC epidemic in the post-MACV era supports accelerated development of an affordable, multivalent conjugate meningococcal vaccine in order to achieve elimination of epidemic meningitis in Africa.

Risk Factors Associated with the Fatal Henipah Virus Outbreak Infection in Sultan Kudarat, Mindanao, Philippines, 2014

P. G. Ching; Epidemiology Bureau, Dept. of Hlth., Manila, Philippines

Introduction: Henipah virus infection outbreak was first reported and investigated in the Philippines on April 17, 2014. The outbreak included 17 cases with 9 deaths from the southern region of Sultan Kudarat in Mindanao. This paper will describe the possible horse to human transmission and subsequent human to human virus transmission and will identify the risk factors associated with the outbreak. **Methods:** A descriptive study and case-control study were conducted. We reviewed the medical records of patients seen and admitted in different hospitals. We did active case finding in the communities. We interviewed cases and relatives of deaths Contact tracing was done for cases and deaths. A *Case* was defined as any well individual from Sultan Kudarat who developed the following symptoms: Acute Encephalitis Syndrome (AES) -Fever, headache with changes in sensorium, OR Influenza like illness (ILI)- Fever, headache, cough and difficulty of breathing, OR Aseptic Meningitis from March 10 - May 23, 2014. A control was any well resident of Brgy. Tinalon who was apparently well from March 10, 2014- May 23, 2014.

Results: A total of 17 cases were identified. There were 13 cases who presented with AES, five with influenza-like illness and one 1 aseptic meningitis. Earliest date of onset was March 10, 2014. Age of cases range from 21 to 60 years (Median=41 years). Sixteen (94%) were males. There were nine deaths (Case Fatality Rate = 53%), all were males. Age ranges from 21- 60 (median=38 years). There were 11 possible human to human transmission documented, with 9 occurring among deaths and affecting two healthcare workers. Two sick horses involved presented with neurological symptoms and two with unknown cause. Significant risk factors are taking care of sick person *(OR 64, 95% CI 4.6-879.58)* and taking care of sick horses *(OR 20, 95% CI 1.6-249.8).* **Conclusion:** We were able to illustrate that a horse to human and human to human transmission occurred in this outbreak. Human and animal health surveillance should be strengthened. We recommended to further establish risk factors and transmission of infection from bats to horses.

Demographic Groups Affected by Increase in Campylobacteriosis, Connecticut, 2005–2014

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Background: After a period of stable, low incidence in Connecticut (CT), campylobacteriosis cases steadily increased 2010-14. Through 2014, all CT laboratories continued to use culture-based testing. To generate hypotheses to explain the increase, we conducted an analysis to determine which demographic groups were most affected. We included census tract-level poverty (SES) as a demographic variable as a previous CT study showed higher incidence as census tract SES increased. **Methods:** CT is a FoodNET site and conducts active laboratory surveillance for campylobacteriosis. Average annual incidence 2012-14 was compared to 2005-07 by age, sex and poverty group. Age groups were 0-9, 10-19, 20-49, 50+ year. Cases were geocoded to the census tract of residence. The 2006-2010 American Community Survey (ACS) was used to determine census tract poverty for 2005-07; the 2009-13 ACS was used for 2012-14. Poverty categories were <5% of households below of the federal poverty level (low poverty), 5-<10%, 10-<20%, and 20% or more (high poverty), applied to 2010 census tract denominators. Age-adjusted rates were used for poverty groups. **Results:** Overall incidence increased 45.6%, from 15.5 in 2005 to 22.5/100,000 in 2014 and 30% when comparing 2005-07 to 2012-14 ($p<0.001$). Increases of at least 15% occurred in all age, sex, and poverty groups. Those with a significantly larger percentage increase than the lowest increase within the group were those ≥ 50 years (41.6%, $p<0.01$) and those of moderate (57.3%) and high (64.6%) poverty levels ($p<0.05$). Persons 50+ years accounted for 72% of the entire increase. Among those 50+ years, the increase in incidence was greatest among the moderate and high poverty groups (134.3% and 170.6%, $p<0.01$ each). **Conclusions:** Campylobacteriosis increased in all groups, but those 50 and older and living in higher poverty areas were disproportionally affected. Hypotheses needing exploration to explain the general increase are whether there has been an increase in *Campylobacter* contamination in food reservoirs versus a change in prevalence of risk factors. A better understanding of risk factors in older age groups, particularly those in higher poverty areas, and whether they are changing over time is needed to understand their being disproportionately affected.

A Collaborative Approach to Reducing the Risk of *Salmonella* Newport Linked to Produce Grown on the Delmarva Peninsula

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Background: Historically, *Salmonella* Newport outbreaks associated with PFGE pattern (*Xba*I PFGE pattern JJPX01.0061) have been linked to red round tomatoes grown on Virginia's Eastern Shore in the Delmarva region. These outbreaks occurred in 2002 (512 persons), 2005 (71 persons), 2006 (107 persons), and 2007 (57 persons), with an additional suspected outbreak in 2010 (46 persons). A definitive contamination source has not been found. Wildlife has been evaluated as a possible source of contamination, but fecal samples from deer, turtles, and birds have been negative and do not support the hypothesis that animals are a source of infection. **Methods:** In August 2014, PulseNet detected a multistate cluster of *Salmonella enterica* serotype Newport infections with a PFGE pattern previously linked to consumption of tomatoes harvested from Virginia's Eastern Shore. To identify the contaminated food and find the source of the contamination, CDC, FDA, state and local health and agriculture departments and laboratories, conducted epidemiological, trace-back, and laboratory investigations. A total of 275 patients in 29 states and the District of Columbia were identified, with illness onsets between May 20 and September 30, 2014. **Results:** Whole genome sequencing (WGS), a highly discriminating subtyping method, was used to further characterize PFGE pattern JJPX01.0061 isolates. Epidemiologic, microbiologic, and product trace-back evidence suggested that cucumbers harvested in Maryland were a source of *Salmonella* Newport infections for some of the Maryland and Delaware cases in the 2014 outbreak. **Conclusion:** The 12 year outbreak history of unique strain of S. Newport associated with produce from the Delmarva Peninsula supports the need for a preventive approach to addressing this public health concern. The Delmarva Produce Safety Task Force was formed in April 2015 as a regional, proactive effort to ensure continued close collaboration between State Departments of Agriculture, Health and Environment with support from FDA. The Task Force is reviewing the science and current research to incorporate any new information into Good Handling Practices and Good Agricultural Practices to enhance food safety and to reduce the risks associated with foodborne pathogens

Outbreak Investigation of Primary Amoebic Meningoencephalitis Caused by *Naegleria fowleri*—Karachi, Pakistan, 2012–2014 (with 2015 update)

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Background: *Naegleria fowleri* is a thermophilic, chlorine-sensitive free-living amoeba that causes a rare and life-threatening infection of the brain called primary amoebic meningoencephalitis (PAM).There have only been 5 well-documented survivors worldwide. Infection results when contaminated water enters the nasal passages usually during swimming in warm fresh water, but infection has also occurred from ritual ablution using drinking water sources. In early September 2014, the media reported many PAM deaths in Karachi. The Department of Health deputed Field Epidemiology & Laboratory Training Program fellows to investigate the outbreak on 15th September, 2014. **Methods:** We identified PAM cases through review of records from the health department, major hospitals, and published reports. Three patients and families of all deceased patients were interviewed and geographical coordinates of last place of residence were recorded. Water supply routes, supply methods and water sources were inspected or investigated. **Results:** Twenty male and three female PAM cases (were diagnosed by CSF and PCR in Karachi. Case fatality rate was 100%. Age range was 4-67 years (mean: 30). All patients were diagnosed from May to October. Fifteen of 23(65.2%) patients lived in 2/6 districts of Karachi in a geographical cluster with one water filtration plant. Fourteen (60.8%) were using municipal water and 11 (47.11%) regularly used water for the rinsing the nasal passages during ablution.

One case-patient reported swimming. **Conclusions:** This is the largest outbreak of *Naegleria fowleri* being reported in Pakistan. A poorly chlorinated water supply and warm temperatures may have caused this outbreak. After the start of the outbreak investigation and media coverage, the government initiated corrective measures including increased chlorination of water and an awareness campaign. In 2015 (June) only one out of five new cases came from the previously affected districts

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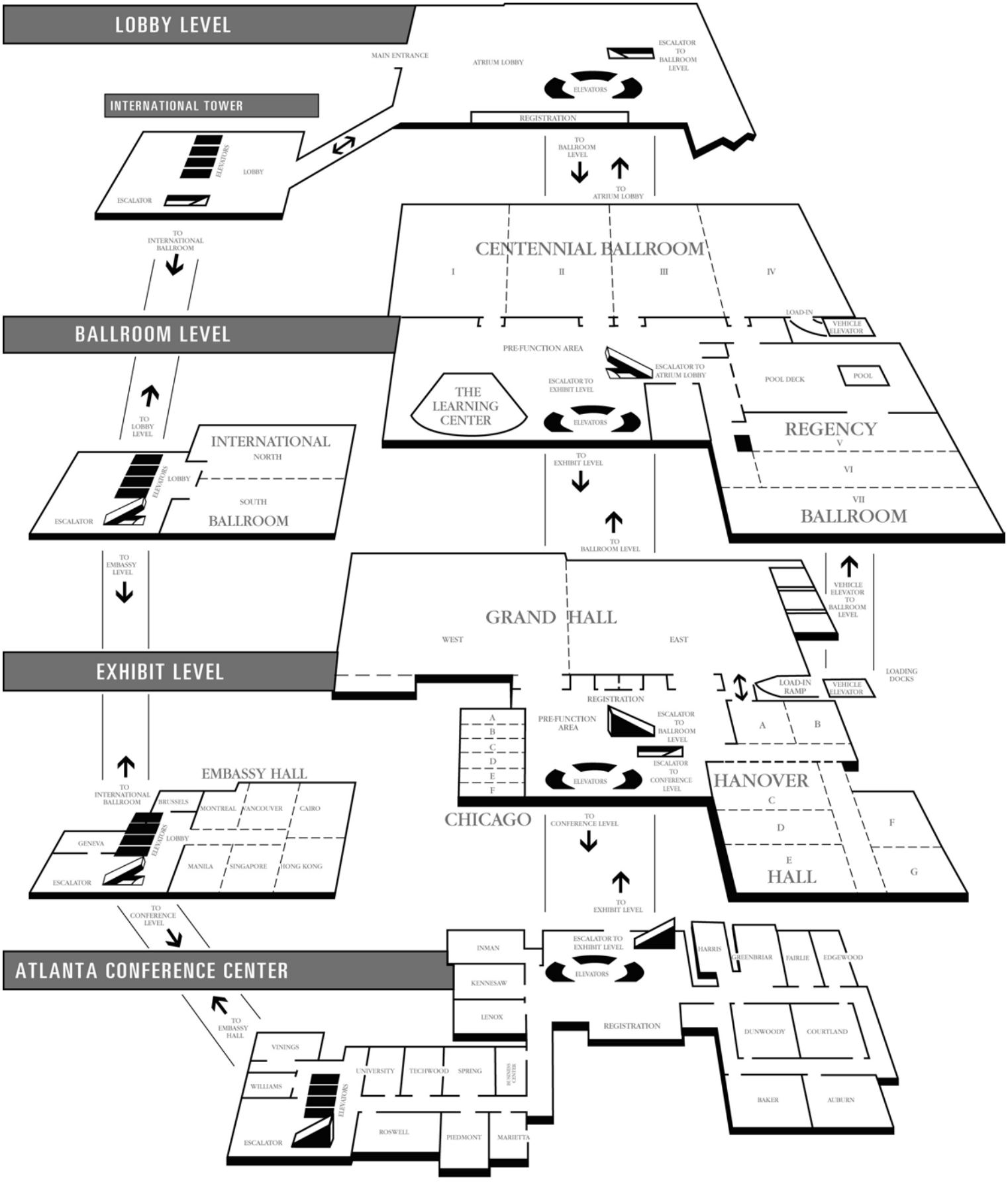

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