2008
International Conference on
Emerging Infectious Diseases

Program and Abstracts Book

ICEID
2008
International Conference
on Emerging Infectious Diseases

March 16 - 19, 2008

Hyatt Regency Atlanta

Atlanta, GA, USA

Organized by

Centers for Disease Control and Prevention

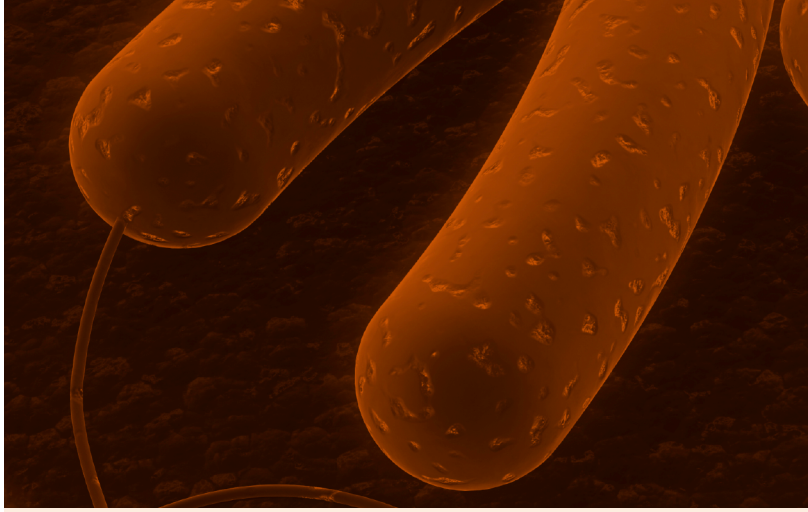
Council of State and Territorial Epidemiologists (CSTE)

Association of Public Health Laboratories (APHL)

World Health Organization (WHO)

American Society for Microbiology (ASM)

Table of Contents



Committees

SCIENTIFIC PROGRAM COMMITTEE — External Representatives

Lin Chen
International Society of Travel Medicine

Carol Chenoweth
Society for Healthcare Epidemiology of America

Susan Daniels
National Institute of Allergy and Infectious Diseases

John R. Dunn
National Association of State Public Health Veterinarians

Emilio Esteban
US Department of Agriculture, Food Safety and Inspection Service

Joel C. Gaydos
US Department of Defense-Global Emerging Infections Surveillance and Response

Kathleen Gensheimer
Council of State and Territorial Epidemiologists

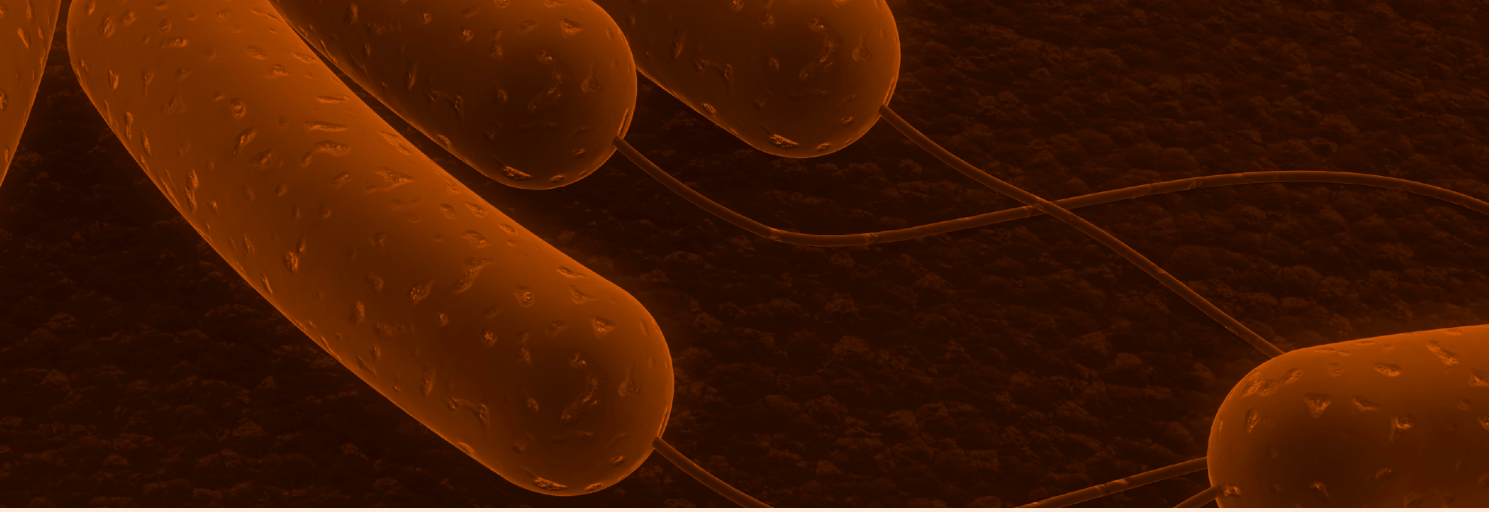
Thomas Gomez
US Department of Agriculture, Animal and Plant Health Inspection Service

James Hughes
Infectious Diseases Society of America

Wanda K. Jones
Office of Women's Health, US Department of Health and Human Services

Marlo Libel
Pan American Health Organization

Tammy Lundstrom
Association for Professionals in Infection Control



Larry Madoff
International Society for Infectious Diseases

Patrick McDermott
US Food and Drug Administration, Center for Veterinary Medicine

Mark Miller
Fogarty International Center, National Institutes of Health

Kenneth Nusbaum
Association of American Veterinary Medical Colleges

Walter A. Orenstein
National Foundation for Infectious Diseases

Mark Starr
American Veterinary Medical Association

Alejandro Thiermann
World Organization for Animal Health

Ray Waters
US Department of Agriculture, Agriculture Research Service

Angela Weaver
US Agency for International Development

Michael P. Williams
National Association of County and City Health Officials

SCIENTIFIC PROGRAM COMMITTEE—CDC Representatives

Steering Committee
Daniel N. Cameron, Chair
Angelica O'Connor

Co-Chairs
Beth Bell
Hazel Dean
Nina Marano
Monica Parise

Coordinating Office for Global Health (COGH)
Michael St. Louis

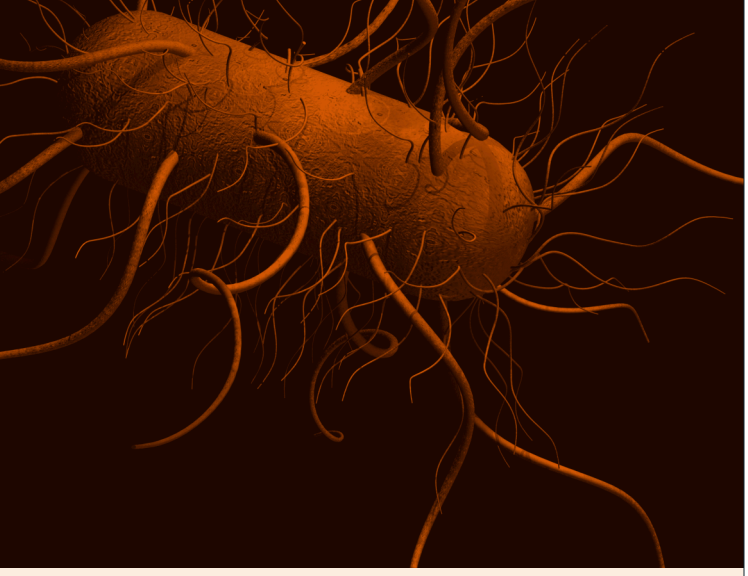
Coordinating Office for Terrorism Preparedness and Emergency Response (COTPER)
Peter Rzeszotarski

National Center for Immunization and Respiratory Diseases (NCIRD)
Susan Goldstein
Daniel Jernigan
Eric Mast
Trudy Murphy
Abigail Shefer

National Center for Zoonotic, Vector-Borne, and Enteric Diseases (NCZVED)
Kate Glynn
S. Patrick Kachur
Ron Rosenberg
David Swerdlow

National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention (NCHHSTP)
Joanna Buffington
Robert Chen
Timothy Holtz
Mary Lou Lindegren
Kimberly Workowski

National Center for Preparedness, Detection, and Control of Infectious Diseases (NCPDCID)
Nancy Anderson
Marian McDonald
Alan Parkinson



ICEID 2008 Conference Organizers and Sponsors

ORGANIZERS

Centers for Disease Control and Prevention (CDC)
Council of State and Territorial Epidemiologists (CSTE)
Association of Public Health Laboratories (APHL)
World Health Organization (WHO)
American Society for Microbiology (ASM)

SPONSORS

In-kind support provided by:

American Association of Blood Banks
American College of Preventive Medicine
Association of Schools of Public Health
American Public Health Association
Alliance for the Prudent Use of Antibiotics
American Sexually Transmitted Diseases Association
American Veterinary Medical Association
Association of American Veterinary Colleges
Department of Defense – Global Emerging Infections Surveillance and Response System
Emory Division of Infectious Diseases
Environmental Protection Agency
Immunization Action Coalition
Infectious Diseases Society of America
International Society of Travel Medicine
National Foundation for Infectious Diseases
National Institutes of Health
OIE (World Organization for Animal Health)
Rollins School of Public Health of Emory University

General Information

Americans with Disabilities Act Compliance

The Hyatt Regency Atlanta is in compliance with the Americans with Disabilities Act to the extent required by the law. If special accommodations would enhance your enjoyment of the conference, please visit the Headquarters Office in the Show Office-Grand Hall. We will make all reasonable accommodations to ensure your comfort at the meeting.

Archives of the Sessions

Most sessions will be recorded and audio recordings available to order onsite and after the conference. See the order form available onsite for pricing and delivery details. After the conference, please visit the website www.iceid.org for ordering information.

Business Center

The Hyatt Regency Hotel business center is located on the Lobby Level.

Hours are:

Monday – Friday . . . . . 7:00 AM to 7:00 PM

Saturday . . . . . 8:00 AM to 1:00 PM

Sunday. . . . . Closed

Continuing Education Credit

Continuing Education will be offered. Our target audience includes physicians, veterinarians, and nurses. Additional details are available at the conference.

E-Central

Sunday, March 16.....2:00 PM - 10:00 PM

Monday, March 17 .....8:00 AM – 10:00 PM

Tuesday, March 18.....8:00 AM – 10:00 PM

Wednesday, March 19.....8:00 AM – 5:00 PM

The organizers and sponsors of the 2008 International Conference on Emerging and Infectious Diseases wish to thank the US Department of Defense – Global Emerging Infections Surveillance and Response System for their financial support of the conference.

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 any e-mail address.

Exhibits

Exhibits will be held in the Grand Hall (Lower Level) of the Hyatt Regency Atlanta. Don't miss the Opening Reception with food, drink, and camaraderie on Sunday, March 16, from 7:00 PM – 9:00 PM. Additional Exhibit Hall hours are 12:00 PM – 6:00 PM on Monday, March 17, and Tuesday, March 18; show hours are from 10:00 AM to 1:00 PM on Wednesday, March 19.

Headquarters Office

The ICEID/ASM Headquarters Office, the Show Office-Grand Hall, will be open and staffed during registration hours. Feel free to come to us with questions or concerns.

Poster Presenters

Posters can be mounted Monday, March 17 – Wednesday, March 19 from 7:30 AM – 8:30 AM in the Exhibit Hall (Grand Hall, Lower Level).

Press Room

Press representatives are welcome at ICEID. Please check in at the Press Room, located on the Grand Hall Level of the Hyatt in the Chicago AB room.

Program Addendum

In addition to this program, registrants receive a program addendum, which incorporates all late-breaker abstracts, additions to the program, and changes made after this program went to press.

Registration

To maintain the quality and size of the conference and ensure meaningful scientific exchange, registration at the ICEID is limited to 2,500 attendees. On-site registration is only available if fewer than 2,500 individuals preregister. Registration will be open during the following times to answer your questions and provide information on the meeting and Atlanta:

Sunday, March 16 . . . . . 2:00 PM - 7:00 PM

Monday, March 17 . . . . . 7:30 AM - 5:00 PM

Tuesday, March 18 . . . . . 7:30 AM - 5:00 PM

Wednesday, March 19 . . . . 8:00 AM - 12:00 PM

General Information *continued*

Speaker Ready Room

Speakers may preview their electronic presentations in the speaker ready room, located in the Regency V ballroom. The room hours are Sunday, March 16, 2:00 PM – 9:00 PM; Monday, March 17 & Tuesday, March 18, 7:30 AM – 7:00 PM, and Wednesday, March 19, 8:00 AM – 4:00 PM, and is equipped with PCs loaded with PowerPoint and other software so that you may view and make changes to your electronic files. Please make sure to submit your presentation to the speaker ready room at least 2 hours prior to the start of the session in which you will be speaking.

Verification of Attendance

Conference attendees requiring a certificate verifying their attendance should visit the Headquarters Office in the Show Office-Grand Hall or the Registration Desk during registration hours beginning Tuesday, March 18. We will be happy to provide you with the needed documentation.

ICEID 2008 Leaders Program

Supported in part by a grant from the Gates Foundation

Larisa Abryutina
Russian Association of Indigenous Peoples of the North (RAIPON)

Chantal Gnankon Akoua-Koffi
Institut Pasteur de Cote d'Ivoire

Abdulhakim Ali Sharaf Al-Kohlani
Ministry of Public Health and Population of Republic of Yemen

Franciso Ardon
Guatemala Ministry of Public Health and Social Welfare

Mengistu Asnake
Ethiopian Public Health Association

Norma Binsztein
Instituto Nacional de Engermedades Infecciosas-ANLIS "Carolos G. Malbrán"

Flabou Bougoudogo
Institute National de Rechereche en Sante Publique

Nasr Mohamad El-Sayed
Ministry of Health and Population

Nihad Fejzic
State Veterinary Office of Bosnia and Hercegovina

Zijian Feng
Chinese Center of Disease Control and Prevention

Lisa Indar
Caribbean Epidemiology Center (CAREC)

Juan Manuel Jimenez-Estrada
Instituto de Salud Del Estado de Mexico (ISEM)

Samuel Kariuki
Kenya Medical Research Institute (KEMRI)

Senanayake A. M. Kularatne
University of Peradeniya, Sri Lanka

S. M. Asib Nasim
UNICEF-Bangladesh

Louis H. Nel
University of Pretoria and South and East African Rabies Group (SEARG)

Patrick Mboya Nguku
Ministry of Health of Kenya

Adriana Pistol
Institute of Public Health Bucharest

José Prado
Ministry of Health of Ecuador

Nilufar Rakhmanova
PRO-MED-mail and Abt Associates, Uzbekistan

Gladys Ramirez
General Directorate of Epidemiology (DGE)

Narendra Singh
Secretariat of the Pacific Community

Guillermo Contreras Soza
Hospital Dr "Hernán Henríquez Aravena"

Tipprapa Tansirisithikul
Thailand Ministry of Public Health

Laxmi Bikram Thapa
Ministry of Health and Population of Nepal

Pedro F. Vasconcelos
Evandro Chagas Institute

Exhibitors

Be sure to spend time visiting the exhibits, located in the Grand Hall.

Exhibits are open:

Sunday, March 16 . . . . . 7:00 PM – 9:00 PM

Monday, March 17 . . . . . 12:00 noon – 6:00 PM

Tuesday, March 18 . . . . . 12:00 noon – 6:00 PM

Wednesday, March 19 . . . . 10:00 AM – 1:00 PM

Applied Maths, Inc. . . . . Booth #504

13809 Research Blvd.
Suite 645
Austin, TX 78750
www.applied-maths.com

Applied Maths develops innovative software solutions for the biosciences. Areas of specialization are pattern matching algorithms, clustering and identification methods, and data mining tools for massive datasets such as sequences, microarrays and gene chips. Since 1991, Applied Maths has set the trend for the analysis of fingerprints with the renowned GelCompar package. Today the company continues to be a pioneer in bioinformatics, with BioNumerics, GelCompar II, GeneMathsXT, and Kodon.

ASM Press . . . . . Booth #704

1517 King George Blvd
Ann Arbor, MI 48104
estore.asm.org

ASM Press, the book publishing division of the American Society for Microbiology, will be exhibiting a selection of texts, references, and general interest titles at the meeting. Be sure to stop by the ASM press booth to see all the new offerings and classic titles in the microbiological sciences. ASM Press offers a 10% discount on all purchases made at the meeting.

Auxilium Pharmaceuticals, Inc. . . . . Booth #703

40 Valley Stream Pkwy.
Malvern, PA 19355
www.auxilium.com

BEI Resources . . . . . Booth #702

10801 University Blvd.
Manassas, VA 20110
www.beiresources.org

The Biodefense and Emerging Infections Research Resources Repository (BEI Resources) was established by NIAID to provide reagents for studying Category A, B, & C priority pathogens and emerging infectious disease agents to facilitate research and product development. BEI Resources is managed under contract by ATCC to acquire, generate, authenticate, store, and distribute these materials to the scientific community.

Biosearch Technologies . . . . . Booth #603

81 Digital Drive
Novato, CA 94949
www.biosearchtech.com

Centers for Disease Control & Prevention . . . . . Booth #710

4770 Buford Highway
Atlanta, GA 30341
www.cdc.gov

Centers for Disease Control & Prevention – Clinician Communication Team . . . . . Booth #709

1600 Clifton Road
Atlanta, GA 30333
www.emergency.cdc.gov/coca

The Clinician Communication Team works with subject matter experts to develop, review and update emergency preparedness content for clinicians. We develop and maintain mechanisms to encourage two-way communication between the clinician community and CDC. We help maintain and advance CDC's emergency preparedness and response capacity at the federal, state, local and international levels.

Centers for Disease Control and Prevention – Coordinating Center for Infectious Diseases . . . . Booth #304

1600 Clifton Road, MS E-05
Atlanta, GA 30333
www.cdc.gov

Centers for Disease Control and Prevention – National Center for Immunization and Respiratory Diseases . . . . . Booth #711

1600 Clifton Road, MS C-23
Atlanta, GA 30333

DiagnosisONE, Inc. . . . . Booth #605

61 Spit Brook Road
Nashua, NH 03060
www.diagnosisone.com

Exhibitors *continued*

US Department of Defense – Global Emerging Infections System . . . . . Booth #310

2900 Linden Lane
Silver Spring, MD 20910
www.geis.fhp.osd.mil

The mission of the DoD-GEIS is to serve force health protection by countering the largest threat to the health of the force, infectious disease. DoD-GEIS conducts surveillance and response to emerging infectious diseases within the military and in foreign civilian populations through the long-standing DoD overseas medical research laboratories. In FY06 GEIS was directed to administer additional congressional supplemental funding for pandemic influenza. With this funding, GEIS has implemented long-term initiatives to increase influenza surveillance, laboratory support, and communication.

European Centre for Disease Prevention & Control . . . . . Booth #708

Tomtebodavagen 11 A
Stockholm, SE-17183
Sweden
www.ecdc.europa.eu

Germfree Labs, Inc. . . . . Booth #502

11 Aviator Way
Ormond Beach, FL 32174
www.germfree.com

Germfree Labs, Inc. manufactures primary and secondary containment equipment found in BSL laboratories with our focus being on Class III BSC and transfer carts. Germfree's product line includes turnkey mobile and modular laboratories in which we retain manufacturing control of all critical primary and secondary containment equipment allowing us to provide a completely integrated laboratory of the highest quality.

IBIS Biosciences Inc. . . . . Booth #609

1896 Rutherford Road
Carlsbad, CA 92008
www.ibisbiosciences.com

International Association of National Public Health Institutes, Emory University . . . . . Booth #308

The Dental School Building
1462 Clifton Rd., NE
Room 446
Atlanta, GA 30322
www.ianphi.org

International Society for Infectious Diseases . . . Booth #611

1330 Beacon Street
Suite 228
Brookline, MA 02446
www.isid.org

The ISID is an educational nonprofit organization with over 10,000 members worldwide. ISID promotes exchange among those in infectious diseases through international scientific meetings, fellowships, grants, a newsletter, and the *International Journal of Infectious Diseases*. ISID staff will be available to provide information about the Society and its activities.

International Society of Travel Medicine . . . . . Booth #411

2386 Clower Street
Suite A102
Snellville, GA 30078
www.istm.org

The International Society of Travel Medicine (ISTM) is committed to the promotion of healthy and safe travel. In cooperation with national and international healthcare providers, academic centers, the travel industry and the media, ISTM advocates and facilitates education, service, and research activities in the field of travel medicine.

Logical Images, Inc.. . . . . Booth #510

3445 Winton Place
Suite 240
Rochester, NY 14623
www.logicalimages.com

VisualDx improves clinicians' capability to evaluate patients presenting with a potential infectious disease. Not only for common conditions, VisualDx merges medical images with actionable text for quick and accurate diagnoses of bioterrorism, infectious diseases, and travel-related infections within each differential. Health alerts and reporting capabilities provide immediate access to information, helping to control and create awareness of emerging infectious diseases.

National Institute of Allergy & Infectious Diseases . . . . . Booth #705

1000 Thomas Jefferson St., NW
Washington, DC 20007
www.niaid.nih.gov

OIE (World Organization for Animal Health). . . . . Booth #302

12 ave de Prony
Paris, 75017
France
www.oie.int

Exhibitors *continued*

Prodesse . . . . . **Booth #615**

PO Box 658
Townsend, TN 37882-0658
www.prodesse.com

A leading provider of "Real Time Solutions," Prodesse manufactures real time PCR reagents that labs worldwide have used for infectious disease pathogens. Prodesse's FDA-cleared ProFlu+™ Assay is a multiplex assay that detects and differentiates influenza A, influenza B and RSV. In clinical trials, it detected 46% more positives than culture. Additional products are CE Marked, and clinical trials for three new products are scheduled and/or under way for 2008.

Public Health Foundation . . . . . **Booth #508**

1300 L Street, NW
Suite 800
Washington, DC, DC 20005
www.phf.org

The Public Health Foundation (PHF) is a national, nonprofit organization working to improve the public health community by providing information, training, and technical assistance to the nation's public health systems. PHF will display resources on travelers' health and on the prevention of MRSA, pandemic influenza, and other infectious diseases.

Sequenom, Inc. . . . . . **Booth #403, 405**

3595 John Hopkins Court
San Diego, CA 92121
www.sequenom.com

Tetracore . . . . . **Booth #409**

9901 Besward Campus Drive
Suite 300
Rockville, MD 20850
www.tetracore.com

Affiliated Events *by invitation only*

WHO Global Salm-Surv Strategic Planning Meeting	**Saturday, March 15** **8:00 AM – 5:00 PM** **Regency VI**
Infectious Disease Prevention & Control Workgroup Meeting	**Sunday, March 16** **7:00 AM – 4:30 PM** **Hanover F**
ACVECC Postgraduate Review Course 2008: Infectious Disease in the Critically Ill Veterinary Patient	**Sunday, March 16** **8:00 AM – 5:00 PM** **Hanover C**
International Circumpolar Surveillance Steering Committee Meeting	**Sunday, March 16** **9:00 AM – 3:00 PM** **Hanover B**
GRaPH-INT Bioportal Beta Testing and Networking Event	**Sunday, March 16** **2:00 PM – 5:00 PM** **Hanover D**
GDD Business Meeting	**Sunday, March 16** **3:00 PM – 7:00 PM** **Hanover E**
WHO Global Salm-Surv & Foodborne Disease Burden Epidemiology Reference Group Reception (by invitation only)	**Tuesday, March 18** **6:00 PM – 8:00 PM** **Hanover C/D**
Influenza Division International Field Staff Teams	**Wednesday, March 19** **4:30 PM – 7:00 PM** **Hanover C/D**

Scientific Program

Sunday, March 16

Scientific Sessions

Opening Keynote Session

5:00 PM – 7:00 PM | Centennial Ballroom

Moderator:

MITCHELL COHEN, Director
Coordinating Center for Infectious Diseases
Centers for Disease Control and Prevention, Atlanta, GA

Introductions

JULIE GERBERDING, Director, Centers for Disease Control and Prevention, Atlanta, GA

Public Health Security in the 21st Century: Working Together under the International Health Regulations
DAVID HEYMANN, Assistant Director-General for Health Security and Environment, World Health Organization, Geneva, Switzerland

Overcoming Poverty and Improving Global Health: Strategies that Work
HELENE GAYLE, President/CEO, CARE, Atlanta, GA

Opening Reception

7:00 PM – 8:00 PM | Grand Hall

Monday, March 17

Poster Set-up for the Day

7:30 AM – 8:30 AM

All posters presented on Monday will be available for viewing in the Grand Hall from 12:00 noon to 6:00 PM. Authors will be present at posters for one hour as noted under the Scientific Sessions schedule for the day.

Scientific Sessions

A1 Concurrent Plenary Session

8:30 AM – 10:10 AM | Centennial I

One Medicine/One Health

8:30 AM - 9:15 AM

Moderator:

NINA MARANO, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

One World, One Health, One Medicine
RONALD DAVIS, American Medical Association, Chicago, IL
ROGER MAHR, American Veterinary Medical Association, St. Charles, IL

Foodborne Illness & Plants/Produce

9:25 AM - 10:10 AM

Moderator:

JOHN DUNN, Tennessee Department of Health, Nashville, TN

Speaker:

The Ecology of Enteric Pathogens on Produce: Life Away from Home
MARIA BRANDL, US Department of Agriculture, Albany, CA

A2 Concurrent Plenary Session

8:30 AM – 10:10 AM | Centennial II

Antimicrobial Resistance

8:30 AM - 9:15 AM

Moderator:

CLIFFORD MCDONALD, Centers for Disease Control and Prevention, Atlanta, GA

Speaker:

For the Duration: Rational Antibiotic Administration in an Era of Antimicrobial Resistance and *Clostridium difficile*
LOUIS RICE, Case Western Reserve University, Cleveland, OH

XDR TB

9:25 AM - 10:10 AM

Moderator:

CAROL CHENOWETH, University of Michigan Health Systems, Ann Arbor, MI

Speaker:

Lessons from MDR TB in the United States: Application to Global XDR TB Response
KEN CASTRO, Centers for Disease Control and Prevention, Atlanta, GA

A3 Concurrent Plenary Session

8:30 AM – 10:10 AM | Centennial III

Global Infectious Disease Disparities & Poverty

8:30 AM - 9:15 AM

Moderator:

MARIAN MCDONALD, Centers for Disease Control and Prevention, Atlanta, GA

Speaker:

Global Infectious Diseases and Poverty
DAVID SATCHER, Center of Excellence on Health Disparities, Atlanta, GA

Novel Surveillance Systems

9:25 AM – 10:10 AM

Moderator:

MICHAEL ST. LOUIS, Centers for Disease Control and Prevention, Atlanta, GA

Speaker:

Emerging Threats: Can We Predict and Prevent Them?
LARRY BRILLIANT, Google.org, Mountain View, CA

Break

10:10 AM – 10:30 AM | Centennial Ballroom Foyer

B1 Concurrent Panel Session

Respiratory Disease Outbreaks

10:30 AM – 12:00 PM | Centennial I

Conveners:

JOEL GAYDOS, US Department of Defense, Silver Spring, MD
TRUDY MURPHY, Centers for Disease Control and Prevention, Atlanta, GA
ABIGAIL SHEFER, Centers for Disease Control and Prevention, Atlanta, GA

Moderator:

LARRY ANDERSON, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Recent Outbreaks of Emerging Respiratory Pathogens: Issues and Challenges
GREGORY GRAY, University of Iowa, Iowa City, IA

Novel Reassortant Influenza Viruses in US Pigs: A Potential Animal-Human Interface
AMY VINCENT, US Department of Agriculture, Ames, IA

Respiratory Disease Outbreaks: A Coordinated Approach to Investigations and Pathogen Identification
LAURI HICKS, Centers for Disease Control and Prevention, Atlanta, GA

B2 Concurrent Panel Session

Infectious Disease Ecologies

10:30 AM – 12:00 PM | Centennial II

Conveners:

JOHN DUNN, Tennessee Department of Health, Nashville, TN
KATE GLYNN, Centers for Disease Control and Prevention, Atlanta, GA
ALEJANDRO THIERMANN, World Organization for Animal Health, Paris, France

Moderators:

ALEJANDRO THIERMANN, World Organization for Animal Health, Paris, France
KATE GLYNN, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Niche Adaptation by *Serratia marcescens*: A Versatile Enterobacterial Pathogen of Many Hosts
JACQUELINE FLETCHER, Oklahoma State University, Stillwater, OK

Changing Ecology of Vectorborne Diseases and Possible Predictability
STEPHANE DE LA ROCQUE, Food and Agriculture Organization, Rome, Italy

Established and Novel Transmission of Chagas Disease from Vectorborne to Orally Acquired
RICARDO MARINS, Ministry of Health, Brazil

B3 Concurrent Panel Session

HIV

10:30 AM – 12:00 PM | Regency VI

Conveners:

ROBERT CHEN, Centers for Disease Control and Prevention, Atlanta, GA
MARY LOU LINDEGREN, Centers for Disease Control and Prevention, Atlanta, GA

Moderators:

DAWN SMITH, Centers for Disease Control and Prevention, Atlanta, GA
BHARAT PAREKH, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Emerging Biomedical Modalities for the Prevention of HIV Transmission
PETER KILMARX, Centers for Disease Control and Prevention, Atlanta, GA

Strategies for National HIV Incidence Surveillance
THOMAS REHLE, Human Sciences Research Council, Cape Town, South Africa

Global Monitoring of HIV Resistance
DIANE BENNETT, World Health Organization, Geneva, Switzerland

B4 Concurrent Panel Session

Globally Mobile Populations & EIDs

10:30 AM – 12:00 PM | Regency VII

Conveners:

LIN CHEN, Harvard University, Boston, MA
NINA MARANO, Centers for Disease Control and Prevention, Atlanta, GA

Moderators:

LIN CHEN, Harvard University, Boston, MA
NINA MARANO, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Vaccine-Preventable Diseases and Mobile Populations
MARTY CETRON, Centers for Disease Control and Prevention, Atlanta, GA

Health Screening of Refugees to Detect Emerging Diseases
PATRICIA WALKER, University of Minnesota, St. Paul, MN

Travelers Visiting Friends and Relatives
JAY KEYSTONE, University of Toronto, Toronto, Ontario

B5 Concurrent Panel Session

Health & Risk Communication

10:30 AM – 12:00 PM | Centennial III

Conveners:

HEATHER BAIR-BRAKE, Centers for Disease Control and Prevention, Atlanta, GA
ABBIGAIL TUMPEY, Centers for Disease Control and Prevention, Atlanta, GA

Moderator:

ABBIGAIL TUMPEY, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Emergency Risk Communications in Rural Populations: Lessons from Rift Valley Fever in Kenya, 2007
EMILY ZIELINSKI-GUTIERREZ, Centers for Disease Control and Prevention, Fort Collins, CO

Grassroots to Global: Successes and Challenges of the Inaugural World Rabies Day Campaign
PETER COSTA, Alliance for Rabies Control, Manhattan, KS

Integrated Approaches to Risk and Crisis Communication
MATTHEW SEEGER, Wayne State University, Detroit, MI

B6 Concurrent Panel Session

Surveillance Role in Detection & Control

10:30 AM – 12:00 PM | Centennial IV

Conveners:

THOMAS GOMEZ, US Department of Agriculture, Atlanta, GA
LARRY MADOFF, Harvard Medical School, Boston, MA

Moderators:

THOMAS GOMEZ, US Department of Agriculture, Atlanta, GA
LARRY MADOFF, Harvard Medical School, Boston, MA

Speakers:

CDC Global Disease Detection Program
SCOTT DOWELL, Centers for Disease Control and Prevention, Atlanta, GA

Informal Information Sources in Emerging Disease Surveillance
MARJORIE POLLACK, ProMED, Brooklyn, NY

Global Early Warning System for Major Animal Diseases, including Zoonoses (GLEWS)
JENNIFER BISHOP, World Health Organization, Geneva, Switzerland

Integrated Disease Surveillance Project of India
SHIV LAL, National Institute for Communicable Diseases, Delhi, India

Lunch *(on your own)*

Poster Session I with Authors

12:00 PM – 1:00 PM | Exhibit Hall

Director's Tour of Posters

RIMA KHABBAZ, Director
National Center for Preparedness, Detection, and Control of Infectious Diseases
Coordinating Center for Infectious Diseases
Centers for Disease Control and Prevention, Atlanta, GA

Vaccines & Vaccine-Preventable Diseases

Board 1: Genetic Diversity and Zoonotic Potential of Human Rotavirus Strains – Hungary 2003-2006

Board 2: Study on Protective Effects for 10 Years after Vaccinated by Vaccines against Hemorrhagic Fever with Renal Syndrome

Board 3: Effectiveness of the 2007-2008 Influenza Vaccine: Preliminary Data from US Military Basic Training Centers

Board 4: Circulation of Type 2 Vaccine-Derived Poliovirus in Nigeria from 2005

Board 5: Opportunities for Prevention of Invasive Pneumococcal Disease among Adults with Diabetes

Antimicrobial Resistance

Board 6: *Salmonella enterica* serovar Heidelberg from Retail Meats: Results of the National Antimicrobial Resistance Monitoring System (NARMS) – 2002-2006

Board 7: Community-Associated Methicillin-Resistant *Staphylococcus aureus* Infection Risk Factor Study

Board 8: Antimicrobial Resistance in *Salmonella* Serotype Schwarzengrund from Human and Retail Poultry Isolates in the United States

Board 9: Multi-Resistant Isolates of *Salmonella* Enteritidis from the Russian Federation

Board 10: Surveillance of Antimicrobial Resistance at the Louisiana Animal Disease Diagnostic Laboratory: The LARSS (LADDL/OPH) Antimicrobial Resistance Surveillance System

Climate Changes

Board 11: Climate Change and the Prediction of Infectious Disease

Foodborne & Waterborne Infections

Board 12: Trends in Toxin Profiles of Human Shiga Toxin-Producing *Escherichia coli* (STEC) O157 Strains, United States, 1999-2006

Board 13: Risk Factors for Shiga Toxin-Producing *Escherichia coli* O157 Infection in Australia

Board 14: Travel-Associated Legionnaires' Disease Cases in the United States

Board 15: Multidrug-Resistant *Salmonella concord* in Adoptee from Ethiopia

Board 16: Analysis of Three Outbreaks of Acute Gastroenteritis Caused by Norovirus between September and November 2006 in Yuhang District Hangzhou City, China

Board 17: Understanding Foodborne Disease Outbreaks Using Environmental Assessments

Board 18: Human Health Burden of Acute Diarrheal Illness in the United States, FoodNet Population Survey, 2006-2007

Board 19: *Salmonella* Bacteriuria in New York StateFoodNet Counties, 2002-2006

Board 20: Foodborne Botulism Associated with Commercial Food in the State of São Paulo, Brazil, 1997-2007

Board 21: Fresh Produce Outbreaks in Australia, 2001-2006

Health Communication

Board 22: Using Technology for Bidirectional Communication with Clinicians on Emergency Preparedness and Response Topics

Board 23: A School-Based Health Promotion Project for Mosquitoborne Disease Prevention in Children

Board 24: Health Marketing: A Tool for Expanding Global Health Partnerships

Board 25: Not Ready, But Willing: Knowledge and Attitudes Regarding Avian Influenza in Kanchanaburi, Thailand

Board 26: China-United States Collaborative Program on Emerging and Reemerging Infectious Diseases: The Construction and Development of Online Knowledge Center of Infectious Disease for Public on National 12320 Public Health Hotline Website of China

Infectious Causes of Chronic Diseases

Board 27: Prevalence of *Helicobacter pylori* Infection in 90 Patients Undergoing Diagnostic Upper Endoscopy – Republic of Georgia, 2003-2005

Board 28: Long-term Recovery Status of West Nile Virus Patients – Utah County, Utah

Board 29: Significant Increase in Guillain-Barré Syndrome Following Sustained Campylobacteriosis Epidemic in New Zealand

Influenza

Board 30: Influenza Pandemic Planning among South Pacific Nations: A Critical Review of Available Plans from a Border Control Perspective

Board 31: Potential Value of Multiple Border Control Interventions to Prevent Pandemic Influenza in Island Settings

Board 32: Seroprevalence of Influenza H1 and H3 Antibody among US Military Accessions

Board 33: Likely Effectiveness of Quarantine for Pandemic Influenza Control at the Borders of Island Countries

Board 34: Age-Specific Hospitalization Rates Associated with Influenza and Respiratory Syncytial Virus (RSV) in the United States, 1989-2005

Board 35: Assessing County Health Department Employees: Willingness to Respond to an Influenza Pandemic

Board 36: Fatal Laboratory-Confirmed Human Influenza Infections in Thailand Identified by the National Avian Influenza Surveillance Program during 2004-2006

Board 37: Use of Rapid Influenza Testing and Antiviral Agent Prescribing Practices Among Primary Care Physicians in Selected Geographical Areas – Connecticut, Minnesota, New Mexico, New York, 2006-2007

New or Rapid Diagnostics

Board 38: Novel Method and Medium for Detecting and Identifying both Methicillin-Susceptible (MSSA) and Methicillin-Resistant (MRSA) *Staphylococcus aureus*

Board 39: Development of a Possible Screening Method for the Detection of Norovirus in Stool Samples

Board 40: Rapid Detection of Animal Pathogens for Global Disease Surveillance

Board 41: Establishment and Application of a Real-Time RT PCR for the Detection of Human Metapneumovirus in Children with Lower Respiratory Tract Infection in Taiwan

Board 42: An Integrated Molecular Platform for Detection, Isolation, and Molecular Serogrouping of Shiga Toxin-producing *Escherichia coli* (STEC)

Nosocomial Infections

Board 43: Cluster of Hepatitis B Infection Among Residents of an Assisted Living Facility – New York, 2007

Board 44: A Massive, Multi-Hospital Outbreak of Surgical Infections Caused by a Rapidly Growing Mycobacterium Previously Unreported in Brazil – Rio de Janeiro, Brazil, 2007.

Board 45: Is the Epidemic Strain of *Clostridium difficile* NAP1 Responsible for Community-Acquired CDAD?

Outbreak Investigation: Lab & Epi Response

Board 46: Building Partnerships to Improve Outbreak Preparedness: the Establishment of an Emergency Vaccine Stockpile for Meningitis Epidemics

Board 47: A Legionnaires' Disease Outbreak Linked to Roof-Collected Rainwater Systems in New Zealand

Board 48: Identification of the Sources of Periodic Epidemics that Maintain the Cholera Bacteria in Ajegunle and Amukoko Districts (Ajeromi/Ifelodun Local Government Area - LGA) in Lagos State, Nigeria

Sexually Transmitted Diseases

Board 49: Prevalence of Sexually Transmitted Diseases and High Risk Behaviors among Female Sex Workers in Indonesia

Surveillance: International & New Strategies

Board 50: Differences in the Clinical Presentation of Confirmed Arboviral Infection in South America

Board 51: Systematic Review of Surveillance Systems for Emerging Zoonotic Diseases

Board 52: Development of Influenza Surveillance Networks in Korea

Board 53: Adherence to Perinatal Group B *Streptococcus* Prevention Guidelines – New York State, 2003-2004

Board 54: Healthcare Utilization Practices for Influenza-like Illness and Severe Acute Respiratory Infection in Guatemala; Implications for Influenza Surveillance

Board 55: Impact of Phone Calls or Supervision Visits on Timeliness and Data Quality in an Electronic Disease Surveillance System in a Resource Limited Setting – Peru

Board 56: Usefulness of Household-based Surveillance for Childhood Pneumonia in Rural Kenya

Travelers' Health & Diseases Importation

Board 57: Cutaneous Anthrax Associated with Drum-Making by Using Goat Hides from West Africa – Connecticut, 2007

Board 58: Screening for Influenza Infection in International Airline Travelers Arriving in New Zealand

Board 59: World Health Organization (WHO) Travel Recommendations During the 2003 SARS Outbreak: Lessons Learned for Mitigating Influenza Pandemic and Globally Emerging Infectious Diseases

Tropical Infections & Parasitic Diseases

Board 60: High Complexity of the Glutathione Transferases Class III Gene in Malaria Vector *Anopheles gambiae*

Board 61: Molecular Profile of Drug-Resistant Mutations Associated with Pfcrt and Pfmdr-1 Genes in *Plasmodium falciparum* Isolates from a Malaria Endemic Region of Venezuela

Board 62: Outbreak of Suspected Brazilian Purpuric Fever in Children with Antecedent Conjunctivitis – Para State, Brazil, 2007

Board 63: Risk Factors for the High Mortality Observed in Visceral Leishmaniasis Patients Treated with Liposomal Amphotericin-B – Brazil, 2005-2006

Vectorborne Diseases

Board 64: Precipitous Increase in the Incidence of Dengue Hemorrhagic Fever in Children: A New Challenge to Public Health in Brazil

Board 65: Evaluation of Five Formulations of *Bacillus thurigiensis* for Dengue Control in the Municipality of Joo Pessoa – PB

Board 66: Primary Investigation on Arbovirus Distribution in China

Board 67: Surveillance for Yellow Fever and other Arboviruses in Free-Ranging Primates in Southern Brazil: An Important Tool for Emerging Diseases Detection

Board 68: An Outbreak of Sylvatic Yellow Fever in Persons Who Had Refused Vaccination in a Yellow Fever Endemic Region – Brazil, 2007

Women, Gender, Sexual Minorities & Infectious Diseases

Board 69: The Validation of a West Nile Virus Survey among Women Living in the Deep South Region of the United States

Zoonotic & Animal Diseases

Board 70: Efficacy of Chloramphenicol in the Treatment of a Hamster Model of Acute Leptospirosis

Board 71: Human Monkeypox in Sudan: Endemic or Introduced?

Board 72: Mycoplasma Species Isolated from California Sea Lions (*Zalophus californianus*)

Board 73: Contrasting the Epidemiology of Evolutionarily Independent Strains of Rabies in a Common Host Species

C1 Slide Session

Foodborne and Waterborne Diseases I

1:15 PM – 2:45 PM | Centennial I

1:15 – 1:30 PM
Outbreaks Associated with Frozen, Stuffed, Pre-Browned, Microwaveable Chicken Entrees in Minnesota: Implications for Labeling and Regulation
CARLOTA MEDUS, Minnesota Department of Health

1:30 – 1:45 PM
A Point-Source Outbreak of Guillain-Barré Syndrome (GBS) Associated with Consumption of City Water – Shuang Yang District, Changchun, Jinlin, China, 2007
RUAN FENG, Chinese Field Epidemiology Training Program (CFETP)

1:45 – 2:00 PM
Oyster-Associated *Vibrio* Infections in the United States, 1998-2006
MARTHA IWAMOTO, Centers for Disease Control and Prevention

2:00 – 2:15 PM
Large Outbreak of Beriberi Possibly Related to Consumption of Mycotoxin-Contaminated Rice, Maranhao, Brasil, 2007
HELENA LIMA, Field Epidemiology Training Program, SVS, Brazilian Ministry of Health

2:15 – 2:30 PM
Salmonella Montevideo Infections Associated with Exposure to Poultry from Mail-Order Hatcheries - United States, 2007
UMID SHARAPOV, Centers for Disease Control and Prevention

2:30 – 2:45 PM
An Investigation Points Towards Contaminated Mud as the Source of a *Campylobacter jejuni* Outbreak Associated with a Mountain Bike Race – British Columbia, Canada, June-July 2007
TAMMY STUART, Canadian Field Epidemiology Program, Public Health Agency of Canada (PHAC)

C2 Slide Session

Influenza I

1:15 PM – 2:45 PM | Centennial II

1:15 – 1:30 PM
Influenza Testing Practices in the Emergency Department: Correlation with Laboratory-Confirmed Influenza Hospitalization Rates, Emerging Infections Program, 2006-2007 Influenza Season
MARK MUELLER, New Mexico Department of Health

1:30 – 1:45 PM
The Burden of Human Influenza in East and Southeast Asia: A Review of the Scientific Literature
JAMES SIMMERMAN, Centers for Disease Control and Prevention

1:45 – 2:00 PM
A Comparison of Clinical and Epidemiological Characteristics of Human Infections with H5N1 Versus Human Influenza Viruses in Thailand, 2004-2006
VIVEK SHINDE, Centers for Disease Control and Prevention

2:00 – 2:15 PM
Comparison of Robust Regression Models for Estimating Influenza-Associated Deaths Using the CDC 122 Cities Mortality Reporting Systems Data
PO-YUNG CHENG, Centers for Disease Control and Prevention

2:15 – 2:30 PM
Emerging Trends in Adamantane Resistance: 2006-2007 Influenza Season
VAROUGH DEYDE, Centers for Disease Control and Prevention

2:30 – 2:45 PM
High Prevalence of Influenza in Hospital Surveillance in Bangladesh
RASHID ZAMAN, ICDDR,B

C3 Slide Session

Surveillance: International

1:15 PM – 2:45 PM | Centennial IV

1:15 – 1:30 PM
Etiology of Encephalitis in England: An Ongoing Multi-Center Prospective Study
JULIA GRANEROD, Health Protection Agency

1:30 – 1:45 PM
Active Population-Based Surveillance for Emerging Infectious Diseases in Resource-Limited Settings: An Evaluation of Pneumonia Surveillance in Thailand
OLIVER MORGAN, Centers for Disease Control and Prevention

1:45 – 2:00 PM
Epidemiology and Incidence of Viral Severe Pneumonia in Population-Based Surveillance among Children Younger than Five Years in Rural Western Kenya, 2006-2007
MAURICE OPE, Centers for Disease Control and Prevention

2:00 – 2:15 PM
Global Surveillance for Infectious Disease Deaths in Active Duty US Military Personnel
ROBERT POTTER, Office of the Armed Forces Medical Examiner

2:15 – 2:30 PM
International Circumpolar Surveillance of Invasive Non-Typeable *Haemophilus influenzae*, 2000-2006
TAMMY ZULZ, Centers for Disease Control and Prevention

2:30 – 2:45 PM
Forecast and Outbreak of Rift Valley Fever in Sudan, 2007
ASSAF ANYAMBA, NASA Goddard Space Flight Center

C4 Slide Session

Zoonotic & Animal Diseases I

1:15 PM – 2:30 PM | Centennial III

1:15 – 1:30 PM
Investigating Disease Emergence from Wildlife — A Transdisciplinary Approach
HUME FIELD, Biosecurity Queensland

1:30 – 1:45 PM
Anticipating the Next Monkeypox: Trends in Rodent Importation, 1999-2006
BETSY SCHROEDER, Centers for Disease Control and Prevention

1:45 – 2:00 PM
Risk Factors for Brucellosis in Siziwang County, Inner Mongolia, China, 2007
YIN WENWU, Chinese Center for Disease Control and Prevention

2:00 – 2:15 PM
A Fatal Case of Inhalation Anthrax in Scotland Associated with West African Goat Skin Drums
COLIN RAMSAY, Health Protection Scotland

2:15 – 2:30 PM
Oral Rabies Vaccination: Implications for Zoonosis Prevention, Control, and Elimination
DENNIS SLATE, US Department of Agriculture, Animal and Plant Health Inspection Service, Wildlife Services

C5 Slide Session

Methicillin-Resistant Staphylococcal Infections

1:15 PM – 2:30 PM | Regency VI

1:15 – 1:30 PM
Trends in Invasive Infection with Methicillin-Resistant *Staphylococcus aureus* (MRSA) in Connecticut, 2001-2006
SUSAN PETIT, Connecticut Department of Public Health

1:30 – 1:45 PM
Short-Term Mortality Associated with Methicillin-Resistant and Methicillin-Susceptible *Staphylococcus aureus* Infections among Veterans Administration Medical Center (VAMC) Patients
CATHERINE LEXAU, Minnesota Department of Health

1:45 – 2:00 PM
Transmission of Methicillin-Resistant *Staphylococcus intermedius* between Animals and Humans
ENGELINE VAN DUIJKEREN, Faculty of Veterinary Medicine, Utrecht University

2:00 – 2:15 PM
Community-Associated (CA) Methicillin-Resistant *Staphylococcus aureus* (MRSA) in Affected Households: Prevalence of Colonization and Incidence of Subsequent Infections
JESSICA BUCK, Minnesota Department of Health

2:15 – 2:30 PM
Detection of Community-Acquired Methicillin-Resistant *Staphylococcus aureus* Associated with Nosocomial Infections
SANDRA TALLENT, Virginia Division of Consolidated Laboratory Services

C6 Slide Session

Vectorborne Diseases

1:15 PM – 2:45 PM | Regency VII

1:15 – 1:30 PM
Long-Term Clinical Sequelae and Rates of Recovery Following Infection with West Nile Virus
KRISTY MURRAY, University of Texas Health Science Center at Houston

1:30 – 1:45 PM
The Changing Epidemiology of Malaria in Brazil: National Surveillance Data and Environmental Correlates, 1990-2006
ANA CAROLINA SANTELLI, Brazilian Ministry of Health

1:45 – 2:00 PM
Pneumonic Plague Mortality and Transmission Potential in the United States
ALISON HINCKLEY, Centers for Disease Control and Prevention

2:00 – 2:15 PM
Molecular and Epidemiologic Analysis of *Francisella tularensis* subsp. tularensis A I and A II in Humans and Animals
KIERSTEN KUGELER, Centers for Disease Control and Prevention

2:15 – 2:30 PM
Clinical Features of Zika Virus Infection During an Outbreak on Yap Island, Federated States of Micronesia, 2007
TAI-HO CHEN, Centers for Disease Control and Prevention

2:30 – 2:45 PM
Japanese Encephalitis in Bangladesh
M. JAHANGIR HOSSAIN, ICDDR,B

Break

2:45 PM – 3:00 PM | Centennial Ballroom Foyer/Regency Foyer

D1 Slide Session

Foodborne & Waterborne Diseases II

3:00 PM – 4:30 PM | Centennial I

3:00 – 3:15 PM
Prognosis of Salmonellosis and Brucellosis: One-Year Follow-Up of a Population-Based Surveillance in Fayoum Governorate, Egypt
SALMA AFIFI, US Naval Medical Research Unit #3

3:15 – 3:30 PM
Analysis of *Listeria* Case Report Forms among Non-Pregnant Cases: FoodNet Sites, 2004-2006
SHARON M. HURD, Yale University, Connecticut Emerging Infections Program

3:30 – 3:45 PM
The Impact of Sodium Dichloroisocyanurate Treatment on Household Drinking Water Quality and Health in Peri-Urban Ghana: A Randomized Placebo-Controlled, Double-Blinded Trial
ELIZABETH BLANTON, Centers for Disease Control and Prevention

3:45 – 4:00 PM
Foodborne Disease Outbreaks Associated with Leafy Greens, 1973-2006
KAREN HERMAN, Centers for Disease Control and Prevention

4:00 – 4:15 PM
Eight Years of National Botulism Surveillance in Brazil: What We Know Now
GREICE CARMO, EPISUS/COVEH, Secretariat of Health Surveillance, Brazilian Ministry of Health

4:15 – 4:30 PM
Prevalence of Noroviruses in Hospitalized Kenyan Children: Comparison of Real-Time RT-PCR and Enzyme-Linked Immunoassays
MARC WIDDOWSON, Centers for Disease Control and Prevention

D2 Slide Session

Influenza II

3:00 PM – 4:30 PM | Centennial II

3:00 – 3:15 PM
Swine Influenza in a Child with Remote Exposure – Iowa, 2006
DEBORAH DUFFICY, Centers for Disease Control and Prevention

3:15 – 3:30 PM
Pandemic Influenza in the Australian Army of World War I
G. SHANKS, Army Malaria Institute

3:30 – 3:45 PM
Pandemic Influenza Policy Model, a Web-Based Tool for Military Planners
BRIAN FEIGHNER, Johns Hopkins University, Applied Physics Laboratory

3:45 – 4:00 PM
Case Report: Dual Infection of H5N1 Avian Influenza and H3N2 Human Influenza in Jakarta, Indonesia, April 2007
VIVI SETIAWATY, Center for Biomedical and Pharmaceutical Research and Development

4:00 – 4:15 PM
Pilot Findings of a Cluster Randomized Trial of Non-Pharmaceutical Interventions for Influenza Prevention in Households in Hong Kong
BENJAMIN COWLING, University of Hong Kong

4:15 – 4:30 PM
Initial Results from the First Comprehensive Influenza Surveillance Activity in Kenya
DAVID SCHNABEL, US Army Medical Research Unit, Kenya

D3 Slide Session

Surveillance: Domestic

3:00 PM – 4:30 PM | Centennial IV

3:00 – 3:15 PM
Incidence of Staphylococcal Toxic Shock Syndrome, 2000-2006
AARON DEVRIES, Minnesota Department of Health

3:15 – 3:30 PM
Rapid Identification of Divergent and Novel Viruses from Previously Untypable California State Department of Public Health Pathogen Surveillance Program Samples
JOSEPH VICTORIA, Blood Systems Research Institute

3:30 – 3:45 PM
Surveillance for Community-Onset *Clostridium difficile*, Connecticut, 2006
THERESE RABATSKY-EHR, Connecticut Department of Public Health

3:45 – 4:00 PM
Correlation of Anti-Influenza Prescription Data to U.S. Sentinel Provider Surveillance Network Data
CRAIG HALES, Centers for Disease Control and Prevention

4:00 – 4:15 PM
Variation in Seasonality among *Salmonella* Serotypes Isolated in Georgia
DANA COLE, Georgia Division of Public Health

4:15 – 4:30 PM
Coccicioidomycosis Surveillance: Improving Assessment of Disease Burden
REBECCA SUNENSHINE, Arizona Department of Health Services and Centers for Disease Control and Prevention

D4 Slide Session

Zoonotic & Animal Diseases II

3:00 PM – 4:30 PM | Centennial III

3:00 – 3:15 PM
Risk Factors for Human Anthrax, Jalalabat and Osh Districts, Kyrgyzstan, August-October 2005
MICHAEL FAVOROV, Centers for Disease Control and Prevention, Central Asia Regional Office

3:15 – 3:30 PM
A Veterinary Curriculum in the Appropriate Use of Antibiotics
PAUL BARTLETT, Michigan State University

3:30 – 3:45 PM
The Emergence of Vaccinia Virus in Brazil
GILIANE TRINDADE, Centers for Disease Control and Prevention

3:45 – 4:00 PM
Methicillin-Resistant *Staphylococcus aureus* (MRSA) Infections among Pets in Minnesota
JEFFREY BENDER, University of Minnesota, Veterinary Public Health

4:00 – 4:15 PM
Risk Factors for Hantavirus Infection among Patients in Rural Areas and Application of Prevention Measures, Minais Gerais, Brazil, 2006
C. BORGES, EPICAMPO, Secretariat of Health of Minais Gerais

4:15 – 4:30 PM
Human Rabies Prophylaxis Due to Bat Attacks in Brazil, 2006
ADRIANA OLIVEIRA, Field Epidemiology Training Program, Secretariat of Health Surveillance, Ministry of Health

D5 Slide Session

Noscomial Infections

3:00 PM – 4:30 PM | Regency VI

3:00 – 3:15 PM
Clinical Severity of *Clostridium difficile* O27 Versus Non-O27 PCR Ribotypes: A Case-Case Study
OLIVER MORGAN, Health Protection Agency: East of England Regional Epidemiology Unit

3:15 – 3:30 PM
National Outbreaks of Mycobacterial Infections Following Fiberoptic-Guided Surgical Procedures, Brazil, 2003-2007
JOSE MELO, Field Epidemiology Training Program (EPISUS), Secretariat of Health Surveillance (SVS), Ministry of Health

3:30 – 3:45 PM
Limiting the Spread of Respiratory Infections in Kenyan Provincial Hospitals: A Report from the Field
CARRIE NGONGO, Centers for Disease Control and Prevention, Kenya

3:45 – 4:00 PM
Investigation of a Multidrug-Resistant *Acinetobacter baumannii* Outbreak - Phoenix, 2007
CYNTHIA LUCERO, Centers for Disease Control and Prevention

4:00 – 4:15 PM
Nosocomial Transmission of Newly Identified Adenovirus Serotype 14 in Healthcare Workers Caring for Patients with Severe Pneumonia - Oregon, 2007
PHILIP GOULD, Centers for Disease Control and Prevention

4:15 – 4:30 PM
Outbreak of Group A Streptococcal Infections in a Long-Term Care Facility – New York, 2006-2007
AMY BURNS, New York State Department of Health

D6 Slide Session–Late Breakers I

3:00 PM – 4:30 PM | Regency VII
See the program addendum for presentations in this session

Poster Session II with authors

5:00 PM – 6:00 PM | Exhibit Hall

Director's Tour of Posters

LONNIE KING, Director
National Center for Zoonotic, Vector-Borne, and Enteric Diseases
Coordinating Center for Infectious Diseases
Centers for Disease Control and Prevention, Atlanta, GA

Vaccines & Vaccine-Preventable Diseases

Board 74: **High Vaccination Coverage Prevented Large-Scale Measles Spread in Poland Following Ukrainian Epidemic in 2006-2007**

Board 75: **An Explosive Outbreak of Modified Measles Posing as a Rash Illness of Unknown Etiology in a High School – TaiYuan, Shanxi Province, China, 2007**

Board 76: Report of the National Rotavirus Strain Surveillance System – United States, 2005-2007

Board 77: *Pneumococcal meningitis* among Adults and Children in the Era of the Pneumococcal Conjugate Vaccine: An Update from Active Bacterial Core Surveillance (ABCs)

Board 78: Epidemiology of Meningococcal Disease in California, 2001-2007

Antimicrobial Resistance

Board 79: Antimicrobial Resistance in *Salmonella* Isolates Recovered from Cattle at Slaughter

Board 80: Prevalence of Antibiotic Use, Knowledge and Attitudes Toward Antibiotic-Free Meat

Board 81: Antimicrobial Resistance in *Salmonella* Serotypes Paratyphi A, Paratyphi B, Paratyphi C, and Paratyphi B var. L(+) Tartarte+ (Formerly Java), NARMS, January 1996 - March 2006

Board 82: First *Escherichia coli* Isolate Resistant to Amikacin and Nine Other Antimicrobial Subclasses, NARMS, 2004-2006

Board 83: Critical or Fatal Illness Due to Community-Associated *Staphylococcus aureus* (CA-SA) Infection – Minnesota, 2005-2007

Emerging Aspects of HIV

Board 84: An Analysis of Histoplasmosis in an Endemic, Resource Poor Area with a High HIV Prevalence Rate – Guatemala, 2007

Board 85: Handbook of Diagnosis, Treatment and Follow-Up Recommendations for *Trypanosoma cruzi*-HIV Co-infection

Board 86: Comparison of Survival after AIDS in Pre-HAART and HAART Eras Confirms High Population Effectiveness of Antiretroviral Treatment in Poland

Foodborne & Waterborne Infections

Board 87: Foodborne Disease Outbreak Trends and Sources and Timeliness of Detection in Connecticut – 2004-2007

Board 88: Indiana Outbreak of *Salmonella* I 4,[5],12:i:- monophasic at a Supermarket Deli - 2006

Board 89: Enhanced Laboratory Testing of Enteric Disease Outbreaks of Unknown Etiology in Minnesota

Board 90: Trends in Incidence of Frequently Identified Non-Typhoidal *Salmonella* Serotypes, Foodborne Diseases Active Surveillance Network, 1996-2006

Board 91: Estimating Underreporting of Foodborne Diseases to Australian Surveillance to Estimate Community Incidence

Board 92: The Prevalence of Reactive Arthritis Symptoms in the General Population, FoodNet Population Survey, 2006-2007

Board 93: Foodborne Disease Outbreaks in the State of São Paulo, Brazil, 1999-2007

Board 94: Rural Exposure to Shiga Toxin-Producing *Escherichia coli* – South Dakota, 1998-2007

Board 95: Tomato Handling Policies and Practices in Restaurants

Board 96: A Study on the State of Diarrhea and Contaminant Seafood Caused by Norovirus in China

Health Communication

Board 97: Community-Based Surveillance Models for Avian Influenza

Board 98: Asymptomatic Carriers of Typhoid Fever and Patient Care

Board 99: Public Health Situational Awareness and the Global Disease Surveillance Platform (GDSP)

Board 100: Individual and Community Influences on Adherence to Directives in the Event of Plague Attack

Influenza

Board 101: Unique Results from Febrile Respiratory Illness Surveillance aboard US Navy Ships

Board 102: Persistent Impairment of T lymphocyte Subset Function in Severe Acute Respiratory Syndrome Patients 2 Years after Discharge

Board 103: Detecting Reduced Susceptibility of Influenza A and B Viruses to Neuraminidase Inhibitors

Board 104: Pandemic Influenza: Do Miami Residents Care?

Board 105: Estimates of Influenza-Associated Deaths by Region in the United States for the 1976-1977 — 2002-2003 Seasons

Board 106: A Cross-Sectional Study on Risk Behaviors for Avian Influenza Human Infection – China, 2007

Board 107: An Historical Perspective of the 1918 Spanish Influenza Pandemic in Michigan

Board 108: Geographical Patterns in Pneumonia and Influenza (P&I) Mortality in Brazil, 1996-2006: Transmissibility and Mortality Impact

Molecular Epidemiology

Board 109: Staphylococcal Cassette Chromosome mec (SCCmec) Characterization and Panton-Valentine Leukocidin Gene Occurrence for Methicillin-Resistant *Staphylococcus aureus* in Turkey – 2003-2006

Board 110: Phylogenetic Analysis of Novel G12 Rotaviruses in the United States: A Molecular Search for the Origin of a New Strain

Board 111: Characterization of a Highly Divergent Picornavirus Prevalent in Stool Samples of Children with Acute Flaccid Paralysis

Board 112: Detection and Characterization of stx Variants Found in Non-0157:H7 Shiga Toxin Producing *Escherichia coli*

Board 113: Human Herpesvirus Type 7 in Cerebrospinal Fluid of a Patient with Acute Demyelinating Encephalomyelitis (ADEM) after Smallpox Vaccination

Outbreak Investigation: Lab & Epi Response

Board 114: Use of a Web-Based Survey Application to Investigate a Large Outbreak of Norovirus among Venture Capitalists

Board 115: Spread of Adenovirus B14 from a Major Military Training Facility to Secondary Training Sites – May to September 2007

Board 116: An Outbreak of Acute Respiratory Tract Infection Caused by Adenovirus Type 11

Board 117: Adenovirus 21 Outbreak at the Coast Guard Training Center in Cape May, New Jersey

Board 118: A Geospatial Analysis of the Spread of Mumps in Iowa during the 2006 Outbreak

Board 119: New Strategies and Collaborations to Investigate Nonevent-Related *Cyclospora cayetanensis* Outbreaks – British Columbia, Canada, 2007

Poverty & Infectious Diseases

Board 120: Socioeconomic Determinants of Prevalence of HIV and HCV Infections in Injecting Drug Users in Poland

Board 121: Prevalence and Antimicrobial Resistance of *Campylobacter* and *Salmonella* in Chickens Sampled at Slaughterhouses in Antananarivo, Madagascar

Board 122: World Rabies Day: A Collaborative Initiative to Make Rabies History

Board 123: Evaluation of the Role of School Children in the Promotion of PuR® and the Safe Water System in Schools and Households

Board 124: High Rates of *Streptococcus pneumoniae* Serotype 1 Bacteremia among Adults in Western Kenya

Surveillance: International & New Strategies

Board 125: Active Surveillance of Infectious Diseases in Northern Canadian Communities: The Northern Antibiotic Resistance Partnership

Board 126: Algorithm for Detecting High Priority Animal Health Events from Global Open Source Surveillance

Board 127: Influenza Surveillance: It Takes a Village

Board 128: New Strategies in National-Level Outbreak Reporting and Response: The Brazilian Center for Strategic Information in Health Surveillance (CIEVS)

Board 129: The Impact of WHO-GSS Training Programs in Brazil

Board 130: Respiratory Disease Surveillance in Royal Thai Army Hospitals

Board 131: Bacteremia among Patients with Community-Acquired Pneumonia in Rural Thailand

Board 132: A Novel Risk Assessment Tool for Emerging Human Infectious Disease and Biowarfare Agents and Its Use in Assessing Preparedness of 20 Pacific Island Countries and Territories

Board 133: Risk Factors and Age Differentials for Death among Children Hospitalized with Diarrhea in Rural Western Kenya – 2005-2007

Tropical Infections & Parasitic Diseases

Board 134: Atypical Presentation of Varicella Zoster Virus Infection in a Family Cluster – Republic of Congo, 2007

Board 135: The Concurrence of Malaria and Typhoid among Adult Patients Admitted in Medical Wards at Iringa Regional Hospital –Tanzania

Board 136: Intestinal Parasitism among Hispanic Migrant and Seasonal Farm Workers in Eastern North Carolina

Board 137: Independent Evolution of Mutant DHFR and DHPS Alleles in an Area of High Transmission in Western Kenya

Vectorborne Diseases

Board 138: Potential Predictors of Tick Species Attached to Persons in Georgia

Board 139: Isolation of Arboviruses in Kenya by Entomological Surveillance – 2006-2007

Board 140: Prospective Study of Symptoms Associated with the Convalescent Period of Dengue Infection in Puerto Rico – 2006-2007

Board 141: La Crosse Encephalitis in a Pregnant Woman and Possible Congenital Infection

Board 142: Seroepidemiology of *Anaplasma phagocytophilum, Bartonella henselae, Coxiella burnetii,* and *Rickettsia typhi* among Farm Worker Populations in the Tianjin Area – China

Zoonotic & Animal Diseases

Board 143: Quantification of Hepatitis E Virus Transmission in Pigs Due to Contact Exposure

Board 144: Enhanced Neurodegenerative Biomarker Expressions Accompanied by Impairment of Ubiquitin-Proteasome System in Experimental Cerebral Toxocariasis

Board 145: Hantavirus in the Eurasian Common Shrew (*Sorex araneus*) in Siberia, Russia

Board 146: Space-Time Clustering of Non-Human Antimicrobial Resistance in Denmark: The case of *Escherichia coli* – 1997-2005

Tuesday, March 18

Poster Set-up for the Day

7:30 AM – 8:30 AM

All posters presented on Tuesday will be available for viewing in the Grand Hall from 12:00 noon to 6:00 PM. Authors will be present at posters for one hour as noted under the Scientific Sessions schedule for the day.

Scientific Sessions

E1 Concurrent Plenary Session

8:30 AM – 10:10 AM | Centennial I

Travel Globalization

8:30 AM - 9:15 AM

Moderator:

LIN CHEN, Harvard University, Boston, MA

Speaker:

Travel, Globalization, and Emerging Infections

MARY WILSON, Harvard University, Boston, MA

Major Global Disease Initiatives: Malaria, Tuberculosis, HIV-AIDS

9:25 AM - 10:10 AM

Moderator:

JAMES HUGHES, Emory University, Atlanta, GA

Speaker:

Title TBA

REGINA RABINOVICH, Gates Foundation, Seattle, WA

E2 Concurrent Plenary Session

8:30 AM – 10:10 AM | Centennial II

Dengue Control/Mosquitoborne Illness

8:30 AM - 9:15 AM

Moderator:

JOEL GAYDOS, US Department of Defense, Silver Spring, MD

Speaker:

Dengue and Yellow Fever: Current Status and Prospects for Prevention and Control

THOMAS MONATH, Pandemic and Bio Defense Fund, Kleiner Perkins Caufield & Byers, Menlo Park, CA

Rift Valley Fever

9:25 AM – 10:10 AM

Moderator:

LARRY MADOFF, Harvard Medical School, Boston, MA

Speaker:

Outbreaks of Rift Valley Fever in Africa in 2006-2007
PIERRE FORMENTY, World Health Organization, Geneva, Switzerland

E3 Concurrent Plenary Session

8:30 AM – 10:10 AM | Centennial III

Avian Influenza Prevention in Poultry

8:30 AM - 9:15 AM

Moderator:

DANIEL JERNIGAN, Centers for Disease Control and Prevention, Atlanta, GA

Speaker:

Avian Influenza in the Animal Reservoir: The Submerged Part of the Iceberg
ILARIA CAPUA, Instituto Zooprofilattico Sperimentale della Venezie, Venice, Italy

Influenza & Emerging Influenza Viruses

9:25 AM – 10:10 AM

Moderator:

BETH BELL, Centers for Disease Control and Prevention, Atlanta, GA

Speaker:

The Global Threat of Avian Influenza: Can We Predict and Prevent an Influenza Pandemic?
NANCY COX, Centers for Disease Control and Prevention, Atlanta, GA

Break

10:10 AM – 10:30 AM | Centennial Ballroom Foyer

F1 Concurrent Panel Session

Avian Influenza

10:30 AM – 12:00 PM | Centennial I

Conveners:

KATHLEEN GENSHEIMER, Centers for Disease Control and Prevention, Augusta, ME
THOMAS GOMEZ, US Department of Agriculture, Atlanta, GA
ALEJANDRO THIERMANN, World Organization for Animal Health, Paris, France

Moderators:

KATHLEEN GENSHEIMER, Department of Health and Human Services, Augusta, ME
THOMAS GOMEZ, US Department of Agriculture, Atlanta, GA

Speakers:

Efficacy of Vaccination in the Control and Prevention of Avian Influenza in Poultry in Asia
LES SIMS, Asia Pacific Veterinary Information Services, Australia

Role of Wild Birds in the Transmission and Maintenance of Avian Influenza
DAVID STALLKNECHT, University of Georgia, Athens, GA

Economic and Trade Implication of Avian Influenza
ALEJANDRO THIERMANN, World Organization for Animal Health

F2 Concurrent Panel Session

Arboviral Disease Risk in a Changing World

10:30 AM – 12:00 PM | Centennial II

Conveners:

SUSAN DANIELS, National Institute of Allergy and Infectious Diseases, Bethesda, MD
KEN NUSBAUM, Auburn University, Auburn, AL
RON ROSENBERG, Centers for Disease Control and Prevention, Fort Collins, CO

Moderator:

ROGER NASCI, Centers for Disease Control and Prevention, Fort Collins, CO

Speakers:

Chikungunya, Zika, and the Equine Encephalitides: Environmental Influence on Recent Epidemics
ANN POWERS, Centers for Disease Control and Prevention, Fort Collins, CO

Sylvatic Dengue: Clearing the Jungle and the Threat to Vaccines
SCOTT WEAVER, University of Texas Medical Branch, Galveston, TX

Mutations and Increased Virulence in the West Nile Virus
AARON BRAULT, University of California, Davis, CA

F3 Concurrent Panel Session

Tuberculosis

10:30 AM – 12:00 PM | Centennial III

Conveners:

CAROL CHENOWETH, University of Michigan Health Systems, Ann Arbor, MI
KATHLEEN GENSHEIMER, Department of Health and Human Services, Augusta, ME
TIMOTHY HOLTZ, Centers for Disease Control and Prevention, Atlanta, GA

Moderators:

KEN CASTRO, Centers for Disease Control and Prevention, Atlanta, GA
CAROL CHENOWETH, University of Michigan Health Systems, Ann Arbor, MI
KATHLEEN GENSHEIMER, Department of Health and Human Services, Augusta, ME

Speakers:

Epidemiology and Challenges of MDR-TB/XDR-TB in Southern Africa and Eastern Europe
PAUL NUNN, World Health Organization, Geneva, Switzerland

Responding to the XDR-TB Epidemic in Rural KwaZulu-Natal, South Africa
NEEL GANDHI, Albert Einstein College of Medicine, New York, NY

Implementing Rapid Anti-TB Drug Resistance Diagnostic Capacity in Resource-Limited Settings
RICHARD O'BRIEN, Foundation for Innovative New Diagnostics, Geneva, Switzerland

The Perfect Storm: HIV Infection and Multidrug-Resistant Tuberculosis
TIMOTHY HOLTZ, Centers for Disease Control and Prevention, Atlanta, GA

F4 Concurrent Panel Session

Travelers as Sentinels & Disease Translocation

10:30 AM – 12:00 PM | Regency VI

Conveners:

LIN CHEN, Harvard University, Boston, MA
NINA MARANO, Centers for Disease Control and Prevention, Atlanta, GA

Moderators:

LIN CHEN, Harvard University, Boston, MA
NINA MARANO, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

GeoSentinel Surveillance of Emerging Infections in Travelers
ELIZABETH BARNETT, Boston Medical Center, Boston, MA

Dengue and Schistosomiasis in Travelers
ELI SCHWARTZ, Center for Geographic Medicine, Tel Hashomer, Israel

Chikungunya and Travel
PHILIPPE PAROLA, Services des Maladies Infectieuses et Tropicales, Marseilles, France

F5 Concurrent Panel Session

Global Burden of Disease

10:30 AM – 12:00 PM | Regency VII

Conveners:

JAMES HUGHES, Emory University, Atlanta, GA
MICHAEL ST. LOUIS, Centers for Disease Control and Prevention, Atlanta, GA
ANGELA WEAVER, US Agency for International Development, Washington, DC

Moderators:

MICHAEL ST. LOUIS, Centers for Disease Control and Prevention, Atlanta, GA
ANGELA WEAVER, US Agency for International Development, Washington, DC

Speakers:

The New Global Burden of Disease Project: Perspective on Infectious Diseases
ROBERT BLACK, Johns Hopkins Bloomsberg School of Public Health, Baltimore, MD

The Neglected Tropical Diseases: New Tools and Opportunities for Their Control
PETER HOTEZ, Sabin Vaccine Institute, Washington, DC

A Look at the Wild Side: Emerging Disease Surveillance in the Field
WILLIAM KARESH, Wildlife Conservation Society, Bronx, NY

Global Trends in Survival of Infants and Children
PETER SALAMA, UNICEF, New York, NY

F6 Concurrent Panel Session

Exotic Animals & Emerging Infectious Diseases

10:30 AM – 12:00 PM | Centennial IV

Conveners

SUSAN DANIELS, National Institute of Allergy and Infectious Diseases, Bethesda, MD
JOHN DUNN, Tennessee Department of Health, Nashville, TN
RAY WATERS, US Department of Agriculture, Ames, IA

Moderators:

SUSAN DANIELS, National Institute of Allergy and Infectious Diseases, Bethesda, MD
JOHN DUNN, Tennessee Department of Health, Nashville, TN
RAY WATERS, US Department of Agriculture, Ames, IA

Speakers:

***Mycobacterium bovis* Infection of White-Tailed Deer: Emergence of a Zoonotic Pathogen at the Interface of Domestic Animals and Wildlife**
MITCHELL PALMER, US Department of Agriculture, Ames, IA

The Epidemiology of Human Monkeypox in the Democratic Republic of Congo
ANNE RIMOIN, University of California, Los Angeles, CA

Nipah Virus Transmission in Bangladesh
STEPHEN LUBY, Centers for Disease Control and Prevention, Dhaka, Bangladesh

Lunch *(on your own)*

Poster Session III with Authors

12:00 PM – 1:00 PM | Exhibit Hall

Director's Tour of Posters

KEVIN FENTON, Director
National Center for HIV/AIDS, Viral Hepatitis, STD and TB Prevention
Coordinating Center for Infectious Diseases
Centers for Disease Control and Prevention, Atlanta, GA

Vaccines & Vaccine-Preventable Diseases

Board 147: **Was Colorado's 2004-2005 Large Increase in Reported Pertussis Cases for Real?**

Board 148: **Estimating Vaccination Coverage: Validity of Household-Retained Vaccination Cards and Parental Recall**

Board 149: **Annual Extra-Seasonal Spike in Incidence of Invasive Pneumococcal Disease**

Board 150: **Safety Review of Quadrivalent Human Papillomavirus (Types 6, 11, 16, 18) Recombinant Vaccine**

Antimicrobial Resistance

Board 151: Impact of the New Clinical and Laboratory Standards Institute Nonmeningitis Penicillin Breakpoints on the Incidence of Penicillin Resistance among Invasive Pneumococcal Disease Isolates

Board 152: Use of Antibiotics among Dairy Veterinarians in Mid-Atlantic States

Board 153: Prevalence and Antimicrobial Resistance of *Campylobacter* from Retail Meats: Results of the National Antimicrobial Resistance Monitoring System (NARMS) – 2002-2006

Board 154: Decreasing Prevalence of Antimicrobial Resistance in Non-Typhoidal *Salmonella* Isolated from Children with Bacteremia in a Rural District Hospital, Kenya

Board 155: Multidrug-Resistant Non-Typhoidal *Salmonella* in New York State's Foodborne Diseases Active Surveillance Network (FoodNet) Counties

Blood, Organ, & Other Tissue Safety

Board 156: Prospective Surveillance of Invasive Fungal Infections (IFIs) among Solid Organ Transplant (SOT) Recipients in the United States, 2001-2006: Review of TRANSNET

Board 157: Robustness of Solvent/Detergent Treatment of Plasma Derivatives: A Data Collection of PPTA Member Companies

Board 158: Prospective Surveillance for Invasive Fungal Infections (IFIs) in Hematopoietic Stem Cell Transplant Recipients (HSCTs), 2001-2006: Overview of the TRANSNET Database

Board 159: A Prospective Study of Multiple Donor Exposure Blood Recipients (PSBR)

Foodborne & Waterborne Infections

Board 160: Resistance of *Salmonella* Isolates to Predation by *Acanthamoeba polyphaga*

Board 161: Surveillance of Salmonellosis and *Escherichia coli* 0157 in Poland during 1995-2005

Board 162: International Travel-Associated Salmonellosis: Foodborne Diseases Active Surveillance Network (FoodNet) – 2004-2006

Board 163: Novel Food Implicated in an Outbreak of Orally Transmitted Acute Chagas Disease in an Urban Area of the Amazon Region – Brazil, 2007

Board 164: Epidemiology of Non-O157 Shiga Toxin-Producing *Escherichia coli* in FoodNet Sites – 2000-2006

Board 165: *Salmonella* Serotype Enteritidis Infections among Workers Producing Poultry Vaccine – Maine, 2006

Board 166: A Case Control Study of Sporadic Human Infection with Shiga Toxin Producing *Escherichia coli* in Australia

Board 167: Botulism in the United States – 1997-2006

Board 168: Foodborne Outbreaks Caused by *Salmonella enterica* serotype Typhi – Brazil, 2000-2005

Board 169: Enteric Bacterial Infections Among Infants and Children – California FoodNet, 1996-2006

Host & Microbial Genetics

Board 170: Genomic Characterization of Human Rotavirus G8 Strains from the African Rotavirus Network (ARN): Relationship to Animal Rotaviruses

Board 171: The Role of IS 1016-bexA Partial Deletion in *Haemophilus influenzae* Serotype A

Board 172: Human Genetic Determinants of Infectious Diseases: An Overview of the Current Research Lines and Consortia

Board 173: Host Genetic Determinants for *Escherichia coli* Susceptibility during Probiotic Prophylaxis for Urinary Tract Infections in Post-Menopausal Women

Board 174: Stepwise Replication Identifies a Low-Producing Lymphotoxin-Alpha Allele as a Major Risk Factor for Early-Onset Leprosy

Influenza

Board 175: US Department of Defense Global Influenza Surveillance Program at the Air Force Institute for Operational Health: Enhancements and Support of Global Partners in Pandemic Preparedness

Board 176: Influenza Virus in Human Exhaled Breath

Board 177: Epidemiology of 1918 Pandemic Influenza in Japan

Board 178: Revisiting the Classical W-Shape of 1918 Pandemic Influenza Mortality: The True Meaning of Catastrophe

Board 179: Impact of Household Crowding on the Risk of Being Hospitalized with Influenza and Pneumonia in a Large Cohort Study

Board 180: Serological Evidence for Influenza A H3N8 Virus Circulation in Canines 1999-2004

Board 181: Clinical Experience of Military Service Members and Their Dependants Who Received an Influenza Antiviral Prescription

Board 182: A Review of Influenza-Like Symptoms Among Laboratory-Confirmed Respiratory Results

Molecular Epidemiology

Board 183: Detection of Human Bocavirus in Children with Lower Respiratory Tract Infection in Taiwan

Board 184: Emergence of Coxsackievirus A24 as the Etiologic Agent for the Recent Outbreak of Acute Hemorrhagic Conjunctivitis in Taiwan

Board 185: Phylogenetic Analysis of Influenza A Virus Subtype H5N1 Strains from Egypt – 2006-2007

Board 186: *Salmonella typhimurium* Variant DT104 in Colombia, Costa Rica, and Argentina: An Emergent Pathogen in Latin America

Board 187: Characterization of the Measles Virus after Declaration of the Nationwide Measles Elimination in Republic of Korea – 2007

New or Rapid Diagnostics

Board 188: A Rapid, High Throughput Vaccinia Virus Neutralization Assay for Testing Smallpox Vaccine Efficacy Based on Detection of Green Fluorescent Protein

Board 189: Evaluation and Validation of a Real-Time Fluorescence RT-PCR for the Detection and Differentiation of Noroviruses in Genogroups I and II

Board 190: Comparison of Reverse Transcriptase Loop-Mediated Isothermal Amplification (RT-LAMP) Tests for H5 Influenza

Board 191: Rapid, Point-of-Care Avian Influenza Diagnostic Evaluation

Outbreak Investigation: Lab & Epi Response

Board 192: Identification of Factors (Environmental and Human) Responsible for the Endemicity of Cholera in Ajegunle and Amukoko Districts (Ajeromi/Ifelodun Local Government Area - LGA) – Lagos State, Nigeria, 1990-2007

Board 193: Using Molecular Identification Methods in Investigating an Apparent Outbreak of *Rhodococcus equi* Infections – New Jersey, 2007

Board 194: *Clostridium perfringens* Foodborne Intoxication Outbreak Associated with Consuming Chili Beans Prepared at a Correctional Facility

Prevention Effectiveness, Cost Effectiveness, & Cost Studies

Board 195: Effectiveness of Hygiene Control Measures for Containing an Outbreak of Norovirus

Board 196: Information Collection and Utilization at Clinical Microbiology Laboratories – Chongqing, China, 2006

Board 197: Observational Study Regarding Incorporation of Measures to Prevent Disease Associated with Animals in Public Settings

Board 198: Cost of Public Health Response to an Outbreak of Malaria among Recently Resettled Refugees – July 2007

Board 199: The Economic Cost of Guillain-Barré Syndrome in the United States

Surveillance: International & New Strategies

Board 200: Detection of Emerging Disease Outbreaks through a Regional Network in the Former Soviet Union: ProMED-RUS

Board 201: Epidemiological Analysis of Influenza by Laboratory Surveillance in Gyeongnam Province, Korea, 2004-2005 — 2006-2007 Seasons

Board 202: A Field Method for Surveillance of Yellow Fever Adverse Events Following Mass Vaccination Campaigns in Togo, 2007

Board 203: Minnesota Medical Examiner (ME) Infectious Deaths Surveillance

Board 204: Sero-Epidemiology as a Novel Approach to Estimate the Incidence of *Campylobacter* and *Salmonella* Infections in the Human Population

Board 205: Pregnancy-Associated Listeriosis in the United States – 2004-2007

Board 206: Operationalizing Climate-Based Epidemic Prediction Models

Board 207: Trained District Health Personnel and the Performance of Integrated Diseases Surveillance and Response (IDSR) in the WHO African Region

Board 208: Health-Seeking Patterns in a Population-Based Surveillance System Offering Free Healthcare in Western Kenya

Board 209: Virological Surveillance of Enteroviruses in North India: A Vital Assessment Before Global Polio Eradication

Vectorborne Diseases

Board 210: Evaluation of Five Formulations of *Bacillus Thuringiensis* for Dengue Control in the Municipality of Caico - Rn.

Board 211: Marked Increase in the Incidence of Dengue and Dengue Hemorrhagic Fever – Brazil, 2007

Board 212: Lyme Disease in New York City — Is It Locally Acquired?

Board 213: Etiology of Fever of Unknown Origin in a Selected Group of Sri Lankan Patients with Prompt Responses to Doxycycline

Board 214: Dengue Virus Infections in Patients Suspected of Malaria/Typhoid Fever in Nigeria

Zoonotic & Animal Diseases

Board 215: Molecular Epidemiology of Cross-Species Transmission of Rabies in the Central Great Plains

Board 216: Comparison of Pig and Ferret Models for Respiratory versus Alimentary Transmission of H5N1 High Pathogenicity Avian Influenza Viruses

Board 217: *Corynebacterium diphtheriae* among Domestic Cats: A Potential Zoonosis?

Board 218: Landscape Genetics of White-Tailed Deer and the Implications for the Spread of Chronic Wasting Disease across Kansas

G1 Concurrent Panel Session

Novel Vaccine Strategies in Preventing Emerging Infectious Diseases in Humans & Protecting Animal Health

1:15 PM – 2:45 PM | Centennial I

Conveners:

TRUDY MURPHY, Centers for Disease Control and Prevention, Atlanta, GA
RON ROSENBERG, Centers for Disease Control and Prevention, Fort Collins, CO

Moderator:

CHARLES RUPPRECHT, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Oral Vaccination to Reduce Reservoir Capacity for the Agent of Lyme Disease
SAM TELFORD, Tufts University, North Grafton, MA

DNA Vaccine for West Nile and Other Flaviviruses
GWONG-JEN (JEFF) CHANG, Centers for Disease Control and Prevention, Fort Collins, CO

Protecting Ourselves Against our Food: Shall We Vaccinate Against *Escherichia coli* O157:H7 or Not?
ALISON O'BRIEN, Uniformed Services University of the Health Sciences, Bethesda, MD

G2 Concurrent Panel Session

Food Safety

1:15 PM – 2:45 PM | Centennial II

Conveners:

JOHN DUNN, Tennessee Department of Health, Nashville, TN
PATRICK MCDERMOTT, US Food and Drug Administration, Laurel, MD
DAVID SWERDLOW, Centers for Disease Control and Prevention, Atlanta, GA

Moderators:

JOHN DUNN, Tennessee Department of Health, Nashville, TN
DAVID SWERDLOW, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Estimating the Global Burden of Foodborne Diseases – WHO's Role and Activities
CLAUDIA STEIN, World Health Organization, Geneva, Switzerland

Estimating the Burden of Foodborne Illness in Australia to Improve Food Safety
MARTYN KIRK, Department of Health and Ageing, Gowrie, Australia

Determining the Burden and Sources of Foodborne Diseases in the United States
ELAINE SCALLAN, Centers for Disease Control and Prevention, Atlanta, GA

An Integrated Food Chain Surveillance System for *Salmonella* in Mexico
MUSSARET ZAIDI, Hospital General O'Horan, Merida, Mexico

G3 Concurrent Panel Session

Antimicrobial Resistance 2008: Use and Consequences

1:15 PM – 2:45 PM | Centennial II

Conveners:

PATRICK MCDERMOTT, US Food and Drug Administration, Laurel, MD
FRED TENOVER, Centers for Disease Control and Prevention, Atlanta, GA

Moderator:

FRED TENOVER, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Emerging Antimicrobial Resistance in Animals: What NARMS Is Telling Us
DAVID WHITE, US Food and Drug Administration, Rockville, MD

The Impact of Antimicrobial Resistance on Treating Sexually Transmitted Diseases
KIMBERLY WORKOWSKI, Centers for Disease Control and Prevention, Atlanta, GA

Changes in Antimicrobial Agent Prescribing Patterns in the Outpatient Setting
LINDA MCCAIG, Centers for Disease Control and Prevention, Hyattsville, MD

G4 Concurrent Panel Session

Emerging & Reemerging Vaccine-Preventable Diseases

1:15 PM – 2:45 PM | Regency VII

Conveners:

ROBERT CHEN, Centers for Disease Control and Prevention, Atlanta, GA
SUSAN GOLDSTEIN, Centers for Disease Control and Prevention, Atlanta, GA
WALTER ORENSTEIN, Emory University, Atlanta, GA
ALAN PARKINSON, Centers for Disease Control and Prevention, Anchorage, AK

Moderators:

WALTER ORENSTEIN, Emory University, Atlanta, GA

Speakers:

Mumps: A Reemerging Vaccine-Preventable Disease
JANE SEWARD, Centers for Disease Control and Prevention, Atlanta, GA

Hepatitis A in Transitional Countries
BETH BELL, Centers for Disease Control and Prevention, Atlanta, GA

Replacement Invasive Pneumococcal Disease: The Moving Target for Expanded/Valency Vaccines
KEITH KLUGMAN, Emory University, Atlanta, GA

G5 Concurrent Panel Session

Barriers & Breakthroughs in Infectious Disease Prevention for Women

1:15 PM – 2:45 PM | Regency VI

Conveners:

WANDA JONES, US Department of Health and Human Services, Washington, DC
MARIAN MCDONALD, Centers for Disease Control and Prevention, Atlanta, GA

Moderator:

WANDA JONES, US Department of Health and Human Services, Washington, DC

Speakers:

Sex Differences and Infectious Disease Prevention
HEATHER MACLEAN, Women's College Hospital, Toronto, Ontario

Digital Cervicography: An Adjunct to VIA-Based Cervical Cancer Screening Program in Zambia
MULINDI MWANAHAMUNTU, University Teaching Hospital, Lusaka, Zambia

Breakthrough in Infectious Disease Prevention: Microbicides
SHARON HILLIER, University of Pittsburgh School of Medicine, Pittsburgh, PA

G6 Concurrent Panel Session

Addressing the Global Threats of Zoonotic Infectious Disease: Perspectives from CDC's International Emerging Infections Program Kenya and Thailand Field Sites

1:15 PM – 2:45 PM | Centennial IV

Convener:

NINA MARANO, Centers for Disease Control and Prevention, Atlanta, GA

Moderators:

LONNIE KING, Centers for Disease Control and Prevention, Atlanta, GA
ALEJANDRO THIERMANN, World Organization for Animal Health, Paris, France

Speakers:

CDC International Emerging Infections Program Overview
SONJA OLSEN, Centers for Disease Control and Prevention, Atlanta, GA

Exploring the Animal-Human Interface in Kenya: The Search for Strategies to Identify Emerging Zoonotic Public Health Threats
ROBERT BREIMAN, Centers for Disease Control and Prevention, Nairobi, Kenya
SARAH CLEAVELAND, University of Edinburgh, Edinburgh, Scotland

***Streptococcus suis* in Thailand: Animal and Human Health Collaborations to Understand Emerging Zoonotic Diseases**
HENRY (KIP) BAGGETT, Centers for Disease Control and Prevention, Nonthaburi, Thailand
TEERASAK CHUXNUM, Thailand Ministry of Public Health, Nonthaburi, Thailand

Break

2:45 PM – 3:00 PM | Centennial Ballroom Foyer/Regency Foyer

H1 Slide Session

Respiratory Diseases

3:00 PM – 4:30 PM | Centennial I

3:00 – 3:15 PM
Incidence and Etiologies of Hospitalized Pneumonia in Young Children in Rural Thailand
JULIA RHODES, IEIP, Thailand MOPH-US CDC Collaboration

3:15 – 3:30 PM
Epidemiology and Incidence of Viral Severe Pneumonia in Population-Based Surveillance among Children Younger than 5 Years in Rural Western Kenya – 2006-2007
TAMARA PILISHVILI, Centers for Disease Control and Prevention

3:30 – 3:45 PM
Impact of 7-Valent Pneumococcal Conjugate Vaccine on Invasive Pneumococcal Disease Among Children and Adults, United States, 2006
MATTHEW MOORE, Centers for Disease Control and Prevention

3:45 - 4:00 PM
Adenovirus 14 Illness among Basic Military Trainees, 2007
JACQUELINE TATE, Centers for Disease Control and Prevention

4:00 – 4:15 PM
Full Genomic Sequence Analysis of Emerging Human Adenovirus (Ad) 14 Isolates from 2006-2007 Acute Respiratory Disease Outbreaks in the US Military
HUO-SHU HOUNG, Walter Reed Army Institute of Research

4:15 – 4:30 PM
Novel Adenovirus Serotype Identified in Healthcare Workers at a Military Hospital - Texas, 2007
FERNANDA LESSA, Centers for Disease Control and Prevention

H2 Slide Session

Health Communications

3:00 PM – 4:30 PM | Centennial II

3:00 – 3:15 PM
Facilitating Community Action to Prevent Avian Influenza
WHITNEY PYLES, CARE USA

3:15 – 3:30 PM
Trying to Get the Message Right: Formative Research on Avian Influenza
LAUREN BLUM, Centers for Disease Control and Prevention

3:30 – 3:45 PM
Physicians' Knowledge, Attitudes, and Practice Regarding Prevention of Infections During Pregnancy
DANIELLE ROSS, Centers for Disease Control and Prevention

3:45 - 4:00 PM
Community Capacity to Implement Nonpharmaceutical Measures for Pandemic Influenza: An Assessment
BARRI BURRUS, RTI International

4:00 – 4:15 PM
Evaluation of a West Nile Virus Prevention Education Intervention among Organ Transplant Recipients – Colorado, 2006
EMILY ZIELINSKI-GUTIERREZ, Centers for Disease Control and Prevention

4:15 – 4:30 PM
Findings from an Evaluation of Malaria Prevention Health Messages Tailored to Travelers Visiting Friends and Relatives in Nigeria and India
STEFANIE STEELE, Centers for Disease Control and Prevention

H3 Slide Session

Blood, Organ, & Tissue Safety

3:00 PM – 4:30 PM | Centennial III

3:00 – 3:15 PM
Fatal Group C Streptococcal Infection Due to Transfusion of a Contaminated Pooled Platelet Unit Despite Routine Bacterial Culture Screening
FERNANDA LESSA, Centers for Disease Control and Prevention

3:15 – 3:30 PM
Risk Reduction for Transfusion Transmissable Emerging Infections: Blood Donor Geographic and Behavioral Risk Deferrals and Their Impact on Blood Availability
SHIMIAN ZOU, American Red Cross

3:30 – 3:45 PM
Transplantation-Transmitted Tuberculosis in Oklahoma – 2007
EMILY PIERCEFIELD, Oklahoma State Department of Health

3:45 - 4:00 PM
Amotosalen and UVA Illumination Inactivate Influenza H5N1 and Chikungunya Virus in Platelet Concentrates and Plasma
LYNETTE SAWYER, Cerus Corporation

4:00 – 4:15 PM
Chagas Disease in Mississippi: Investigation of Suspected Autochthonous Infections in the United States
PAUL CANTEY, Centers for Disease Control and Prevention

4:15 – 4:30 PM
Preliminary Description of the Organ Transplant Infection Project (OTIP), a Multi-Year Cohort Study of Stem Cell and Lung Transplant Recipients
DEBRA WAGNER, Centers for Disease Control and Prevention

H4 Slide Session

Tropical Diseases

3:00 PM – 4:30 PM | Centennial IV

3:00 – 3:15 PM
Paederus Dermatitis: An Outbreak in Thai Soldiers
PICHA SUWANNAHITATORN, Phramongkutklao College of Medicine

3:15 – 3:30 PM
A Coordinated Epidemiologic and Water Assessment to Investigate a Cholera Outbreak in a Temporary Shelter for Displaced Persons in Thailand
VALERIE NYUNT, Aide Médicale Internationale

3:30 – 3:45 PM
First Reported Outbreak of Eosinophilic Meningitis Caused by *Angiostrongylus cantonensis* in Brazil
M. GARCIA, Brazilian Field Epidemiology Training Program (EPISUS), Secretariat of Health Surveillance, Brazilian Ministry of Health

3:45 – 4:00 PM
Clinical and Epidemiologic Characteristics of Patients with Orally Transmitted Acute Chagas Disease – Brazil, 2005-2006
ERICA TATTO, Secretariat of Health Surveillance (SVS), Brazilian Ministry of Health

4:00 – 4:15 PM
Yellow Fever Resurgence in Africa: Public Health Measures to Assess the Risk of YF Outbreaks
TIM NGUYEN, World Health Organization, Epidemic and Pandemic Alert and Response Department

4:15 – 4:30 PM
Integration of Neglected Disease Programs in Togo: Evaluation of a Pilot Project
JENNIFER VERANI, Centers for Disease Control and Prevention

H5 Slide Session–Late Breakers II

3:00 PM – 4:30 PM | Regency VII

See the program addendum for presentations in this session.

Poster Session IV with Authors

5:00 PM – 6:00 PM
Exhibit Hall

Director's Tour of Posters

BETH BELL, Associate Director for Epidemiologic Science
National Center for Immunization and Respiratory Diseases
Coordinating Center for Infectious Diseases
Centers for Disease Control and Prevention, Atlanta, GA

Vaccines & Vaccine-Preventable Diseases

Board 219: Outbreak of Measles in Norway among Nomadic Travelers from England

Board 220: Comparative Study of Pertussis Dynamics in the Pre- and Post-Vaccination Era in 30 Countries

Board 221: Nationwide Outbreak of Rubella Caused by a Single Viral Genotype during Rubella and Congenital Rubella Syndrome Elimination Phase – Brazil, 2007

Board 222: An Explosive Outbreak of Modified Measles Posing as a Rash Illness of Unknown Etiology in a High School – TaiYuan, Shanxi Province, China, 2007

Antimicrobial Resistance

Board 223: Impact of the New Clinical and Laboratory Standards Institute Nonmeningitis Penicillin Breakpoints on the Incidence of Penicillin Resistance among Invasive Pneumococcal Disease Isolates

Board 224: Antimicrobial Resistance in *Salmonella* Serotype I 4,[5],12:i:-, NARMS 1996-2005

Board 225: Longitudinal Study of Antimicrobial Resistance among *Escherichia coli* Isolated from Integrated Multi-Site Cohorts of Humans and Swine

Board 226: Antibiotic Restriction Policy and Practice in Selected U.S. Hospitals: Results of a Regional Survey

Board 227: *Staphylococcus aureus* and Methicillin-Resistant *Staphylococcus aureus* on Surfaces in a University and a Jail Setting

Bioterrorism Preparedness

Board 228: Clinical Experience, Infection Control Practices, and Diagnostic Algorithms for Poxvirus Infections — an Emerging Infections Network Survey

Board 229: Societal Implications of Biodefense and Emerging Infectious Disease Research: Perspectives from the SERCEB Policy, Ethics, and Law Core

Board 230: Enhanced Public Health Surveillance Activities in Miami-Dade County for a Special Event

Emerging Opportunistic Infections

Board 231: Toxicity of *Kingella kingae* on Human Cells

Board 232: Estimating the Global Burden of Cryptococcal Meningitis

Board 233: Changing Epidemiology of Human Pneumocystosis in India

Board 234: *Acanthamoeba spp.* Cysts Are Resistant to Desiccation for at Least 20 Years

Board 235: Trends in Hospital Admissions for Skin and Soft Tissue Infections (SSTIs) among Medicare Enrollees – 2001-2005

Foodborne & Waterborne Infections

Board 236: Description of Shiga-Toxin Producing *Escherichia coli* Infections in Georgia

Board 237: *Vibrio vulnificus* Infections in Georgia

Board 238: Outbreaks in Australia from Imported Foods – 2001-2007

Board 239: Antimicrobial-Resistant *Salmonella* from Retail Chickens in Pennsylvania 2006-2007

Board 240: Rotavirus Diarrhea in Children in Cambodia

Board 241: First Report of Spontaneous Clinical Recovery in the Presence of Circulating Botulinum Toxin Type F in an Adult

Board 242: Serotypes, Antimicrobial Susceptibility and Molecular Characterization of *Salmonella* from Infections in Humans in Henan Province, China

Board 243: Evidence that Fresh Chicken Is the Main Source of New Zealand's Sustained Campylobacteriosis Epidemic

Board 244: Global Survey by the World Health Organization (WHO) to Assess Public Health Surveillance Systems for *Salmonella* – WHO Global Salm-Surv, 2006

Healthcare Worker Safety

Board 245: Investigations of Close Contacts of Patients with Laboratory-Confirmed H5N1 Virus Infection in Indonesia

Board 246: Evaluation of Effectiveness of Commercial Sanitizers/Disinfectants to Inactivate Human Norovirus Using Two Surrogate Model Strains (*Feline calicivirus* and *Murine norovirus*)

Influenza

Board 247: Protective Effect of Maritime Quarantine in South Pacific Islands During the 1918-1919 Influenza Pandemic

Board 248: Impact of Respiratory Syncytial Virus on Seasonal Influenza Surveillance – New York, 2005-2007

Board 249: Knowledge, Attitudes, and Practices About Influenza Control Practices among Hispanics in San Diego County, California – 2006

Board 250: Sentinel Surveillance for Influenza in Kenya

Board 251: A Cross-Sectional Study on Risk Behaviors for Avian Influenza Human Infection – China, 2007

Board 252: Preventing the Spread of Seasonal Flu: Measuring the Impact of a Voluntary Program on Influenza Immunization Coverage among Long-Term Care Facility Residents and Employees

Board 253: Predominant Circulating Seasonal Influenza Strain May Predict Nosocomial Influenza Outbreak Severity – New York State, 2002-2007

Laboratory Proficiency Testing/Quality Assurance

Board 254: Biological Enrichment of Low-Level Mycoplasma Contaminants Using Co-Cultivation with Permissive Cell Cultures

Modeling

Board 255: A SEIR Model for Assessing the Effects of School Dismissal during a Severe Seasonal Influenza Outbreak

Board 256: A Prediction Market for H5N1 Influenza

Board 257: Using Geographic Information System (GIS) for Malaria Surveillance in a Township in the Brazilian Amazon Region – 2006

Board 258: A Modified Agent-Based Model for Assessing Effectiveness of Disease Surveillance for Detection of Acute Respiratory Outbreaks in Resource-Limited Settings

Board 259: Geographic Information System for the Detection, Risk Stratification, and Targeting of *Triatoma dimidiata* Control in Guatemala

Board 260: Accessing and Utilizing Remote Sensing Data for Vectorborne Infectious Diseases Surveillance and Modeling

Board 261: Detection of Influenza Positive Cases Using Laboratory Databases in the Military Health Care Setting

Board 262: Stochastic Model of HPAI Spread among Commercial Poultry Operations in Georgia

Nosocomial Infections

Board 263: Endophthalmitis Outbreak Due to *Pseudomonas aeruginosa* Infection after Ophthalmic Surgery – Roraima State, Brazil, 2006

Board 264: 30-Day and 180-Day Case Fatality Rates among Invasive Methicillin-Resistant *Staphylococcus aureus* Patients – Tennessee, 2004-2007

Board 265: A Pilot Surveillance Strategy for Hospital-Acquired Respiratory Illness in Bangladesh

Outbreak Investigation: Lab & Epi Response

Board 266: Seven Years of Field Epidemiology Training in Brazil: A National Strategy to Strengthen National Surveillance and Outbreak Response

Board 267: Mumps Outbreak Among Military Populations in Lima and Ayacucho, Peru – 2007

Board 268: Dissemination of Community-Associated Methicillin-Resistant *Staphylococcus aureus* CMRSA7 (USA400) in Northern Saskatchewan, Canada

Surveillance: International & New Strategies

Board 269: Health-Seeking Patterns in a Population-Based Surveillance System Offering Free Health Care in Western Kenya

Board 270: Can Current Disease Reporting Systems Capture All Animal Bites? – Miami-Dade County, Florida, 2006

Board 271: Global ID Surveillance and Diplomacy: Case Study in Strategic Local Investment

Board 272: WHO Global Salm-Surv: Worldwide *Salmonella* Distribution, 1995 - 2006

Board 273: *Campylobacter* Serology Is Consistent with High Infection Pressure

Board 274: Assessing the Public Health Impact of the First 6 Years of WHO Global Salm-Surv

Board 275: Optimizing Influenza Sentinel Surveillance at the State Level

Board 276: US Department of Defense Public Health Laboratory Services Internet-Accessible Databases

Board 277: Online News Monitoring for Global Infectious Disease Intelligence: Evaluation of the HealthMap System

Board 278: Use of Oral Rehydration Solution among Persons with Diarrhea in Rural Guatemala – 2006

Vectorborne Diseases

Board 279: Insecticide-Treated Mud as a Means of Malaria Control

Board 280: Dengue Fever with Complications: An Intermediate Reporting Category between Dengue Fever and Dengue Hemorrhagic Fever Used in the Brazilian National Dengue Surveillance System: Case Characteristics and Classification Issues

Board 282: Emergence of Autochthonous Cutaneous Leishmaniasis in Northeast Texas and Oklahoma

Board 283: Epidemiology of Malaria and Vector Distributions in the Republic of Korea

Viral Hepatitis

Board 284: Epidemiologic Profile of Hepatitis C Cases – Brazil, 2002-2006

Board 285: Use of Viral Hepatitis Surveillance to Detect a Cluster of Hepatitis C Virus Infection – New York, 2007

Board 286: Characterization of Perinatal Hepatitis B Cases – California, 2000-2005

Zoonotic & Animal Diseases

Board 287: Time to Classify Zoonoses

Board 288: Lagos Bat Virus in Kenya

Board 289: The Prevalence of Q Fever in the United States: Data from NHANES 2003-2004

Board 290: Assessing the Risk for Introduction of Rabies and Other Zoonoses via Importation of Dogs to the United States

Wednesday, March 19

Poster Set-up for the Day

7:30 AM – 8:30 AM

All posters presented on Wednesday will be available for viewing in the Grand Hall from 10:00 AM to 1:00 PM. Authors will be present at posters for 1 hour as noted under the Scientific Sessions schedule for the day.

Scientific Sessions

I1 Concurrent Plenary Session

8:30 AM – 10:10 AM | Centennial I

Climate Change

8:30 AM - 9:15 AM

Moderator:

DAVID SWERDLOW, Centers for Disease Control and Prevention, Atlanta, GA

Speaker:

Climate Change: The Public Health Response

HOWARD FRUMKIN, Centers for Disease Control and Prevention, Atlanta, GA

Role of Political/Social Disruption

9:25 AM - 10:10 AM

Moderator:

J. TODD WEBER, Centers for Disease Control and Prevention

Speaker:

Political and Social Issues and Emerging Infectious Diseases

BARRY LEVY, Tufts University School of Medicine, Boston, MA

I2 Concurrent Plenary Session

8:30 AM – 10:10 AM | Centennial II

Advances in New Pathogen Detection

8:30 AM - 9:15 AM

Moderator:

MONICA PARISE, Centers for Disease Control and Prevention, Atlanta, GA

Speaker:

A Staged Strategy for Pathogen Surveillance and Discovery

IAN LIPKIN, Columbia University, New York, NY

Emerging Infections & Animals

9:25 AM - 10:10 AM

Moderator:

THOMAS GOMEZ, US Department of Agriculture, Atlanta, GA

Speaker:

Emerging Virus Infections: a Continuing Threat from the Animal World

ALBERT OSTERHAUS, Erasmus MC, Rotterdam, The Netherlands

I3 Concurrent Plenary Session

8:30 AM – 10:10 AM | Centennial III

Emerging Vaccine Issues

8:30 AM - 9:15 AM

Moderator:

WALTER ORENSTEIN, Emory University, Atlanta, GA

Speaker:

Vaccine Controversies: Communicating Science to the Public

PAUL OFFIT, Children's Hospital of Philadelphia, Philadelphia, PA

Outbreaks of Emerging Infections

9:25 AM - 10:10 AM

Moderator:

NANCY COX, Centers for Disease Control and Prevention, Atlanta, GA

Speaker:

Profile of the Emerging Infectious Disease in India During the Last 5 Years

NAMUL GANGULY, Indian Council of Medical Research, New Delhi, India

Break

10:10 AM – 10:30 AM | Grand Hall/Exhibit Hall

J1 Concurrent Panel Session

Issues in Vaccination & Vaccine-Preventable Diseases

10:30 AM – 12:00 PM | Regency VII

Conveners:

ERIC MAST, Centers for Disease Control and Prevention, Atlanta, GA
WALTER ORENSTEIN, Emory University, Atlanta, GA
ABIGAIL SHEFER, Centers for Disease Control and Prevention, Atlanta, GA

Moderators:

ERIC MAST, Centers for Disease Control and Prevention, Atlanta, GA
ABIGAIL SHEFER, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Co-administration of Vaccines – an Increasing Complex Interaction

RON DAGAN, Ben Gurion University of the Negev, Beer-Sheva, Israel

Waning Immunity and Other Issues in Vaccination

WALTER ORENSTEIN, Emory University, Atlanta, GA

New Insights into Measuring Vaccine Herd Protection

JOHN D. CLEMENS, International Vaccine Institute, Seoul, Republic of Korea

J2 Concurrent Panel Session

Pathogen Discovery

10:30 AM – 12:00 PM | Centennial I

Conveners:

KATE GLYNN, Centers for Disease Control and Prevention, Atlanta, GA
PATRICIA WILKINS, Centers for Disease Control and Prevention, Chamblee, GA

Moderators:

KATE GLYNN, Centers for Disease Control and Prevention, Atlanta, GA
RICHARD DRAKE, Eastern Virginia Medical School, Norfolk, VA

Speakers:

Microbial Ecology of the Gastrointestinal Tract

DAVID RELMAN, Stanford University, Palo Alto, CA

Molecular Microbiology of Human-Associated Niches and Novel Pathogen Discovery

DAVID FREDRICKS, Fred Hutchinson Cancer Research Center, Seattle, WA

Identification and Characterization of a Novel Human Virus, WU Polyomavirus

DAVID WANG, Washington University School of Medicine, St. Louis, MO

J3 Concurrent Panel Session

Sexually Transmitted Diseases

10:30 AM – 12:00 PM | Regency VI

Conveners:

JOANNA BUFFINGTON, Centers for Disease Control and Prevention, Atlanta, GA
JOEL GAYDOS, US Department of Defense, Silver Spring, MD
TAMMY LUNDSTROM, Providence and Providence Park Hospitals, Detroit, MI

Moderators:

JOEL GAYDOS, US Department of Defense, Silver Spring, MD
JOHN DOUGLAS, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Chlamydial LGV: Global Epidemiology and Emergence of Mutants

ANGELIKA STAREY, University of Vienna, Vienna, Austria

Syphilis—A Growing Concern

JEFFREY KLAUSNER, San Francisco Department of Public Health, San Francisco, CA

Multidrug-Resistant Gonorrhea—the GC Isolate Surveillance Program

EILEEN YEE, Centers for Disease Control and Prevention, Atlanta, GA

J4 Concurrent Panel Session

International Networks that Work

10:30 AM – 12:00 PM | Centennial II

Conveners:

JAMES HUGHES, Emory University, Atlanta, GA
ALAN PARKINSON, Centers for Disease Control and Prevention, Anchorage, AK

Moderators:

JAMES HUGHES, Emory University, Atlanta, GA
ALAN PARKINSON, Centers for Disease Control and Prevention, Anchorage, AK

Speakers:

International Circumpolar Surveillance (ICS): A Network for Monitoring Infectious Disease Emergence in Arctic Regions

ALAN PARKINSON, Centers for Disease Control and Prevention, Anchorage, AK

The Unique Capabilities of the US Department of Defense Global Emerging Infections Surveillance and Response System

RALPH ERICKSON, Department of Defense, Silver Spring, MD

The Role of the International Association of National Public Health Institutes (IANPHI) in Strengthening Global Public Health Activities

ONI IDIGBE, Nigerian Institute of Medical Research, Lagos, Nigeria

The International Emerging Infections Programs: Combating Emerging Threats Using Proven Public Health Tools

SONJA OLSEN, Centers for Disease Control and Prevention, Atlanta, GA

J5 Concurrent Panel Session

Public Health Genomics

10:30 AM – 12:00 PM | Centennial III

Conveners:

MARY REICHLER, Centers for Disease Control and Prevention, Atlanta, GA
VENKATACHALAM UDHAYAKUMAR, Centers for Disease Control and Prevention, Atlanta, GA

Moderators:

MUIN KHOURY, Centers for Disease Control and Prevention, Atlanta, GA
MOHAMED KARMALI, Canadian CDC, Ottawa, Canada

Speakers:

Genetic Determinants for Host Control of HIV-1 Infection
RICHARD KASLOW, University of Alabama, Birmingham, AL

Host Genomics of Sexually Transmitted Diseases
SERVAAS MORRE, Free University Medical Center, Amsterdam, The Netherlands

Genetic Determinants of Susceptibility to Tuberculosis
STEVEN HOLLAND, National Institutes of Health, Bethesda, MD

J6 Concurrent Panel Session

Methicillin Resistant *Staphlyococcus aureus*

10:30 AM – 12:00 PM | Centennial IV

Conveners:

CLIFFORD MCDONALD, Centers for Disease Control and Prevention, Atlanta, GA
NINA MARANO, Centers for Disease Control and Prevention, Atlanta, GA

Moderators:

CLIFFORD MCDONALD, Centers for Disease Control and Prevention, Atlanta, GA
JOHN JERNIGAN, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

Healthcare-Associated Methicillin-Resistant *Staphylococcus aureus*
SUSAN HUANG, Brigham and Women's Hospital, Boston, MA

Community-Associated Methicillin-Resistant *Staphylococcus aureus*
RACHEL GORWITZ, Centers for Disease Control and Prevention, Atlanta, GA

Methicillin-Resistant *Staphylococcus aureus* in Animals and Links to Human Disease
SCOTT WEESE, University of Guelph, Guelph, Ontario

Lunch *(on your own)*

Poster Session V with Authors

12:00 PM – 1:00 PM | Exhibit Hall

Vaccines & Vaccine-Preventable Diseases

Board 291: An Outbreak of Severe Community-Associated Methicillin-Resistant *Staphylococcus aureus* in Children in Vietnam Following Vaccination: Implications for Infection Control in Immunization Programs

Board 292: Acute Asthma Exacerbation Following Immunization with Live Attenuated Influenza Vaccine among US Service Members during the 2006-2007 Influenza Season

Board 293: A Large Measles Outbreak in Dar es Salaam, Tanzania — Support for the Need for a Two-Dose Measles Vaccination Strategy

Antimicrobial Resistance

Board 294: Daptomycin Resistance and hVISA Development in MRSA Endocarditis

Board 295: Laboratory Analysis of *Staphylococcus aureus* in Florida: January 1, 2003, to December 31, 2005, with an Emphasis on Methicillin Resistance

Board 296: Bactericidal Activity of Sphingosine on Coryneform (Diphtheroid) Species

Board 297: Antimicrobial Resistance Surveillance Tool for US Department of Defense Facilities

Emerging Opportunistic Infections

Board 298: Impact of Coccidioidomycosis (Valley Fever) in Arizona: Data from Enhanced Surveillance

Board 299: Identification of Novel Discistro-Like Virus from Stool Samples of Children with Acute Flaccid Paralysis

Board 300: Clinical and Epidemiological Characterization of WU Polyomavirus Infection in St. Louis, MO

Board 301: *Staphylococcus aureus* Community-Acquired Pneumonia in Children During the 2006-2007 Influenza Season

Board 302: *Nocardia mikamii sp. nov.* Isolated from Pulmonary Infections in the United States

Board 303: Characterization of a Novel *Francisella sp.* Isolated from Human CSF and Blood

Foodborne & Waterborne Infections

Board 304: Clinical Characteristics of O157 and non-O157 Shiga Toxin-Producing *Escherichia coli* (STEC) Infections in Minnesota – 2000-2006

Board 305: Are There Gender Differences in Food Consumption? The FoodNet Population Survey, 2006-2007

Board 306: Prevalence of Multidrug Salmonella in Eggs from Poultry and Ducks in South India

Board 307: Non-O157 Shiga Toxin-producing *Escherichia coli* in Connecticut: Predominant Serogroups, Measures of Disease Severity and Risk Factors vs. O157 – 2000-2007

Board 308: Environmental Mycobacteriosis and Drinking Water: What Are the Connections?

Board 309: An Outbreak of Orally Transmitted Acute Chagas Disease in an Urban Area – Para State, Brazil, 2006

Board 310: The Global Burden of *Salmonella*

Board 311: *Shigella* from Humans in Thailand during 1993 to 2006: Spatial-Time Trends in Species and Serotype Distribution

Immigrant & Refugee Health

Board 312: Establishing Respiratory Disease Surveillance in Two Refugee Camps in Kenya – 2006-2007

Board 313: Pyogenic Liver Abscesses with *Klebsiella pneumoniae* in a Public Hospital in Queens, New York

Board 314: Assessing Exposure to West Nile Virus in the Migrant Agricultural Workers of the Niagara Peninsula, Canada

Board 315: Being Free of Tuberculosis: Not Just a Matter of Health

Influenza

Board 316: Use of Hospital Discharge Data to Assess Completeness of Reporting of Adult Influenza-Associated Hospitalizations – Colorado, 2006-2007

Board 317: Latitudinal Variations in Seasonal Patterns of Influenza and Respiratory Syncytial Virus (RSV): A Multinational Comparative Study

Board 318: Effectiveness of Inactivated Influenza Vaccines Varied Substantially with Antigenic Match in the United States during the 2004-2005 — 2006-2007 Seasons

Board 319: Variations in Primary Care Physician Influenza Testing Practices

Board 320: The 1918 Pandemic Experience in Japan: Age and Geographic Mortality Patterns

Board 321: Use of Pyrosequencing for Rapid Sequence Confirmation and Characterization of Real-Time RT-PCR Amplicons of A/H5N1 Highly Pathogenic Avian Influenza Viruses

Board 322: Respiratory Outbreaks Identified by Ongoing Surveillance at US Military Basic Training Centers

New or Rapid Diagnostics

Board 323: Potential Point of Care Technology Tested as Part of an Avian Influenza Pandemic Preparedness Initiative

Board 324: Development of a High-Throughput Multiplex PCR and Capillary Electrophoresis Technique for Serotype Determination of *Salmonella enterica* Food Animal Isolates

Board 325: Rapid Molecular Determination of Serotype from Clinical Isolates of *Salmonella enterica*

Board 326: *Salmonella* Molecular Serotyping with a DNA Microarray: An Approach for Non-Agglutinable *Salmonella enterica* Serotypes

Nosocomial Infections

Board 327: An Application of Social Network Theory to Optimize Influenza Vaccination among Healthcare Workers

Board 328: Using Active Microbiologic Surveillance During an Outbreak of Healthcare-Associated Extended Spectrum Beta-Lactamase-Producing *Klebsiella pneumoniae* Infections – New Jersey, 2007

Board 329: Microbiological Agents as a Contributing Cause of Death in Wounded Service Members During Iraqi Freedom and Enduring Freedom

Outbreak Investigation: Lab & Epi Response

Board 330: PulseNet International and WHO Global Salm-Surv: A Collaborative Effort to Reduce the Global Burden of Enteric Diseases

Board 331: The Usefulness of a Web Forum and Online Questionnaire in the Investigation of an Outbreak of *Campylobacter jejuni* Associated with a Mountain Bike Race – British Columbia, Canada, June-July, 2007

Board 332: An Outbreak of Acute Respiratory Disease Caused by *Mycoplasma pneumoniae* in a Shipboard Environment

Board 333: Challenges to Contact Tracing Investigations Following International Airline Travel by Persons with Infectious Tuberculosis

Board 334: *Escherichia coli* O157 and Non-O157 Shiga Toxin-Producing *Escherichia coli* (STEC) Testing Among Clinical Laboratories Serving the FoodNet Catchment Area

Board 335: Laboratory and Epidemiologic Description of Children Infected with *Shigella sonnei* in Northwest Georgia

Social Determinants of Infectious Disease Disparities

Board 336: Predictors of Household Water Treatment among a Rural Population in Kenya

Board 337: Occupational Brucellosis in Xilinhaote, Inner Mongolia, China – 2007

Surveillance: International & New Strategies

Board 338: WHO Global Salm-Surv Country Databank

Board 339: WHO Global Salm-Surv: *Salmonella* Surveillance in China – 2006-2007

Board 340: FDA Tomato Safety Initiative: Preliminary Finding – Virginia, 2007

Board 341: An International Survey of Bioscience Research and Biosecurity Practices

Board 342: Evaluation of an Animal Health Electronic Laboratory Reporting Surveillance System: Characterizing an Outbreak of Anthrax in North Dakota

Board 343: Forecast and Validation of the Rift Valley Fever Outbreak in East Africa – 2006-2007

Board 344: WHO Global Salm-Surv: Providing a Platform for Training on Zoonosis, Food Security, and Antimicrobial Resistance Issues – 2006-2007

Board 345: Identification of Respiratory Disease Cases Using Outpatient ICD-9-CM Codes

Board 346: The Development of a Pediatric Population-based Encephalitis Study

Board 347: Risk Factors for Brucellosis in Samarqand Oblast, Uzbekistan

Tuberculosis

Board 348: Detection of *Nocardia* from Patients Diagnosed as Tuberculosis in Egypt

Board 349: Brazilian Tuberculosis Surveillance and Health Information System – 2001-2003

Board 350: Tuberculosis among Non-Residents Receiving Treatment in Brazil – 2001-2006

Board 351: Determining the Impact of HIV Infection on the Outcome of Patients Infected with Tuberculosis Meningitis

Board 352: Febrile Respiratory Illness and Tuberculosis in the CNMI: A Perspective Over a Decade

Vectorborne Diseases

Board 353: Dengue Outbreak at a Fishing Port – Guangdong Province, China, 2007

Board 354: Serologic Evidence of *Ehrlichia chaffensis* Infection in Peru

Board 355: Occupational Risk Factors Associated with a Large Increase in Malaria Cases on the Brazil-French Guiana Frontier – 2006

Board 356: Downregulated Expression of IL-4 and IL-10 in Mice Brain during Japanese Encephalitis Virus Infection

Board 357: Detection of *Rickettsia typhi* and *R. felis* in *Xenopsylla cheopis* from Hawaii

Board 358: The Potential for Introduction of Japanese Encephalitis Virus into California

Zoonotic & Animal Diseases

Board 359: Anthrax in Wabessa Village in the Dessie Zuria District of Ethiopia

Board 360: Animal Rabies Surveillance – Jordan, 2000-2007

Board 361: Host Ecology in Urban and Rural Habitats: Modeling Exposure Risk to Rabies in the Midwest

Board 362: A Comparison of the Impact of Rabid Foxes with Rabid Raccoons – New York State

Additional Poster Abstracts

(not submitted to a specific topic category)

Board 363: Profile of Meningococcal Infection: Report from a Developing Country

Board 364: Influenza

Board 365: Diversity of Picornaviruses – Rural Bolivia, 2002-2003

Board 366: Analysis of Genetic Diversity and Natural Selection in the Apical Membrane Antigen 1 of *Plasmodium falciparum* and *P. vivax* from India

Board 367: Analyzing Global Trends in EIDs, and Predicting the Origin of the Next New Zoonosis

Board 368: Increasing Resistance to Antimicrobials Among *Neisseria gonorrhoeae* Isolates in a Developing Country

Board 369: Prevalence of Hepatitis B Amongst Healthy Pregnant Women in a Developing Country

Board 370: The Preven Urban Community Randomized Trial of a Combined Intervention for Sexually Transmitted Disease Prevention in Nepal

Board 371: Modeling the Effects of Land-Use Changes on the Emergence of Hendra Virus

Board 372: S. Woo-Jin *(Note: No title was given.)*

Board 373: Nipah Virus Emergence in Malaysia 1998-1999 Was Due to Epidemic Enhancement in the Domestic Pig Population

Board 374: Five-Year Review of Etiology of Food and Waterborne Disease Outbreaks in the Philippines

Board 375: Case Report: Dual Infection of H5N1 Avian Influenza and H3N2 Human Influenza – Jakarta, Indonesia, April 2007

K1 Concurrent Panel Session

Malaria

1:15 PM – 2:45 PM | Centennial I

Conveners:

LIN CHEN, Harvard University, Boston, MA
S. PATRICK KACHUR, Centers for Disease Control and Prevention, Atlanta, GA

Moderators:

LIN CHEN, Harvard University, Boston, MA

Speakers:

Counterfeit Antimalarials and Public Health
PAUL NEWTON, Wellcome Trust – Mahoset Hospital – Oxford Tropical Medicine Research Collaboration, Vientiane, Lao PDR

"Can We Eradicate Malaria in Africa: An Historical Perspective"
RANDALL PACKARD, John Hopkins University, Baltimore, MD

"Update on Vivax Malaria"
ELI SCHWARTZ, Center for Geographic Medicine, Tel Hashomer, Israel

K2 Concurrent Panel Session

New Advances in Laboratory Techniques

1:15 PM – 2:45 PM | Centennial II

Conveners:

J. MICHAEL MILLER, Centers for Disease Control and Prevention, Atlanta, GA
JANET NICHOLSON, Centers for Disease Control and Prevention, Atlanta, GA

Moderators:

J. MICHAEL MILLER, Centers for Disease Control and Prevention, Atlanta, GA
JANET NICHOLSON, Centers for Disease Control and Prevention, Atlanta. GA

Speakers:

Genomic Approaches to Viral Detection and Identification
DAVID WANG, Washington University School of Medicine, St. Louis, MO

Proteomic Characterizations of Emerging Pathogens, Vaccine Responses, and Host Response Proteins in Clinical Fluids
RICHARD DRAKE, Eastern Virginia Medical School, Norfolk, VA

Translating Bacterial Genomics to Medical Microbiology
JAMES VERSALOVIC, Texas Children's Hospital, Houston, TX

K3 Concurrent Panel Session

Political/Social Issues & EIDs

1:15 PM – 2:45 PM | Regency VII

Conveners:

LARRY MADOFF, Harvard Medical School, Boston, MA
MICHAEL ST. LOUIS, Centers for Disease Control and Prevention

Moderator:

LARRY MADOFF, Harvard Medical School, Boston, MA

Speakers:

Social and Political Aspects of an Emerging Zoonosis Outbreak
PIERRE FORMENTY, World Health Organization, Geneva, Switzerland

HIV/AIDS Care in Resource Poor Settings
SERENA KOENIG, Brigham and Women's Hospital, Boston, MA

Contemplating Epidemics: Social, Economic, Political, and Cultural Aspects of Contagious Crises Across Time
HOWARD MARKEL, University of Michigan, Ann Arbor, MI

K4 Concurrent Panel Session

International New Vaccine Initiatives

1:15 PM – 2:45 PM | Centennial III

Conveners:

SUSAN GOLDSTEIN, Centers for Disease Control and Prevention, Atlanta, GA
ABIGAIL SHEFER, Centers for Disease Control and Prevention, Atlanta, GA
ANGELA WEAVER, US Agency for International Development, Washington, DC

Moderators:

ABIGAIL SHEFER, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:

The Science and Programmatic Issues of the Switching from OPV to IPV in the Context of the Global Polio Eradication Program
STEVE COCHI, Centers for Disease Control and Prevention, Atlanta, GA

HPV Vaccine: Issues for Introduction in Developing Countries
VIVIEN TSU, Program for Appropriate Technologies in Health (PATH), Seattle, WA

Rotavirus Vaccines: The Continuing Challenges Ahead
ROGER GLASS, Fogarty International Center, National Institutes of Health, Bethesda, MD

K5 Concurrent Panel Session

Bloodborne Pathogens

1:15 PM – 2:45 PM | Centennial IV

Conveners:

JOANNA BUFFINGTON, Centers for Disease Control and Prevention, Atlanta, GA
CAROL CHENOWETH, University of Michigan, Ann Arbor, MI
TAMMY LUNDSTROM, Wayne State University, Detroit, MI

Moderators:

JOSEPH PERZ, Centers for Disease Control and Prevention, Atlanta, GA
CARMEM LUCIA PESSOA-SILVA, World Health Organization, Geneva, Switzerland

Speakers:

Applying Standard Precautions Universally
CARMEM LUCIA PESSOA-SILVA, World Health Organization, Geneva, Switzerland

Trends in Transfusion-Transmissible Infections and Progress in Blood Safety
LAWRENCE MARUM, Centers for Disease Control and Prevention, Atlanta, GA

Update on Safe Injection Global Network (SIGN) Initiatives
SELMA KHAMASSI, World Health Organization, Geneva, Switzerland

Ebola in Kikwit and Kasai: Infection Control Challenges
PETER KILMARX, Centers for Disease Control and Prevention, Atlanta, GA

Break

2:45 PM – 3:00 PM | Centennial Foyer/Regency Foyer

L1 Slide Session

New Rapid Diagnostics

3:00 PM – 4:30 PM | Centennial I

3:00 – 3:15 PM
Application of Proteomics Methods for Pathogen Discovery
DONGXIA (DON) WANG, Centers for Disease Control and Prevention

3:15 – 3:30 PM
Evaluation of QuickVue Influenza A+B Rapid Diagnostic Test in a Community Setting
BENJAMIN COWLING, The University of Hong Kong

3:30 – 3:45 PM
Evaluation of an Antigen-Capture ELISA to Detect *Histoplasma capsulatum* Antigenuria in Immunocompromised Patients
CHRISTINA SCHEEL, Centers for Disease Control and Prevention

3:45 – 4:00 PM
***Mycobacterium tuberculosis:* Direct from Sputum Identification and Determination of Drug Resistance within Hours for all Antimycobacterial Agents**
NICOLE PARRISH, Johns Hopkins University

4:00 – 4:15 PM
Rapid Identification of Class A Biothreat and Other Clinically Relevant Bacterial Pathogens Using Universal PCR Coupled with High Resolution Melt Curve Profile Analysis
SAMUEL YANG, Johns Hopkins University

4:15 – 4:30 PM
The Use of a Real-Time Multiplex PCR for Detection of Sporadic and Outbreak Cases Caused by Free-Living Amoeba
KAKALI BANDYOPADHYAY, Centers for Disease Control and Prevention

L2 Slide Session

Mobile Populations & Infectious Diseases

3:00 PM – 4:30 PM | Centennial II

3:00 – 3:15 PM
Survey of US Travelers to Asia to Assess Compliance with Recommendations for Japanese Encephalitis Vaccine
MARK DUFFY, Centers for Disease Control and Prevention

3:15 – 3:30 PM
***Brucella melitensis* Infection Following Duty in Iraq**
L. CARPENTER, Tennessee Department of Health, Communicable and Environmental Disease Services

3:30 PM – 3:45 PM
Persistent Gastroenteritis Outbreak Due to a New Variant Norovirus Spanning Multiple Cruises of a Domestic Riverboat and Affecting On-Shore Contacts – Ohio and Mississippi Rivers, 2006
GWEN EWALD, Centers for Disease Control and Prevention

3:45 – 4:00 PM
Occurrence of Infectious Diseases in US Veterans of Recent Military Conflict
GARY ROSELLE, US Department of Veterans Affairs, Veterans Health Administration (VHA) Central Office Infectious Diseases Program, and Cincinnati VA Medical Center, and University of Cincinnati

4:00 – 4:15 PM
Five-Year Experience with Type 1 and Type 2 Reactions in Hansen's Disease at a US Travel Clinic
JESSE JACOB, Emory University

4:15 – 4:30 PM
Exposure to Infectious Tuberculosis (TB) during Air Travel: Outcome of Passenger Contact Investigations Initiated during June-October, 2007
KAREN MARIENAU, Centers for Disease Control and Prevention

L3 Slide Session

Vaccine-Preventable Diseases

3:00 PM – 4:30 PM | Regency VII

3:00 – 3:15 PM
Reducing Global Disparities in the Use of Hib Vaccine
LINDA OJO, Centers for Disease Control and Prevention

3:15 – 3:30 PM
Rotavirus Burden in Central Asia: The Value of New Rotavirus Vaccines
ELMIRA FLEM, Norwegian Institute of Public Health

3:30 – 3:45 PM
An Evaluation of the Implementation of the Reaching Every District (RED) Approach – Sudan, Africa, 2007
TOVE RYMAN, Centers for Disease Control and Prevention

3:45 – 4:00 PM
Pneumococcal Meningitis among Adults and Children in the Era of the Pneumococcal Conjugate Vaccine: An Update from Active Bacterial Core Surveillance (ABCs)
HEATHER E. HSU, University of Pennsylvania

4:00 – 4:15 PM
Disease and Economic Burden of Rotavirus Diarrhea in Western Kenya
JACQUELINE TATE, Centers for Disease Control and Prevention

4:15 – 4:30 PM
Etiologies of Bacterial Meningitis in Bangladesh
EMILY GURLEY, ICDDR,B

L4 Slide Session

Tuberculosis

3:00 PM – 4:30 PM | Centennial III

3:00 – 3:15 PM
Evaluation of Microscopic Observation Drug Susceptibility Assay for the Concurrent Detection of Tuberculosis/Multidrug-Resistant Tuberculosis
GIRUM EJIGU, Medical Faculty, College of Health Sciences, Hawassa University

3:15 – 3:30 PM
Differences in Tuberculosis Knowledge between U.S.-Born and Foreign-Born Adults
HEATHER FREE, Centers for Disease Control and Prevention

3:30 – 3:45 PM
Overseas Screening for Tuberculosis (TB) in US-Bound Immigrants and Refugees – 1999-2004
YECAI LIU, Centers for Disease Control and Prevention

3:45 – 4:00 PM
Investigation of a Multidrug-Resistant *Mycobacterium tuberculosis* Outbreak in a Foreign-Born Community - Tennessee, 2007
ROQUE MIRAMONTES, Centers for Disease Control and Prevention

4:00 – 4:15 PM
Rapid Multidrug-Resistance Profiling of *Mycobacterium tuberculosis*
CHRISTIAN MASSIRE, Ibis Biosciences, Inc.

4:15 – 4:30 PM
Descriptive Analysis of TB Patients Treated in a Binational Setting
MIGUEL ESCOBEDO, Centers for Disease Control and Prevention

L5 Slide Session

Sexually Transmitted Diseases

3:00 PM – 4:30 PM | Centennial IV

3:00 – 3:15 PM
High Incidence of HIV-I Infection among Pregnant Youth in Four Provinces of Cameroon
MINN SOE, Emory University

3:15 – 3:30 PM
Cost Effectiveness of Chlamydia Screening Policies among Male Military Recruits
REMINGTON NEVIN, Army Medical Surveillance Activity

3:30 – 3:45 PM
Evaluation of Congenital Syphilis Surveillance in Brazil: High Prevalence, Low Treatment Rates, and Substantial Underreporting
ALESSANDRA SIQUEIRA, Field Epidemiology Training Program, Secretariat of Health Surveillance, Ministry of Health

3:45 – 4:00 PM
Host Genetic Determinants Predispose to Complications of *Chlamydia trachomatis* Infections
SANDER OUBURG, VU University Medical Center

4:00 – 4:15 PM
Three-Fold Increase in the Rate of Syphilis among US Air Force Personnel, 2000-2006
NICOLE PEDUZZI, Air Force Institute for Operational Health

4:15 – 4:30 PM
Herpes Simplex Virus (HSV) Infection in New York State Excluding New York City (NYS) – 1994-2003
PERRY SMITH, New York State Department of Health

Poster & Slide Session Abstracts

Poster Sessions

Monday, March 17, 12:00 PM – 1:00 PM	Posters 1 – 73
Monday, March 17, 5:00 PM – 6:00 PM	Posters 74- 146
Tuesday, March 18, 12:00 PM – 1:00 PM	Posters 147- 218
Tuesday, March 18, 5:00 PM – 6:00 PM	Posters 219 – 290
Wednesday, March 19, 12:00 PM – 1:00 PM	Posters 291 – 375

Slide Sessions

Monday, March 17, 1:15 PM – 2:45 PM	Slide Session C
Monday, March 17, 3:00 PM – 4:30 PM	Slide Session D
Tuesday, March 18, 1:15 PM – 2:45 PM	Slide Session H
Wednesday, March 19, 3:00 PM – 4:30 PM	Slide Session L

Poster & Slide Session Abstracts

Vaccines & Vaccine-Preventable Diseases

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 1. Genetic Diversity And Zoonotic Potential Of Human Rotavirus Strains, Hungary (2003-2006)

K. Banyai[1], A. Bogdan[2], G. Domonkos[1], P. Kisfali[2], P. Molnar[3], B. Laszlo[4], I. Mihaly[3], B. Melegh[2], J. Konya[4], V. Martella[5], J. R. Gentsch[6], G. Szucs[1];

[1]ANTSZ Baranya County Institute of State Public Health Service, Pecs, HUNGARY, [2]University of Pecs, Pecs, HUNGARY, [3]"St. Laszlo" Central Hospital for Infectious Diseases, Budapest, HUNGARY, [4]University of Debrecen, Debrecen, HUNGARY, [5]University of Bari, Bari, HUNGARY, [6]Centers for Disease Control and Prevention, Atlanta, GA.

Background: Rotavirus strain surveillance is being conducted in many countries before and after introduction of newly licensed vaccines to assess the impact of the vaccines on rotavirus strains. The huge serotype diversity of human rotaviruses and detection of numerous reassortants with genetic relationships with animal and human rotaviruses suggests that it will be important to continue routine strain surveillance to better understand rotavirus evolution and track strains that may escape vaccine elicited immunity. In this report we describe a strain surveillance study in the Budapest area of Hungary. **Methods:** Laboratory methods of our strain surveillance included RNA profile analysis, genotyping of the outer capsid genes, VP7 (G) and VP4 (P), using type-specific primers in multiplex PCR and consensus primers specific to VP7, VP4, VP6 and NSP4 genes in nucleotide sequencing. **Results:** During the 3-year surveillance period a total of 1983 rotavirus strains were G typed. The relative frequencies of individual G types were: G1 (22%), G2 (4.8%), G3 (3.5%), G4 (18.5%), G6 (1.1%), G8 (<0.1%, n=1), G9 (42%), and G12 (3.4%). Information on P genotype incidence was determined for a subset of samples (n=814). In addition to the globally important strains a variety of uncommon antigen combinations (P[8],G12; P[4],G3; P[8],G2; P[6],G4; P[9],G3; P[9],G6; P[14],G6 and P[14],G8) were also found. Sequence and phylogenetic analysis of the VP7, VP4, VP6 and NSP4 genes of selected strains with uncommon antigen combinations demonstrated high similarity with bovine, porcine, and feline rotaviruses, respectively. **Conclusions:** Unlike the globally distributed variants of human P[8],G9 and P[8],G12 strains most of which carry a single gene (VP7) of animal origin, the P[6],G4; P[9],G3; P[9],G6; P[14],G6; and P[14],G8 rotaviruses identified thus far in several countries may have multiple genes of animal origin. In this study evidence is presented for the (i) independent zoonotic transmission of the same type specificities and that (ii) circulation of animal-like strains might be sustained in humans when they undergo gene reassortment with human rotaviruses. Comprehensive genome sequence data on human and animal rotavirus strains is a key to understand the significance of the zoonotic potential of rotaviruses.

Board 2. Study on Protective Effects For 10 Years After Vaccinated by Vaccines Against Hemorrhagic Fever With Renal Syndrome

G. Zhenyu[1], w. jingqing[1], f. chunfu[2], C. Enfu[1], L. Jinbao[3], W. Zhen[1], H. Fan[1], L. Biyao[1], l. junfen[1], C. liming[1], D. Gangqiang[1];

[1]Zhejiang center for disease control and prevention,P.R.CHINA, Hangzhou, CHINA, [2]Quzhou center for disease control and prevention,P.R.CHINA, Hangzhou, CHINA, [3]Longyou center for disease control and prevention,P.R.CHINA, Longyou, CHINA.

Background: In China, hemorrhagic fever with renal syndrome(HFRS), caused by Hantaan (HNT) and Seoul (SEO) viruses, has an average morbidity and mortality rate of is 3.5 and 0.07 per 100,000 and affects mainly farmers. Three inactivated HFRS inactivated vaccines (HNT, SEO and bivalent) have been developed. We carried out a field trial of HNT vaccine in an endemic area (HFRS incidence rate = 22 per 100,000) of Zhejiang Province, China, to evaluate its immunogenicity and effectiveness. **Methods:** We selected 15 villages (10460 persons) for vaccination and 25 villages (16203 persons) as unvaccinated controls in an endemic county. We obtained informed consent from all subjects in the vaccination group to be vaccinated and from a sample of 67 to have periodic blood specimens taken. We administered 1 ml of HNT, inactivated HFRS vaccine on 0, 7, and 28 days in August, 1995, and a single booster in August, 1996. Our vaccinated group consisted of 10178 persons received all 4 doses of vaccine. We followed subjects actively for 50 days in 1995 and 15 days in 1996. Local doctors maintained surveillance for clinical HFRS throughout the 10 year trial. We tested sera of a sample of 67 persons in the vaccinated group before and 2 weeks after the initial series, before and 2 weeks, 12 months, 18 months, 2 years, 3 years, and 5 years after the booster dose. We used the immunofluorecent antibody (IFA) assay for IgG antibody and the Micro-CPE method for neutralizing antibody(NA). **Results:** Two weeks after the full-course vaccination, the sero-conversion rate was 100% (67/67)(95% *CI* is 96~100%) with a GMT = 72 by IFA and 44% (8/18)(95% *CI* is 22~69%) with a GMT = 4.6 by NA. IFA positive rates were 29% before boosting and rose to 83% two weeks after boosting. They then fell progressively to 10% after 3 years. NA positive rate were 15% before boosting rose to 56% after boosting and fell progressively to 10% after 3 years. Nine years after boosting, the IFA positive rate was 7.1%. No HFRS cases occurred in the vaccinated group compared to 34 HFRS in the control group (mean yearly incidence rate = 21 per 100,000). The ten-year vaccine effectiveness in this population approached 100% (95% *CI* is 96~100%). **Conclusions:** Although immunogenicity was not sustained at high levels, HFRS vaccine was highly effective to preventing HRFS in a typical rural population in an endemic area in China.

Board 3. Effectiveness of the 2007-08 Influenza Vaccine: Preliminary Data from US Military Basic Training Centers

A.W. Hawksworth, R. M. Grass, D. J. Faix, K. L. Russell;

Naval Health Research Center, San Diego, CA.

Background: Influenza vaccine effectiveness (VE) can vary each season, depending primarily on how well vaccine strains match circulating strains of influenza. Laboratory analyses of early season influenza A/H3 strains suggest a potential mismatch with the 2007-08 northern hemisphere vaccine. Ongoing febrile respiratory illness (FRI) surveillance at US military basic training centers captures

data and specimens that are leveraged to estimate influenza vaccine effectiveness on an annual basis. These data have demonstrated high VE in this setting during each of the past 4 years. **Methods:** Data from ongoing FRI surveillance at basic training centers were used to estimate VE against both laboratory-confirmed influenza (LCI) and nonspecific FRI (oral temperature of ≥ 100.5° F and either cough or sore throat) during periods when all trainees on base received influenza vaccination. Vaccine protection was assumed to begin 14 days post-vaccination in the primary analysis of VE. Alternative analyses were conducted using 7 days to vaccination coverage or less than complete vaccination among trainees. **Results:** Beginning in 2003-04, estimates of VE in this population were 94%, 86%, 92%, and 87% against LCI during 4 successive seasons. VE against nonspecific FRI was markedly lower each season. Preliminary data from 2007-08 will be presented in this poster using the same methodology used in previous seasons. **Conclusions:** This methodology allows season to season comparison of vaccine effectiveness in a manner that is cost-effective and timely. Influenza vaccination was highly protective against LCI in this population during the previous 4 seasons and will serve as a baseline for evaluation of 2007-08 vaccine performance. Protection against nonspecific FRI was much lower due to a preponderance of adenovirus among trainees, serving to validate the high VE seen against LCI. Influenza strains from vaccinated individuals are captured in this laboratory-based surveillance program and are valuable as potentially drifted strains. Surveillance strategies sensitive to changes in vaccine effectiveness are important as we heighten preparedness for pandemic influenza strains.

Board 4. Circulation of Type 2 Vaccine-Derived Poliovirus in Nigeria from 2005

J. Shaw, C. Burns, A. Williams, P. Chenoweth, M. Pallansch, O. Kew;

CDC, Atlanta, GA.

Background: From 2005 - 2007, an outbreak of type 2 circulating vaccine-derived poliovirus (cVDPV) occurred in nine northern states of Nigeria. Between July 2005 and September 2007, 79 cVDPV cases were identified in children with acute flaccid paralysis (AFP). In addition, viruses related to Sabin 2 oral poliovirus vaccine (OPV) strain with 0.5% - 0.9% divergence in the VP1 capsid coding region (903 nt) were isolated from stool specimens from 24 AFP cases in the same areas. About half of the cases were from Kano state, which also had wild type 1 and 3 poliovirus circulating at the same time. The spread of the poliovirus was mostly limited to neighboring states. **Methods:** Isolation of poliovirus RNA, Reverse-transcription polymerase chain reaction, Nucleotide sequencing, Phylogenetic analysis**. Results:** At least seven genetic lineages were circulating in 2005-2007, which suggested independent emergence of multiple cVDPV chains of transmission. All isolates shared a nucleotide substitution in the VP1 capsid protein at position T428C, which causes an amino acid reversion of I143T. This position is one of the two sites that have been identified as a determinant of attenuation for Sabin 2 OPV. The cVDPV cases within the same lineage were mostly locally restricted, and the viruses were closely related to each other. The majority of the isolates had recombined with Sabin 3 in the 5' UTR, with the remainder being Sabin 2- like or having recombined with other human enterovirus species C (HEV-C) viruses, either other circulating wild polioviruses or nonpolio enteroviruses. A collection of different 3Dpolymerase (3Dpol) sequences were observed. In addition to >10 different categories of 3Dpol recombinants containing sequences from unidentified HEV-C viruses, two Sabin recombinant viruses were identified: one each containing Sabin 1 or Sabin 3 3Dpol sequences. **Conclusions:** The identification of an outbreak of circulating vaccine-derived poliovirus in an area of low OPV coverage has important implications for maintaining a polio-free global population following eradication of wild poliovirus circulation.

Board 5. Opportunities for Prevention of Invasive Pneumococcal Disease among Adults with Diabetes

R. D. Muhammad[1], O. D. Johnson[2], K. M. Narayan[2], W. Schaffner[3], A. Thomas[4], C. Lexau[5], N. Bennett[6], M. M. Farley[7], L. Harrison[8], A. Reingold[9], J. Hadler[10], B. Beall[1], K. Klugman[2], M. R. Moore[1];

[1]Respiratory Diseases Branch, Centers for Disease Control and Prevention, Atlanta, GA, [2]Emory University, Rollins School of Public Health, Atlanta, GA, [3]Vanderbilt University School of Medicine, Nashville, TN, [4]Oregon Department of Human Services, Public Health Division, Portland, OR, [5]Minnesota Department of Health, Minneapolis, MN, [6]Monroe County Health Department and University of Rochester, Rochester, NY, [7]Emory University School of Medicine and the Atlanta Veterans Affairs Medical Center, Atlanta, GA, [8]University of Pittsburgh, Pittsburgh, PA, [9]University of California at Berkeley, School of Public Health, Berkeley, CA, [10]Connecticut Department of Public Health, Epidemiology Program, Hartford, CT.

Background: Adults with diabetes are at increased risk of invasive pneumococcal disease (IPD) compared to healthy adults. Since the introduction of 7-valent pneumococcal conjugate vaccine (PCV7) for children, rates of IPD among adults have declined. To identify prevention opportunities, we evaluated IPD outcomes and serotype distributions among persons with and without diabetes. **Methods:** Cases of IPD were defined by isolation of pneumococcus from a normally sterile site in adults ≥18 years of age residing in 8 Active Bacterial Core surveillance areas under continuous surveillance during 1998-2006. We compared the proportions of cases with DM alone (DM), diabetes and ≥1 underlying illness (DM+UI), ≥1 underlying illness without diabetes (UI), and no recorded underlying illness (NUI) during 2006 to the pre-PCV7 baseline period of 1998-1999. We determined serotype using the Quellung reaction and grouped cases into those potentially preventable with 23-valent pneumococcal polysaccharide vaccine (PPV23), PCV7, and a developmental 13-valent conjugate vaccine (PCV13). **Results:** During 1998-2006, we identified a total of 19,853 cases of IPD. Overall rates of IPD declined from 22 cases per 100,000 to 16 cases per 100,000 (-31%, 95% CI -34,-27). During the baseline, 3%, 7%, 43%, and 47% of IPD cases had DM, DM+UI, UI, and NUI, respectively. In comparison, in 2006, 6%, 15%, 51%, and 28% of IPD cases had DM, DM+UI, UI, and NUI, respectively ($P<0.0001$, X^2 comparing proportions with DM, DM+UI, and UI to NUI at baseline to 2006). In 2006, case-fatality ratios (CFRs) among IPD case-patients with DM, DM+UI, UI, and NUI were 2.5, 15, 16, and 7.5%, respectively. After adjusting for age, cases of IPD with diabetes did not have increased CFRs compared to cases without diabetes ($P=0.74$). Of the 428 cases with DM or DM+UI in 2006, 385 (90%) had available serotype results. The most common serotypes were 19A (15%), 3 (11%), 22F (9%), 7F (8%), and 6A (7%); 10%, 52%, and 61% of these cases would potentially be covered by PCV7, PCV13, and PPV23, respectively. **Conclusions:** Although rates of IPD among adults have declined dramatically since PCV7 introduction, diabetics now account for a larger proportion of IPD cases than before PCV7 introduction. Either PCV13 or PPV23 could potentially prevent a substantial proportion of cases.

Antimicrobial Resistance

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 6. *Salmonella enterica* serovar Heidelberg from Retail Meats: Results of the National Antimicrobial Resistance Monitoring System (NARMS): 2002-2006.

S. Zhao, E. Hall-Robinson, A. Glenn, S. Friedman, J. Abbott, S. Ayers, P. McDermott;

Food & Drug Administration, Laurel, MD.

Background: *Salmonella enterica* serovar Heidelberg is frequently associated with foodborne illness in humans, and is commonly isolated from poultry and their derived meats. A recent upsurge in antimicrobial resistance in this serovar has been recognized. There are few data on the prevalence, antimicrobial susceptibility, and genetic diversity of *S.* Heidelberg isolates in retail meats. **Methods:** We compared the prevalence of *S.* Heidelberg in a sampling of 20,294 meats, including chicken breast, ground turkey, ground beef and pork chops collected during 2002-2006 for the National Antimicrobial Resistance Monitoring System (NARMS). Isolates were analyzed for antimicrobial susceptibility and compared genetically using pulsed-field gel electrophoresis (PFGE). **Results:** A total of 297 *S.* Heidelberg isolates were recovered, representing 22% (297/1372) of all *Salmonella* serovars from retail meats. Among the 297 isolates, 178 (60%) from ground turkey, 109 (37%) from chicken breast and 10 (2%) from pork chop; no *S.* Heidelberg was found in ground beef. A total of 197 (66%) of the isolates were resistant to at least one of the 15 antimicrobial agents tested and 49 (16%) of the isolates were resistant to ≥5 antimicrobials. Five isolates (1.7%) were resistant to ≥9 antimicrobials, all of which were recovered form ground turkey. The proportion of resistance to different antimicrobials were: tetracycline (40%), streptomycin (38%), sulfamethoxazole (30%), gentamicin (27%), and kanamycin (21%), ampicillin (19%), amoxicillin-clavulanic acid (10%), cefoxitin (9%), ceftiofur (9%), chloramphenicol (1%), and nalidixic acid (1%). Resistance was consistently more prevalent in *S.* Heidelberg from ground turkey than from chicken breast. All isolates were susceptible to amikacin, ceftriaxone, ciprofloxacin and trimethoprim/ sulfamethoxazole. PFGE using *Xba*I and *Bln*I generated 107 patterns. Certain clones were widely dispersed in different types of meats and meat brands from different store chains in all three sampling years. **Conclusions:** These date indicate that *S.* Heidelberg is a common serovar in retail poultry meats, and includes clones of multidrug-resistant strains.

Board 7. Community-Associated Methicillin-Resistant *Staphylococcus aureus* Infection Risk Factor Study

K. Como-Sabetti[1], K. Harriman[2], S. Fridkin[3], R. Lynfield[4];

[1]Minnesota Department of Health, Minneapolis, MN, [2]California Department of Public Health, Richmond, CA, [3]Centers for Disease Control and Prevention, Atlanta, GA, [4]Minnesota Department of Health, Saint Paul, MN.

Background: Little is known about risk factors for methicillin-resistant *Staphylococcus aureus* (CA-MRSA) infection in non-outbreak settings. **Methods:** MN Department of Health initiated a hypothesis-generating CA-MRSA case control study in 2003. 150 patients with *S. aureus* infections, including both CA-MRSA and CA methicillin-sensitive SA (MSSA), were identified by 3 sentinel labs. 2-3 age-group matched healthy community controls (CC) were identified by sequential digit dialing. Participants were interviewed about possible risk factors and an antibiotic history was obtained from healthcare providers. Univariate and multivariate conditional logistic regression were conducted using SAS for 3 separate analyses to avoid biased estimates: CA-MRSA cases vs. CA-MSSA cases, CA-MRSA cases vs. CA-MRSA CCs, and CA-MSSA cases vs. CA-MSSA CCs. **Results:** 75 CA-MRSA and CA-MSSA cases and 438 CCs were enrolled. Antibiotic use in the prior 1-6 months (recent ABX) was more frequent among CA-MRSA cases than CA-MSSA cases or CCs (33% vs. 17% vs. 14%). History of boils was infrequent (10% CA-MSSA, 1% CA-MSSA, 1% CCs). Race, education, income, household members per room, dog in the home, history of boils, and towel sharing were associated with CA-MRSA when compared to CA-MSSA or CA-MRSA CCs. Recent ABX and number of recent ABX courses were associated with CA-MRSA when compared to CA-MSSA cases ($p=0.03$; OR=2.5, and $p<0.01$; OR=2.2 respectively) and persisted when compared to CA-MRSA CCs ($p=0.05$; OR=2.3, and $p=0.02$; OR=1.9 respectively), but were not associated with CA-MSSA cases compared to CA-MSSA CCs. After adjusting for socioeconomic factors, history of boils was associated with CA-MRSA compared to CA-MSSA ($p=0.002$; AOR=76.8) but not when compared to CA-MRSA CCs. Recent ABX and ABX courses were associated with CA-MRSA compared to CA-MSSA ($p=0.02$, AOR=1.9, and $p=0.01$, AOR=2.2 respectively) and compared to CA-MRSA CCs ($p=0.05$, AOR=2.4, and $p=0.02$ and AOR = 1.9 respectively). **Conclusions:** In non-outbreak settings, antibiotic use and history of boils (which may be a proxy for prior CA-MRSA skin disease) appear to be risk factors for CA-MRSA. Further investigation of antibiotic use and specific antibiotic classes is needed. Although not definitive, this study reinforces the importance of careful antibiotic stewardship.

Board 8. Antimicrobial Resistance in *Salmonella* Serotype Schwarzengrund from Human and Retail Poultry Isolates in the United States

R. Rickert[1], F. Medalla[2], E. Robinson-Hall[3], J. M. Whichard[2], G. Pecic[1], A. Glenn[3], S. Ayers[3], E. J. Barzilay[2], P. F. McDermott[3], D. White[3];

[1]Atlanta Research and Education Foundation/Centers for Disease Control and Prevention, Atlanta, GA, [2]Centers for Disease Control and Prevention, Atlanta, GA, [3]Food and Drug Administration, Center for Veterinary Medicine, Laurel, MD.

Background: Non-Typhi *Salmonella* (NTS), a common cause of human gastroenteritis, is estimated to cause 1.4 million cases each year in the U.S. *Salmonella* serotype Schwarzengrund is among the 40 most frequently identified human NTS serotypes in the U.S., and ranked 5th among retail meat isolates in 2004. A study of human and poultry *Salmonella* Schwarzengrund isolates in Denmark, Thailand and the U.S. in which human and poultry isolates showed resistance to quinolones (nalidixic acid, ciprofloxacin) suggests that resistant *Salmonella* Schwarzengrund is disseminated internationally by poultry products from Thailand. **Methods:** The National Antimicrobial Monitoring System (NARMS) at CDC monitors antimicrobial resistance in NTS isolates from ill people. From 1996-2005, sites submitted NTS isolates to CDC for susceptibility testing. Participation increased from 14 sites in 1996 to all 50 states and 3 local health departments in 2003. NARMS retail meat surveillance began in 2002 with 5 sites and increased to 10 sites in 2005. Minimum inhibitory concentrations were determined by broth microdilution and interpreted using Clinical Laboratory Standards Institute criteria when available. We compared resistance in U.S. *Salmonella* Schwarzengrund isolates from humans (1996-2005) and retail poultry (2002-2005). **Results**: Of 73 clinical isolates of *Salmonella* Schwarzengrund from humans tested from 1996-2005; 5 (7%) were nalidixic acid-resistant and 3 (4%) were ciprofloxacin-resistant. Schwarzengrund was the 2nd most common ciprofloxacin-resistant NTS serotype, accounting for 3 (16%) of 19 ciprofloxacin-

resistant NTS identified in NARMS from 1996-2005. There were 34 *Salmonella* Schwarzengrund isolates from retail poultry: 7 chicken breast and 27 ground turkey. Resistance to ciprofloxacin or nalidixic acid was not observed in isolates from retail poultry. **Conclusions:** *Salmonella* Schwarzengrund is the 2nd most common ciprofloxacin-resistant serotype among human NTS in NARMS. Resistance to ciprofloxacin and nalidixic acid was observed in isolates from humans but not from retail poultry. Continued monitoring of resistance in clinical and poultry isolates is important to gain a greater understanding of the emergence and dissemination of quinolone resistance in *Salmonella* Schwarzengrund.

Board 9. Multi-Resistant Isolates of *Salmonella* Enteritidis from the Russian Federation

E. G. Simonova[1], S. S. Rozhnova[1], S. A. Greene[2], E. J. Barzilay[3];

[1]Central Reseach Institute of Epidemiology, Moscow, RUSSIAN FEDERATION, [2]Atlanta Research and Education Foundation, Decatur, GA, [3]Centers for Disease Control and Prevention, Atlanta, GA.

Background: In 2004, the incidence of salmonellosis in the Russian Federation was 33.9 per 100,000 inhabitants. More than 70% of all Salmonella infections are due to *Salmonella* Enteritidis. This serotype has also been isolated in 37-56% of retail food products and 21-74% of environmental samples. While most infections are self-limiting, antimicrobial agents are critical for the treatment of severe illness. **Methods:** From January 2006 to March 2007, 250 strains of *Salmonella* Enteritidis were collected from stool of children ages <1 - 15 years, median age 33 months, hospitalized for salmonellosis in several children's health clinics in Moscow. Isolates were tested for susceptibility against a panel of 7 classes of 21 antibiotics using ATB-G plates (BioMérieux, Lyon, France). Minimum Inhibitory Concentrations (MIC) were interpreted according to Clinical and Laboratory Standards Institute (CLSI) criteria. **Results:** Resistance to aminoglycosides was highest, followed by 1st generation cephalosporins, and quinolones. Of the 250 *Salmonella* Enteritidis isolates resistant to aminoglycosides, 50.4% (126) were tobramycin-resistant, 42.8% (107) were gentamicin-resistant, 42.4% (106) were netilmicin-resistant, and 30.8% (77) were amikacin-resistant. Resistance to 1st generation cephalosporins, nalidixic acid, and ß-lactamase inhibitor (amoxicillin-clavulanic acid) was 42.4% (106), 26.7% (67) and 8% (20) of isolates, respectively. Resistance to ciprofloxacin and 4th generation cephalosporins was not observed. **Conclusions:** This study provides critical information about multi-drug resistance in *Salmonella* Enteritidis isolates in the Russian Federation. A national monitoring system should continue to be implemented to determine prevalence estimates of antimicrobial resistance. Salmonella surveillance and antimicrobial resistance data can guide efforts to optimize efficacy of clinical treatments.

Board 10. Surveillance of Antimicrobial Resistance at the Louisiana Animal Disease Diagnostic Laboratory: The LARSS (LADDL/OPH Antimicrobial Resistance Surveillance) System

G. A. Balsamo[1], R. Ratard[1], A. Roy[2];

[1]Louisiana Office of Public Health, New Orleans, LA, [2]Louisiana Animal Disease Diagnostic Laboratory, Baton Rouge, LA.

Background: Development of resistance to antimicrobial drugs complicates medical therapy and increases health care costs in both human and veterinary medicine. In human medicine surveillance for development of microbial resistance is often carried out in healthcare facilities, such as hospitals and nursing homes. However antimicrobial use in veterinary medicine, agriculture and human medicine certainly influences antimicrobial resistance across disciplines. In an effort to monitor development of antimicrobial resistance in veterinary medicine in Louisiana, data from LADDL are examined by a surveillance system that monitors changes in resistance patterns of antimicrobials against common genera of organisms, differences in resistance profiles by source of submission (from general veterinary practices or from the referral hospital at LSUSVM), and tracks the microbes most commonly isolated in samples submitted from different anatomic sites or organ groups. **Methods:** Trends in resistance are analyzed using the Cochrane-Armitage test for trend. Differences in resistance by source of submission are analyzed by a chi-square analysis or Fisher Exact Test, and the microbial makeup of infections in specific anatomical sites is displayed in annual and multi-year cohorts to facilitate surveillance determining changes in predominant microorganisms identified in common infections. **Results:** Antimicrobial sensitivity profiles for each anti-microbial/bacterial genera combination is displayed online for public access. Detected increasing and decreasing trends in resistance are displayed in graphic form. Proportions of organisms cultured from different anatomical sites are displayed in tabular form. **Conclusions:** Surveillance for detection of resistance and knowledge of in vitro sensitivity histories for anti-microbial/bacterial combinations are helpful to practitioners for decisions related to evidence based antimicrobial therapy and judicious use of antimicrobials. The information regarding resistance trends can be used in comparisons across different species and may result in hypotheses generation for studies of antimicrobial resistance in the varied disciplines that constitute veterinary medicine. All significant results will be displayed on the OPH website.

Climate Changes

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 11. Climate Change and the Prediction of Infectious Disease

V. Dhara;

Computer Sciences Corp@Centers for Disease Control, Atlanta, GA.

Background: Climate change has the potential for influencing the earth's biological systems and its impact on human health is still emerging. The 2007 IPCC report noted that 'there is evidence of climate-change related shifts in the distribution of disease vectors and other infectious diseases.' **Methods:** Development of predictive models for infectious disease is vital for the identification of susceptible populations, implementation of early warning systems, and provision of health care services. Improvements in meteorology have enabled better understanding of long-term changes in weather patterns. This paper reviews examples of two diseases in the Indian sub-continent, malaria and cholera, and the Ross River virus disease in Australia. **Results:** The multifactorial nature of malaria causation does not permit a simple model of disease prediction. To determine the role of climate change in malaria transmission, research efforts incorporating a disease surveillance system that combine trend analyses from multiple sites to account for local factors are required. The discovery of V. cholera's existence in the natural environment changed the understanding that cholera was transmitted only from person-to-person. A relationship has been observed between increases in sea-surface temperature and the onset of cholera epidemics, with cholera outbreaks following the seasonal rise and fall in sea-surface height and temperature. Weather data from two regions in southeastern Australia were matched with Ross River virus disease data for 1991-99. By mapping multiple

datasets into geographic information systems (GIS), the study was able to detect emerging patterns of disease and demonstrate spatial and temporal association with excessive rainfall. **Conclusions:** Both Ross River virus disease and cholera have been noted to be associated with climate change. Molecular analysis and application of epidemiological datasets to GIS have permitted the development of predictive models of disease occurrence. Because of the complex social and demographic multifactorial causes of malaria, a comprehensive research effort will be required to determine if associations with climate change exist. Monitoring of infectious disease spread will be needed to develop early warning systems which have both health and economic benefits.

Foodborne & Waterborne Infections

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 12. Trends in Toxin Profiles of Human Shiga Toxin-producing *Escherichia coli* (STEC) O157 Strains, United States, 1999-2006

M. Joyner, C. Bopp, P. Gerner-Smidt, L. Gould, P. Griffin, N. Strockbine;

Centers for Disease Control, Atlanta, GA.

Background: Shiga toxin-producing *E. coli* (STEC) cause diarrhea, hemorrhagic colitis, and hemolytic uremic syndrome (HUS). All STEC produce one or both of two Shiga toxins, Stx1 and Stx2. STEC strains that produce Stx2 are more strongly associated with HUS than strains that produce both Stx1 and Stx2 or only Stx1. We examined trends in toxin profiles of human STEC O157 isolates from 1999 to 2006. **Methods:** The PulseNet *E. coli* national database contains subtype patterns of STEC strains isolated from humans. PulseNet participants electronically submit subtype patterns of STEC O157 isolates and toxin profiles to the national database. Toxin profiles were determined by PCR of the toxin genes for Stx1 and Stx2. Human isolates of STEC O157 submitted to the national database during 1999-2006 were classified based on their toxin profiles into Stx1-only, Stx2-only, or Stx1 + Stx2. **Results:** During 1999-2006, information was submitted on 2293 isolates; the number of isolates reported increased each year, in parallel with the maturation of the database. The overall proportion with Stx1-only was 2%, Stx2-only 43%, and Stx1 + Stx2 56%. The percent of isolates that were Stx2-only increased from a low of 11% in 1999 to a high of 56% in 2006. The percent of isolates that were Stx1 + Stx2 decreased from a high of 87% in 1999 to a low of 43% in 2006. Fewer than 10% of strains were Stx1-only in any year. **Conclusions:** This dramatic shift in the toxin profile of human STEC O157 strains is unexplained. The increased proportion of strains producing only Stx2 may result in a higher incidence of HUS relative to the incidence of STEC O157 infections. Further work is needed to determine the subtype of Stx2 genes in these strains, to characterize isolates from animal reservoirs and foods, and to compare these shifts with patterns in other countries.

Board 13. Risk factors for Shiga toxin producing *Escherichia coli* O157 infection in Australia

M. McPherson[1], J. Raupach[2], M. Kirk[3], B. Combs[1];

[1]OzFoodNet, Adelaide, AUSTRALIA, [2]Communicable Disease Control Branch, Deparment of Health, Adelaide, AUSTRALIA, [3]OzFoodNet, Canberra, AUSTRALIA.

Background: Shiga toxin producing *Escherichia coli* (STEC) causes acute gastroenteritis characterised by abdominal cramps and bloody diarrhoea. In Australia, serotype O157 is the predominant strain of STEC, causing 60% of all infections. To investigate risk factors for STEC O157 infection, we conducted an Australia-wide case control study between 2003 and 2007. **Methods:** Patients infected with STEC O157 that were notified to health departments were eligible for the study and three controls per case were selected from a bank of controls based on sex and five year age groups. Cases were recruited in South Australia from July 2003, with all other Australian states participating from 2005. A standardised questionnaire was used to collect information regarding demographic data, food, behavioural and environmental exposures. All factors associated at the univariate level ($p<0.1$) were included in a categorical logistic regression model. **Results:** There were 43 cases of STEC O157 and 117 controls recruited in the study. For cases, mean duration of diarrhoea was six days (range 2-22 days) and 49% were hospitalised with a mean stay of four nights. In multivariate analysis, STEC O157 infection was associated with eating hamburgers (OR=6.6, 95% CI=2.2-20.0), eating out of the home (OR=4.8, 95% CI=1.7-13.6) and living on or visiting a farm (OR=4.6, 95% CI=1.2-17.6). Eating home grown fruit or vegetables was negatively associated with infection (OR=0.2, 95% CI=0.1-0.8). **Conclusions:** This is the first study in Australia to identify that contact with animals and eating hamburgers may increase the risk of STEC O157 infection. Similar findings have been reported internationally, suggesting that these risk factors are not geographically specific.

Board 14. Travel-Associated Legionnaires' Disease Cases in the United States (U.S.)

N. T. Alexander[1], M. Moore[2], B. Fields[2], L. Hicks[2];

[1]CDC/AREF, Atlanta, GA, [2]CDC, Atlanta, GA.

Background: Legionnaires' disease (LD) is a severe pneumonia caused by inhalation of aerosolized water containing *Legionella* bacteria. An estimated 21% of all LD is travel-associated. Travel-associated LD clusters can go unrecognized, as case-patients often develop symptoms after returning home. With proper identification of clusters and remediation of the implicated water source, further cases of LD are preventable. **Methods:** We analyzed U.S. surveillance data from CDC's LD surveillance system (LDSS) from 2005-2006. Travel-associated cases had clinical or x-ray confirmed pneumonia and laboratory confirmation of LD infection with travel away from home ≥1 night during 2-14 days before illness onset. We also reviewed travel-associated clusters (≥2 cases with travel to the same location in ≤1 year). **Results:** In 2005-2006, 1393 confirmed LD cases were reported; 341 (24%) were travel-associated. Nearly all (315, 92%) travel-associated cases occurred among U.S. residents; 26 (8%) occurred among visitors to the U.S. Thirty-two states (64%) reported at least one travel-associated case. The median age among case-patients was 60 years (range 20-89); 225 (73%) of 307 were male, 279 (97%) of 287 were hospitalized, and 18 (7%) of 262 died. Of 291 U.S. resident case-patients with detailed travel information, 232 (78%) reported domestic travel only, 35 (12%) reported international travel only and 24 (8%) reported both. U.S. resident case-patients reported travel to 42 states, 3 territories and 25 countries. Among U.S. residents with domestic travel only, 115 (50%) reported a hotel stay; 78 (34%) in a private residence, vehicle or campsite; 7 (3%) in an other accommodation; and 46 (20%) in an unknown accommodation. Ten clusters were identified affecting 25 case-patients. **Conclusions:** LD cases have been identified in association with travel to most U.S states. Hotels were the most common travel exposure. Enhanced surveillance and improved communication with international and state public health partners will assist in the identification of additional clusters and contribute to the prevention of travel-associated LD cases.

Board 15. Multi Drug Resistant *Salmonella* Concord In Adoptee From Ethiopia

R. S. Hendriksen[1], M. Mikoleit[2], C. Kornschober[3], F. Angulo[2], M. Biggerstaff[2], M. Cormican[4], H. Hasman[1], J. Threlfall[5], D. Mevius[6], C. Kjelsø[7], F. M. Aarestrup[1];

[1]WHO Collaborating Centre for Antimicrobial Resistance in Foodborne Pathogens and Community Reference Laboratory for Antimicrobial Resistance, National Food Institute (DTU), Copenhagen V, DENMARK, [2]WHO Collaborating Centre for Surveillance, Epidemiology and Control of Salmonella and other Foodborne Diseases, Centers for Disease Control and Prevention, the Enteric Disease Epidemiology Branch, Atlanta, GA, [3]Austrian Agency for Health and Food Safety (AGES), Institute for Medical Microbiology and Hygiene, Graz, AUSTRIA, [4]National University of Ireland, Galway, IRELAND, [5]Laboratory of Enteric Pathogens, Central Public Health Laboratory, London, UNITED KINGDOM, [6]Central Institute for Animal Disease Control Lelystad – CIDC Lelystad, Lelystad, THE NETHERLANDS, [7]Statens Serum Institute (SSI), Copenhagen S, DENMARK.

Background Several countries in Europe and The USA have observed cases of salmonellosis caused by the rare serovar *Salmonella* Concord specifically in adopted infants from Ethiopia. The objective of the present study is to examine the epidemiology of the *S.* Concord infections in humans and if possible to identify the source of the infection. **Methods** A total of 51 infections with *S.* Concord have been identified in Europe and The USA from 2001 -2007. Most cases are from adopted children from Ethiopia however eight are from adults whereof four have been associated with travel to the southern part of Africa. A questionnaire was used to obtain more information on cases from Denmark and The USA. The purpose was to obtain further information to determine whether the infection was acquired in Ethiopia and to identify the orphanages. All 51 isolates were tested for antimicrobial susceptibility. All isolates with reduced susceptibility to 3rd & 4th generation cephalosporins were examined by PCR for the presence of genes encoding beta-lactamases. Amplicons were sequenced and five isolates resistant to cephalosporin were conjugated by plate mating using BHI agar and relevant antimicrobials. All isolates were analyzed for genetic relatedness by PFGE using *Xba*I and a comparison of the profiles was performed. **Results** The questionnaires showed that all Danish adopted children and six from the USA had a history of diarrhoea whereas the remaining five from USA were asymptomatic. The Danish children were adopted through one adoption agency, whereas the Americans came from two other agencies. All isolates from Ethiopian children were multi drug resistant, including resistant to cephalosporins and encoding by $bla_{CTX\text{-}M\text{-}15}$, $bla_{SHV\text{-}12}$ and $bla_{TEM\text{-}1}$ genes. A total of 41 different PFGE types were observed. *S.* Concord isolates from other areas of East Africa were pansucseptible or showed limited (streptomycin and ceftiofur) resistance. **Conclusion** Antimicrobial susceptibility testing and PFGE suggest that the Ethiopian *S.* Concord clones circulating among adoptee are distinct from other *S.* Concord clones circulating in Africa. The diversity of PFGE types observed suggests that *S.* Concord may be a common serovar in the region with an unknown reservoir. Further investigation is needed to address these questions.

Board 16. Analysis of three outbreaks of acute gastroenteritis caused by NoV between September and November 2006 in Yuhang District Hangzhou City, China

R. LI[1], S. SONG[2], M. CHENG[1], W. TAN[2], X. ZHANG[3], Y. SONG[1], Y. SUN[2];

[1]China CDC, Beijing, CHINA, [2]Yuhang District CDC, Hangzhou, CHINA, [3]Yuhang CDC, Hanzhou, CHINA.

Background Norovirus (NoV) is one of the most common causes of acute gastroenteritis in children and adults and usually causes a considerable number of outbreaks of gastroenteritis worldwide. But few outbreaks of gastroenteritis caused by NoV in China have been reported. The authors developed a fast detection of NoV from fecal and food specimens by real-time PCR and determined three outbreaks of acute gastroenteritis caused by NoV between September and November 2006 in Yuhang District Hangzhou City by the fast detection and epidemiological investigation. **Methods** The epidemiological characters of NoV-caused acute gastroenteritis outbreaks in 2006 are analysised by field epidemiological methods. 20 fecal specimens collected from three outbreaks are detected by the real-time PCR technology and epidemic genotype is identified by the sequencing analysis. **Results** Three outbreaks occured in rural area of south eastern China between September and November 2006. 10, 13 and 77 cases are involved respectively and there is no fatal case in three outbreaks. The total male: female ratio is 1:1.2. There is no significant aggregation of age. Diarrhea and vomit are the major clinical expressions. 95% of the total cases have acute diarrhea and 72% of those have vomit symptom. The incubation period is approximately 12-36 hours. The highest attack rate in family among three outbreaks is 43.33%, which suggest that there is a family aggregation. But all cases have no raw seafood history and other suspicious diet history and 70 cases have no common diet history. The cases involved in each outbreak all have frequent contact. Thus the authors speculate that the contact transmission could be the reason of spread and the fecal-oral route could not be excluded. Three outbreaks all detect positive specimens by real-time PCR. 11 NoV GGII positive specimens from 20 fetal specimens are identified by the sequencing analysis. All positive specimens are proved to be NoV GGII 4, which is consistence with epidemic genotype reported worldwide.**Conclusions** There are NoV-caused gastroenteritis outbreaks in rural area in China and NoV GGII 4 is the major epidemic genotype. Contact spread is the possible transmission mode of the outbreaks in rural areas of south-eastern China in Autumn and Winter, but fetal-oral route can not be excluded.

Board 18. Human Health Burden of Acute Diarrheal Illness in the United States, FoodNet Population Survey, 2006-2007

L. B. Moyer[1], P. Clogher[2], C. Fuller[3], T. F. Jones[4], A. Lasher[5], D. M. Norton[6], S. Solghan[7], M. Tobin-D'Angelo[8], O. Henao[9];

[1]CDC and VA Medical Center, Atlanta, GA, [2]CT EIP, New Haven, CT, [3]MN Dept of Health, St Paul, MN, [4]TN Dept of Health, Nashville, TN, [5]FDA, College Park, MD, [6]CA EIP, Oakland, CA, [7]NY Dept of Health, Albany, NY, [8]GA Div of Publ Health, Atlanta, GA, [9]CDC, Atlanta, GA.

Background: Foodborne pathogens cause an estimated 76 million illnesses each year. Although most illnesses are self-limiting, the human health burden is substantial and includes healthcare provider visits, medications, laboratory tests, hospitalizations, and time missed from work. We describe the human health burden of acute diarrheal illness using data from the 2006-2007 FoodNet Population Survey. **Methods:** During 2006-2007, FoodNet conducted a 12-month population-based survey in 10 sites using a standard random-digit dialing methodology. Demographic information was collected and respondents were asked about illness and activities in the month before the interview. Acute diarrheal illness was defined as ≥ 3 loose stools in 24-hours lasting >1 day or resulting in impairment of daily activities. Persons with a chronic illness in which diarrhea was a major symptom were excluded. Weighted proportions were calculated to adjust for study design and age and sex. **Results:** The weighted prevalence of acute diarrheal illness in the month prior to interview was 6.9% (95% CI 6.6-7.2). Acute diarrheal illness prevalence was greatest among those <5 years old (12.9%, 95% CI 9.7-16.1) and least among those ≥65 years old (4.4%, 95% CI

3.5-5.3). The mean duration of diarrhea was 4 days (median 2) and 1.7% reported bloody diarrhea. Of the 20.0% who visited a medical care provider, 26.7% went to a doctor's office or clinic more than once, 13.0% went to an emergency department, 1.0% were admitted to a hospital overnight and an additional 2.3% spent more than one night in the hospital. Stool specimens were submitted from 4.0% of persons reporting acute diarrheal illness, 32.9% took anti-diarrheal medications and 10.6% used antibiotics. Of those who had a job during this time period (52.0%), 33.2% missed time from work because of their or their child's illness (median 2 days). Of those attending school (7.2%), 66.3% missed time from school because of the illness (median 2 days). **Conclusion:** Acute diarrheal illness remains an important human health burden causing substantial personal and societal costs from multiple healthcare contacts and days missed from work or school. Continued efforts are needed to identify the causes and risk factors for illness; thus, helping to direct intervention and prevention efforts to reduce the burden of illness.

Board 19. *Salmonella* Bacteriuria in New York State FoodNet Counties, 2002-2006

G. L. Smith[1], S. M. Zansky[2], D. L. Hoefer[2], J. B. Karr[3], N. L. Spina[2], S. M. Solghan[2], T. P. Root[4];

[1]NYSDOH, Geneva, NY, [2]NYSDOH, Albany, NY, [3]NYSDOH, Rochester, NY, [4]Wadsworth Center Laboratories-NYSDOH, Albany, NY.

Background: Salmonellosis is a major cause of foodborne illness in the U.S. Commonly associated with gastrointestinal illness, it can also cause extra-intestinal illness including urinary tract infections. Recent national trends indicate *Salmonella* bacteriuria increasing in incidence and as a proportion of all *Salmonella*, especially among elderly women. Analysis of *Salmonella* bacteriuria in 34 New York State (NYS) Emerging Infections Program (EIP) FoodNet counties was conducted to look for similar trends. **Methods:** The NYS FoodNet program has conducted population-based active surveillance for laboratory-confirmed cases of infection of *Salmonella*. Using the NYS Department of Health (NYSDOH) Communicable Disease Electronic Surveillance System (CDESS) and the Clinical Laboratory Information System (CLIMS), confirmed cases of *Salmonella* identified between 2002-2006 were included in this analysis. The most invasive source for each case is recorded. Data was examined to compare incidence rates of *Salmonella* isolated from urine and proportion of urine isolates by gender and age group. **Results:** 2337 confirmed cases of *Salmonella* were identified between 2002-2006. Of 2333 cases with a known specimen source, 189 cases were isolated from urine (8.1%). The annual proportion of urine isolates ranged from 5.1% (2002) to 11.1% (2005). The incidence rate of *Salmonella* bacteriuria increased from 0.8 cases per 100,000 persons in 2002 to 1.1/100,000 in 2006 with the highest rate of 1.3/100,000 in 2005. Most cases isolated from urine occurred among women (88.4%). For both sexes, incidence from urine increased with age, beginning around 50 years of age with the greatest percentage of cases attributable to those ≥70 years. **Conclusions:** *Salmonella* bacteriuria has long been identified in NYS residents but recently represent a greater proportion of the total cases. The majority of cases occur in elderly females similar to national reports. Collecting and reporting specimen source is an important component of foodborne disease surveillance, helping to identify changes in the epidemiology of those illnesses. Possible change in test practices, role of urine catheters, and urine predilection of some *Salmonella* serotypes may contribute to the increased incidence of *Salmonella* bacteriuria in NYS and warrant further study.

Board 20. Foodborne Botulism Associated with Commercial Food in the State of São Paulo, Brazil, 1997-2007

M. B. Eduardo[1], N. P. Bassit[1], E. M. Nunes[1], M. T. Jahnel[1], C. A. Ristori[2], R. E. Rowlands[2], M. Jakabi[2];

[1]SP Center for Epidemiological Surveillance, São Paulo, BRAZIL, [2]Adolfo Lutz Institute, São Paulo, BRAZIL.

Background: Foodborne botulism is a severe neuroparalytic disease caused by the ingestion of food containing preformed *Clostridium botulinum* neurotoxin. In Brazil, reported cases of botulism have been usually caused by toxin type A associated with canned vegetable, fruits or meat, in generally, homemade products. We report the findings of the botulism outbreaks investigation from 1997 to August 2007 in the State of São Paulo caused by the ingestion of commercial foods. **Methods:** We reviewed foodborne botulism outbreaks reported to the Center for Epidemiologic Surveillance, from 1997 to 2007. Confirmed cases were defined as those with botulinum toxin detected in serum, stool or gastric fluid or with compatible clinical illness that ate the same contaminated food as the confirmed case. An outbreak was defined as two or more cases of botulism caused by consuming a common source-contaminated food. An event was defined as the occurrence of a sporadic case or an outbreak of botulism. **Results:** A total of nine events affected 13 people (incidence rate = 1.2 cases/year; fatality rate = 23.1%): three sporadic cases caused by toxin type A and ingestion of industrialized canned hearts of palm (23.1%), two of them, imported from Bolivia; one case by non-identified toxin type and consumption of meals in restaurant (7.7%); one outbreak with four cases, toxin type A, by the consumption of canned tofu imported from China (30.8%); five cases (one case was type A, one type AB and three non-identified toxin) by the consumption of commercial chicken pie with hearts of palm and/or cream cheese (38.5%), three of them, sporadic cases and two from one outbreak. The laboratorial analysis of canned tofu, in addition to the presence of botulinum toxin, showed that the product was contaminated by *B. cereus*. Roasted pies were kept in inadequate temperature and were consumed without reheating. **Conclusions:** Foodborne botulism, while rare, remains an important public health emergency, and commercial foods were responsible for the cases and outbreaks in the State of São Paulo. Cases associated with canned hearts of palms and roasted foods showed failures in manufacturing or preparation/conservation processing of foods requiring new sanitary regulations and alert to consumers. Sanitary and educational measures were being implemented to prevent new cases.

Board 21. Fresh produce outbreaks in Australia, 2001-2006

M. D. Kirk[1], K. Fullerton[1], J. Gregory[2];

[1]OzFoodNet, Canberra, AUSTRALIA, [2]OzFoodNet, Department Human Services, Victoria, AUSTRALIA.

Background: Recent outbreaks in Australia and abroad have highlighted the role of fresh produce in foodborne disease outbreaks. Since fresh produce is often eaten without cooking, its outbreak potential can be significant. **Methods:** Data from the OzFoodNet Outbreak Register from January 2001 to June 2005 were reviewed. OzFoodNet Quarterly and Annual Reports (published and unpublished) from July 2005 through December 2006 were also reviewed. Produce-related outbreaks were defined as outbreaks of foodborne or suspected foodborne transmission where the confirmed or suspected vehicle included fresh, uncooked produce. **Results:** From January 2001 through June 2005 there were 1767 reported gastroenteritis outbreaks recorded. Of these outbreaks, 426 (24%) were either foodborne (157, 37%) or suspected foodborne (269, 63%). Sixteen (4%) of these outbreaks were identified as produce-related. An additional 9 produce-related outbreaks were identified in the review of quarterly and annual reports. These 25 outbreaks

affected at least 686 people, with 51 people hospitalized and no fatalities. The mean number of people affected in these outbreaks was 30 people, with a range from 2 to 125 people. These outbreaks occurred in association with food served at restaurants (44%), primary produce (20%), and fast-food/takeaway food (20%). These outbreaks were caused by *Salmonella* (60%), followed by unknown aetiology (20%), norovirus (12%), and *Campylobacter* (8%). **Conclusions:** Fresh produce causes considerable foodborne disease in Australia. Fresh produce is particularly vulnerable to causing outbreaks due to the lack of an adequate kill-step for pathogens.

Health Communication

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 22. Using technology for bidirectional communication with clinicians on emergency preparedness and response topics

J. Schwendinger, D. Batts, A. Downs, J. Dills;

CDC, Atlanta, GA.

Background: The Clinician Communication Team (CCT) is part of CDC's Emergency Communication System which coordinates all health information to CDC audiences during a public health emergency. The CCT provides emergency preparedness and response information to clinicians through the Clinician Outreach Communication Activity (COCA). COCA has two main components: the Clinician Registry and collaboration with clinician organizations. CCT defines clinicians as health care providers, public health professionals, preparedness planners and first responders. **Methods:** Through COCA, CCT provides informational updates in the form of an email newsletter called the CDC Clinician Communication Updates. These updates take two forms - weekly informational and monthly training announcements. These provide a synopsis of the latest clinical and scientific guidance on CDC websites with links to content and a summary of training opportunities and links to relevant web site information. In times of public health emergency the distribution frequency increases as new information and resources are available. CCT facilitates monthly COCA conference calls presented by CDC subject matter experts (SMEs). Participants download presentation materials, dial-in toll-free to listen and ask questions and receive free continuing education credits. COCA calls are scheduled monthly and may be conducted more frequently in response to a public health emergency. CCT also provides an avenue for inquiries related to emergency preparedness and response and current public health events via a COCA email box. Clinicians can submit questions which are answered using cleared content or by appropriate CDC SMEs. **Results:** From 2003 to present, CCT distributed 377 updates and hosted 59 COCA conference calls (average attendance = 400, highest = 2,148) and responded to 1,545 email inquires. The Clinician Registry currently has 42,000 individual subscribers and COCA has 143 clinician organizational partners. **Conclusions:** CCT uses email, electronic newsletters, websites and distance learning opportunities to provide a messaging channel to clinicians in times of public health emergency and for preparedness planning. CCT uses several valuable channels for timely distribution of evidence based health information applicable to clinicians.

Board 23. A School-Based Health Promotion Project for Mosquito-Borne Disease Prevention in Children

A. D. LaBeaud, A. Glinka, C. H. King;

Case Western Reserve University, Cleveland, OH.

Background: Children are at high risk for mosquito-borne disease exposure because they spend large amounts of time outdoors and often do not wear protective clothing or mosquito repellent. Our objective was to assess whether a school-based educational intervention focused on mosquito bite prevention and mosquito-borne disease, particularly West Nile virus (WNV), was able to: 1) improve WNV-related knowledge, 2) change WNV-related attitudes, 3) maintain these improvements, and 4) promote personal protective behaviors (PPBs) among participants and their families. **Methods:** A single one-hour session was evaluated for its ability to improve mosquito and WNV knowledge, attitudes, and practices (KAP) among elementary school students in Cuyahoga County, Ohio. A 4th grade cohort was randomized to "case" and "control" classrooms. "Cases" learned about mosquito safety and PPBs through a modified CDC "Neato Mosquito" (NM) program. "Controls" learned about tobacco prevention through the AAFP "Tar Wars" (TW) program. Pre- and post-intervention KAP surveys were compared to assess immediate KAP changes. Follow-up surveys, administered after the summer break 5-6 months later, assessed long-term KAP changes. **Results:** 345 students participated: 181 in NM and 164 in TW. 242 students completed follow-up testing: 123 in NM and 119 in TW. Age, gender, and baseline knowledge scores were equivalent between arms. Immediate post-test knowledge scores increased significantly, and remained significantly higher at follow-up in NM vs. TW ($p<0.001$). Post-intervention attitude scores showed increased fear of WNV, but this fear was not retained at follow-up testing. Follow-up behavior scores increased significantly in reported PPBs among NM participants, but not TW ($p=0.03$). Increased discussion about mosquito-borne diseases between NM participants and their families was reported ($p<0.001$). **Conclusions:** Immediate and long-term improvements in WNV-related knowledge resulted from our intervention. Importantly, significant increases in PPBs and discussion about mosquito-borne diseases were reported among NM participants. School-based educational interventions can play a significant role in promoting mosquito-bite prevention and can serve as an effective tool to communicate public health information to children.

Board 24. Health Marketing: A Tool for Expanding Global Health Partnerships

V. P. Carlson[1], C. L. Robinson[2], D. Lo Wo Fong[3], F. J. Angulo[2], S. M. DeLong[4], and WHO Global Salm-Surv;

[1]Public Health Prevention Service, Centers for Disease Control and Prevention, Atlanta, GA, [2]Centers for Disease Control and Prevention, Atlanta, GA, [3]World Health Organization, Geneva, SWITZERLAND, [4]Centers for Disease Control and Prevention and United States Veterans Administration, Atlanta, GA.

Background: WHO Global Salm-Surv (WHO GSS) is a network of institutions and individuals committed to enhancing the capacity of countries to detect, respond to, and prevent foodborne and other infectious enteric diseases through training and other activities. The network promotes integrated laboratory-based surveillance through collaboration between microbiologists and epidemiologists. In 2006, WHO GSS began to develop its health marketing and communications strategies to increase visibility of WHO GSS worldwide and strengthen the WHO GSS brand among existing partners. **Methods:** WHO GSS uses print marketing collateral and e-communication tools to advocate its mission and goals. Print marketing collateral includes official publications, magnets, and Regional Information Packets. E-Communication tools include the public web site, Global Listserv, and published

articles. **Results:** The WHO GSS Progress Report and Strategic Plan offer perspectives on the network's past accomplishments and future directions. The WHO GSS Webcard and Magnet introduced the program's logo and use non-traditional formats to disseminate information about the WHO GSS programs. The WHO GSS Global Listserv has become essential in distributing information on trainings, program issues, and outbreaks to WHO GSS members. The Listserv has > 950 active members worldwide, and distribution has been expanded from four to seven languages. The network has been featured in national publications in several member countries, including an article on CDC Connects, an intranet portal reaching 15,000 CDC employees, and was referred to in a CDC E-Brief to the U.S. Congress. **Conclusions:** Each marketing method has been critical in "branding" WHO GSS, leading to higher recognition of the program at all levels of public health infrastructure. Future directions for WHO GSS include continued expansion of e-communication tools and distribution of print marketing collateral. WHO GSS marketing tools will be incorporated into plans for expanding inter-sectoral partnerships, and special attention will be given to increasing online presence using new online media. Marketing WHO GSS increases recognition of the network and its activities. Continuation of WHO GSS marketing efforts will provide sustainability and growth of the network and its global impact.

Board 25. Not Ready, But Willing: Knowledge and Attitudes regarding *Avian Influenza* in Kanchanaburi, Thailand

J. N. Larson[1], K. Chartchai[2], J. F. Mahoney[1];

[1]University of Pittsburgh School of Medicine, Pittsburgh, PA, [2]Department of Infectious Control, Kanchanaburi, THAILAND.

Background: Avian Influenza (AI), due to H5N1 virus, is a serious emerging global public health threat causing significant human mortality, especially in Southeast Asia. Development of sustained human-to-human transmission could trigger an influenza pandemic. Information about knowledge of and attitudes towards AI in high risk areas, such as Kanchanaburi Thailand, where human AI fatalities have already occurred, is greatly needed. **Methods:** Adults in a hospital clinic in Kanchanaburi, Thailand were asked to complete a 54 item written survey in Thai consisting of multiple choice questions and Likert Scales. Results analysis utilized standard qualitative and quantitative techniques. **Results:** 286 people were approached; 242 surveys were completed. 24% of respondents were health care workers. 10% correctly identified AI symptoms and only 0.5% could correctly answer all four basic knowledge questions covering symptoms, transmissibility, and prognosis. Despite 29% believing that a pandemic will never occur and 14% thinking that people cannot survive AI infection, 73% expressed a desire to learn more about AI and 80% want the government to provide more AI education. 83% report no longer touching birds with bare hands and 21% no longer own poultry since AI concerns first arose. Preferred educational sources include TV, health care professionals, and newspapers. **Conclusions:** Comprehensive Avian Influenza knowledge is low among surveyed participants in western Thailand. Significant gaps in knowledge exist regarding symptom identification and modes of transmission, even among health care workers in an area with prior human H5N1 deaths, which could lead to delayed disease recognition, containment, and treatment. The great majority of respondents want to learn more about AI. Targeted educational interventions need to be implemented so that the Thai public can be better prepared to prevent infection, identify illness early and contain outbreaks.

Board 26. China-U.S. Collaborative Program on Emerging and Re-emerging Infectious Diseases

The construction and development of online knowledge center of infectious disease for public on national 12320 public health hotline website of China

Y. SUN, D. Liang, R. LI;

China CDC, Beijing, CHINA.

Background Within the field of public health, the prevention and control of infectious diseases in China, apart from improving the environment and infrastructure for the public, is to search and apply effective ways to get the basic and scientific health information and knowledge reachable for them. The advantage of Internet's capacity such as 'website knowledge center' mediated by computer to serve as a virtual space for health information can be taken here to inform and educate the public. **Method** Qualitative and quantitative research methods were employed respectively to conduct the studies in terms of the needs of the public, the experts' opinions and the following-up browse rate of the website. Moreover, the statistics from each 12320 call center nationwide on the infectious diseases the public consulted most frequently were taken into account as well. **Results** 9 root directories with about 5,000 health and sanitary information and knowledge elements have been selected and put in the database on the website (www.12320.gov.cn). The basic information and knowledge of five infectious diseases-flu, measles, rabies, tuberculosis and hepatitis B were chosen to put in the knowledge center for the public. The browse rate increases steadily. The study on evaluating the public's response to the contents of the knowledge center on the 12320 website and their further needs in health information and knowledge has been conducted and the result will be concluded in the near future. **Discussion** The results suggest that online health communication can be taken as one of effective ways for health professionals to control diseases and promote health as it can reach and inform large number of audiences. However, under the current circumstance in China, the majority of the rural populations and some urban residents are likely to remain excluded from the benefits of new technologies such as computer and internet because of their inadequate education and economic condition Currently, we carried out the professional and popularized editions of the health information and knowledge package and promoted it by integrating with the 12320 public health hotline in order to get it more accessible to the public.

Infectious Causes of Chronic Diseases

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 27. Prevalence of *Helicobacter pylori* Infection in 90 Patients Undergoing Diagnostic Upper Endoscopy _ Republic of Georgia, 2003-2005\

N. Tarkhashvili[1], J. Guarner[2], R. Beriashvili[3], N. Chakvetadze[3], U. Gabunia[3], D. Kordzaia[3], P. Imnadze[3], J. Sobel[2];

[1]CDC, Pierre, SD, [2]CDC, Atlanta, GA, [3]NCDC, Tbilisi, GEORGIA.

Background: *Helicobacter pylori* causes gastritis, peptic ulcers and gastric cancer. Approximately 50% of the world's population is infected but only about 20% of infected persons progress to clinical disease. Previous studies in the Republic of Georgia (ROG) have demonstrated that >70% of adults are infected with *H. pylori* and gastric cancer rate is 18/100,000 (about 6-9 fold

higher than the United States). However, prevalence of infection among gastritis, peptic ulcer and cancer patients has never been studied in the ROG. **Methods:** We performed a cross-sectional study of patients referred to 23 tertiary medical centers of ROG for diagnostic upper endoscopy during 2003-2005. Eligibility criteria included: availability of the medical records and biopsy slides. We abstracted demographic data from medical records and our study pathologist diagnosed patients according to histopathological findings. We defined infection as *H. pylori* graded ≥1 on hematoxylin and eosin section of the biopsies using the Revised Sydney Classification System for Gastritis. Adjusted prevalence ratios (aPRs) were generated using multivariable Poisson regression. **Results:** Of all the records reviewed 90 patients were eligible for the study: 41 (46%) were female and median age was 61 (range 6-81 years). The overall prevalence of *H. pylori* infection was 59 (72%) in 82 patients with adequate slide specimens. *H. pylori* was detected in 45 (78%) of 58 biopsies showing gastritis, 7 (58%) of 12 with peptic ulcer and 7 (58%) of 12 with gastric cancer. Older age (age ≥50 years) was not associated with the greater prevalence of *H. pylori* infection (aPR = 0.9; 95% Confidence Intervals (CI) 0.8-1.2) as well as the male sex (aPR = 1.0; 95% CI: 0.9-1.2). **Conclusions:** In this first cross-sectional study of biopsy slides archived at the medical centers of the ROG the prevalence of *H. pylori* in patients undergoing diagnostic procedures was 72%. *H. pylori* was more prevalent in patients clinically diagnosed with gastritis than among patients diagnosed with peptic ulcer disease or cancer, as in previous studies. Older age and male sex did not confer increased risk of *H. pylori* infection. Understanding these variables is important for devising a public heath testing, treatment and secondary prevention strategies in the ROG.

Board 28. Long-term Recovery Status of West Nile Virus Patients_Utah County, Utah

J. Holbrook[1], J. K. Miner[1], L. Wyman[2];

[1]Utah County Health Department, Provo, UT, [2]Utah Department of Health, Salt Lake City, UT

Background Although considered an acute infection, patients with West Nile Virus (WNV) infection often report chronic problems with achieving full recovery. This study was conducted to further define the recovery process for WNV patients and note differences between recovery status of West Nile Fever (WNF) patients and West Nile Neuroinvasive Disease (WNND) patients in a cohort from Utah. **Methods** This study included a cohort of 16 patients diagnosed in 2005. Patients were interviewed by a trained researcher at 6, 12 and 18 months post diagnosis. Questions were asked regarding three health status domains: physical, cognitive and functional. Answers were scored according to the frequency of symptoms. Within each domain, the ratio of the 18-month composite score to the baseline score was calculated and used as the measure of recovery. Patients were categorized as having achieved "marginal recovery" at >50% of baseline. **Results** Only 20% of participants achieved marginal recovery in all three domains. The greatest improvement in recovery occurred between 6 and 12 months; no significant improvement was detected between 12 and 18 months. No significant differences were determined between the marginal recovery groups in terms of age, gender, clinical syndrome (WNF vs, WNND), and hospitalization status. Neither clinical syndrome nor age was predictive of marginal recovery in any of the three domains. **Conclusions** In this study, the effects of WNF and WNND appear to be chronic for at least 18 months after infection. The vast majority of patients failed to reach even marginal recovery status in the three domains, suggesting serious, long-lasting disease effects. Younger age and less severe clinical presentation were not protective in terms of achieving recovery. Further data collection is currently occurring for a larger cohort of patients to determine whether these findings were unique.

Board 29. Significant Increase in Guillain-Barré Syndrome Following Sustained Campylobacteriosis Epidemic in New Zealand

M. G. Baker, N. Wilson, K. Venugopal;

University of Otago, Wellington, Wellington, NEW ZEALAND.

Background: New Zealand (NZ) experienced a steadily increasing incidence in campylobacteriosis from 1980 to 2006. The notified rate of 383 / 100,000 in 2006 was the highest national rate reported in the literature. Given the documented association between *Campylobacter* infection and Guillain-Barré syndrome (GBS), we investigated whether there was a concomitant increase in rates of this condition. **Methods:** We correlated rates of first hospitalisation for GBS (ICD.9CM 357.0 and ICD.10AM G61.0 from 1998) with notification rates for campylobacteriosis for the period 1988-2005. We also analysed hospitalisations for campylobacteriosis (ICD.9CM 008.43 from 1995 and ICD.10AM code A04.5 from 1998) for the period 1995-2005 to see whether the rate of subsequent GBS was any higher in this group compared to that seen for the total New Zealand population. **Results:** The incidence of GBS rose significantly over the 1988-2005 period (Chi square test for trend p=0.04) and this increase was correlated with the increase in campylobacteriosis notifications over that same period (Spearman's rho 0.535, p=0.02). The estimated increase in GBS rate from 2.2 / 100 000 in 1988 to 3.0 / 100 000 in 2005 is consistent with an additional 33 cases a year attributable to the campylobacteriosis epidemic in NZ. We detected three GBS cases in people previously hospitalized for campylobacteriosis, giving a rate of 60/100,000 (3/5090). This rate is approximately 30 times higher than the expected annualized rate in NZ (RR 28.0, 95%CI 9.0-86.6, p<0.001). **Conclusions:** Campylobacteriosis appears to be an important cause of GBS and now may account for at least 25% of GBS cases occurring in NZ. Controlling NZ's food borne campylobacteriosis epidemic is therefore likely to be an important strategy to reduce GBS in this country and other adverse sequelae of this enteric infection.

Influenza

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 30. Influenza Pandemic Planning among South Pacific Nations: A Critical Review of Available Plans from a Border Control Perspective

N. Wilson[1], M. McLeod[1], H. Kelly[2], M. Baker[1];

[1]University of Otago, Wellington, Wellington, NEW ZEALAND, [2]Victorian Infectious Diseases Reference Laboratory,, Melbourne, AUSTRALIA.

Background: There is historical evidence and theoretical reasons as to why border control for pandemic influenza may be of value for island nations. We therefore aimed to critically review border control strategies included in the publicly available pandemic preparedness plans for Australia, New Zealand and smaller South Pacific Islands.**Methods:** Based on previously implemented and currently nominated border control measures, we developed a checklist of 10 important criteria rated on a 0 to 3 scale. We applied this checklist to each of the pandemic preparedness plans for which copies were publicly available, giving a detail rating out of 30. **Results:** From a search for pandemic plans in 24 Pacific Island countries/territories, we identified 6 pandemic plans from Nauru, Palau, Tonga, New Caledonia, New Zealand and Australia. The least detailed plans were from Palau and Tonga, both with a score

of 9/30. Nauru, the island with the smallest population and lowest GDP with a pandemic plan available, scored 22/30, similar to the plan from New Caledonia (20/30). The most detailed plans were from the larger and more developed countries, New Zealand (29/30) and Australia (27/30). **Conclusions:** There was a substantial difference in the quality of the border control components of the influenza pandemic plans examined. Some of this difference could be explained by the need to rationalise the range of border control strategies to match available resources. Pacific islands could benefit from additional support to improve their pandemic planning and preparedness. Future work could include broadening the assessment criteria used here and applying them to a larger number of plans, as part of a constructive dialogue with the countries concerned.

Board 31. Potential Value of Multiple Border Control Interventions to Prevent Pandemic Influenza in Island Settings

N. Wilson[1], H. Kelly[2], M. Baker[1], G. Sertsou[1];

[1]University of Otago, Wellington, Wellington, NEW ZEALAND, [2]Victorian Infectious Diseases Reference Laboratory, Melbourne, AUSTRALIA.

Background: There have been historical successes with influenza pandemic control by island nations using maritime quarantine. Some islands have also recently included border control in their pandemic plans. We aimed to quantify potential border control measures for preventing or delaying pandemic influenza in island settings.**Methods:** We used a published method to model the proportion of cases developing symptomatic pandemic influenza on airline flights. We applied this method to air travel from Hong Kong, the assumed source area, to six island nations in the South Pacific: American Samoa, Fiji New Caledonia, New Zealand (NZ), Samoa, and Tuvalu. We then performed a threshold analysis using parameters from the epidemiological, modeling and historical literature and the deterministic modeling software *InfluSim* to determine the likely outcome of the implementation of incoming and outgoing travel restrictions, routine six-day facility-based quarantine, entry screening and tracing of contacts at risk from in-flight transmission. **Results:** NZ, the largest island population considered and Tuvalu, the smallest, were at the extremes. We found that 57% (NZ) to 93% (Tuvalu) of cases with a median time of infection 24 hours before commencing travel would have developed symptoms of pandemic influenza by the time of arrival in the capital city. During early WHO pandemic phase 6, it was estimated that all six countries could prevent cases being released into the community at the threshold of <1 case per 20 weeks. At the peak of phase 6, Tuvalu would require 99% travel reduction by citizens and 100% reduction by non-citizens, but no other interventions, to meet the threshold of <1 case in 20 weeks. However, even with all plausible border control interventions detailed above, it was likely that NZ would still release 1.3 undetected cases per week into the community. This would be sufficient to initiate and sustain a pandemic in the absence of additional interventions. **Conclusion:** The threshold analysis suggests that, for these island nations, border control interventions would probably be successful in the early stages of an influenza pandemic. But at the peak of phase 6, very rigorous measures would be required for island nations with substantail travel volumes if the release of cases into the community was to be prevented.

Board 32. Seroprevalence of Influenza H1 and H3 Antibody among U.S. Military Accessions

A. Eick, Z. Hu, R. Nevin, S. Tobler;

U.S. Army Center for Health Promotion and Preventive Medicine, Silver Spring, MD.

Background: U.S. military recruits are historically at high risk for respiratory infections, including influenza. The scientific literature is lacking recent seroprevalence data on seasonal influenza among this young adult age group. Although recruits are vaccinated against influenza during accession, full protection may not take effect until weeks after vaccination, leaving a window of susceptibility if the recruit lacks pre-existing immunity. The objective of this study was to provide influenza antibody seroprevalence data on recruits just prior to accession. **Methods:** Data from the Defense Medical Surveillance System and serum specimens maintained at the Department of Defense Serum Repository were used for this study. A random sample of 1000 recruits was selected from the new accession cohort entering service in 2005-2006. Serum specimens were collected prior to accession at the applicant's military entrance processing. Specimens were tested by hemagglutination inhibition assay for H1N1 and H3N2 influenza antibodies. Geometric mean titers ≥ 40 were considered seropositive. Univariate and multivariate Poisson regression models were used to determine factors associated with seropositivity **Results:** Approximately 43% and 66% of recruits were seropositive for H1 and H3 influenza antibodies, respectively. Almost a quarter of the recruits were seronegative to both H1 and H3. Only 32% were seropositive to both viruses. No seasonality in seropositivity was found. Increasing age was significantly associated with decreased odds of seropositivity to each virus. Gender, home country, home state, and education were not associated with seropositivity. **Conclusions:** New accessions into the U.S. military represent a sampling of the young adult population throughout the U.S. Seropositivity to both viruses may indicate previous influenza vaccination, whereas seropositivity to only 1 virus may represent natural infection. If that assumption holds, then approximately half of the recruits had a natural infection prior to accession, possibly pointing out a need to increase vaccination rates in this age group. The nearly quarter of new accessions entering service as seronegative could be a potential source for outbreaks in the recruit setting and requires additional investigation.

Board 33. Likely Effectiveness of Quarantine for Pandemic Influenza Control at the Borders of Island Countries

N. Wilson[1], H. Kelly[2], M. Baker[1], G. Sertsou[1];

[1]University of Otago, Wellington, Wellington, NEW ZEALAND, [2]Victorian Infectious Diseases Reference Laboratory, Melbourne, AUSTRALIA.

Background: Strict maritime quarantine, with facility quarantine on land, appeared to reduce the effect of the 1918-19 influenza pandemic in some island jurisdictions. Many island nations now include quarantine in their pandemic plans. We explored the theoretical effectiveness of quarantine and whether it could potentially be shortened with appropriate laboratory testing of quarantined travellers. **Methods:** We used a published method to estimate the time to symptom emergence, given infection at the time of departure and 11-hours of air travel time before quarantine. It was also assumed that 9% of cases remained asymptomatic during the infectious period (also based on a recently published estimate). In particular, we assumed that, in the event of another pandemic, it will be possible to test for the virus using nucleic acid assays with a similar performance profile to assays used for routine diagnosis and surveillance of influenza A (ie, a sensitivity of at least 90% and specificity approaching 100%). **Results:** Using these assumptions we estimated the likelihood of an infected traveller still being asymptomatic and infectious after 3 days quarantine was 4.2% and 1.5% after 6 days. Quarantine effectiveness would be enhanced by longer travel times (eg, estimated to average over 37 hours from Asia to Tuvalu). But such effectiveness could be compromised in islands with limited quarantine facilities and the need to use home quarantine. Quarantine times could potentially be truncated by laboratory testing of those in quarantine. For example, if the prevalence of pandemic influenza infection in arriving passengers in the early part of *Pandemic Phase 6* were 1%, the negative predictive value (NPV) of a negative nucleic acid test would be

99.9%. This would decline to only 99.5% for a higher prevalence of 5%. **Conclusions:** In theory the use of facility-based quarantine for 6 days by island nations would substantially reduce the risk of the arrival of pandemic influenza. The use of diagnostic tests, if available through stockpiling in advance or rapid delivery, may permit a reduction in the quarantine period.

Board 34. Age-specific Hospitalization Rates Associated with Influenza and Respiratory Syncytial Virus (RSV) in US States, 1989-2005

C. Ringholz[1], L. Simonsen[2], W. Thompson[3], C. Steiner[4], D. Fernandez[5], E. van Wijngaarden[5], J. Treanor[5], A. Falsey[5], A. Budd[3], A. Fowlkes[3], C. Panozzo[3], M. Miller[1], C. Viboud[1];

[1]Fogarty International Center, National Institutes of Health, Bethesda, MD, [2]George Washington University, Washington, DC, [3]Centers for Disease Control and Prevention, Atlanta, GA, [4]Agency for Healthcare Research and Quality, Rockville, MD, [5]University of Rochester School of Medicine and Dentistry, Rochester, NY.

Background: The relative contribution of influenza and RSV to respiratory hospitalizations remains unclear. We estimated hospitalization rates associated with influenza and RSV epidemics in the US, taking advantage of unique state-specific data on hospitalizations and laboratory surveillance available for multiple seasons. **Methods:** We compiled weekly hospital admissions with any diagnosis of pneumonia or influenza (P&I), or RSV from the Healthcare Cost and Utilization Project's State Inpatient Databases for 9 states for 1989-2005, representing 31% of the 2000 US population. We modeled age-specific rates of P&I hospitalizations associated with influenza and RSV viral activity and projected model estimates to the entire US population. Three models were compared: 1, a Serfling seasonal regression model; 2. a Poisson model using covariates of either influenza- and RSV-specific hospital admissions or 3. viral laboratory surveillance. **Results**: Analysis of state-specific laboratory surveillance and hospitalization data consistently suggested that timing and magnitude of influenza activity varied markedly between seasons ($P<0.001$), while timing of RSV epidemics varied mostly between states ($P<0.001$). Estimates of influenza-associated hospitalization rates were consistent by the 3 modeling approaches (range of estimates, 31-51 per 100,000 for all ages and 167-245 for adults ≥65 years old). Higher rates were associated with RSV than influenza in children <5 years old (155-185 vs. 42-115 per 100,000), but RSV estimates in other age groups were highly sensitive to the model structure and choice of covariates. **Conclusions:** The projected national influenza hospitalization burden estimates were robust for most age groups and similar to previously published estimates for different time periods and modeling approaches. RSV estimates were generally more sensitive to modeling assumptions, and may be confounded by a lag between timing of viral activity and the associated hospitalizations, which may vary between age groups. This pattern will be explored in further work.

Board 35. Assessing County Health Department Employees' Willingness to Respond to an Influenza Pandemic

N. E. Basta[1], S. E. Edwards[2], J. Schulte[3];

[1]Department of Epidemiology, University of Washington, Seattle, WA, [2]Florida Department of Health, Bartow, FL, [3]Centers for Disease Control and Prevention, Atlanta, GA.

Background: During an influenza pandemic, local health department employees are expected to play a significant role in carrying out response and control protocols. However, little is known about how informed employees are about pandemic response or how willing they are to respond. The Florida Department of Health, in an effort led by the state health office and its 67 county health departments, has been actively planning the response efforts to be undertaken in the event of a pandemic. Here, we determine how knowledgeable local health department employees are about pandemic influenza, how likely they are to respond, and which factors are significantly associated with a willingness to respond to a pandemic. **Methods:** We conducted an anonymous, online survey of 4,746 Florida county health department employees randomly selected using a stratified random cluster sample. We gathered information about demographics, knowledge of pandemic response, and the likelihood of reporting to a pandemic given 4 different scenarios that specified the stage of the pandemic (early vs. peak) and the type of duties required (lower risk - no face-to-face contact vs. higher risk - face-to-face contact). Responses were weighted based upon the sampling fraction and the response rates. Multivariate logistic regression was used in the main analysis. **Results:** Of the 2,414 (51%) unique responses received, willingness to respond to a pandemic varied by the stage of the pandemic and the type of job duties. 92% were very or somewhat likely to respond early in the pandemic and perform lower risk jobs, 66% early in the pandemic with higher risk jobs, 83% at the peak of the pandemic with lower risk jobs, and 56% at the peak with higher risk jobs. Those who have read either the state or county pandemic flu plan and nurses were significantly more likely to report a willingness to respond. Having attended a pan flu training was not significantly associated with willingness to respond to any scenario. **Conclusions:** These results indicate that the majority of Florida county health department employees surveyed are willing to respond to an influenza pandemic, but that their willingness declines during the peak of the pandemic and when face-to-face contact is required. These results highlight underlying issues that must be addressed prior to a pandemic event.

Board 36. Fatal Laboratory-confirmed Human Influenza Infections in Thailand Iidentified by the National Avian Influenza Surveillance Program during 2004-2006

W. Hanshaoworakul[1], V. Shinde[2], U. Narueponjirakul[1], W. Sanasuttipun[3], S. Kaewchana[3], D. Areechokechai[1], J. M. Simmerman[3], K. Ungchusak[1];

[1]Bureau of Epidemiology, Department of Disease Control, Ministry of Public Health, Nonthaburi, THAILAND, [2]CDC/CCID/NCIRD, Atlanta, GA, [3]CDC/International Emerging Infections Program, Nonthaburi, THAILAND.

Background: In Thailand, while attention is focused on the severity of avian influenza A(H5N1) infection, human influenza infections are believed to cause only mild illnesses. Between 2004 and 2006 only 1 influenza death was reported through national passive surveillance in a population of 65 million. We reviewed the frequency of deaths in which human influenza strains were detected using data from the national Avian Influenza Surveillance system (AIS). **Methods:** The AIS investigates all suspected human AI infections and includes testing for influenza types A, B and influenza A subtypes H5, H3, H1 using RT-PCR. From the AIS database, we identified fatal cases where laboratory testing indicated an infection with human influenza viruses. A retrospective chart review was conducted on all fatal cases. **Results:** Between January 2004 and December 2006, 11,641 investigations for suspected AI infection were conducted, during which 2,076 (18%) cases of human influenza virus infection were identified. Among these cases, 22 deaths were recorded (four deaths in 2004, 8 in 2005 and 10 in 2006) compared with 17 deaths attributable to avian influenza A (H5N1) infection. In 2004 subtypes H1, H3 and type B accounted for 32%, 32% and 27% of all infections, respectively. In 2005, 64% of human influenza infections were due to H3 while the H1 subtype caused 74% of infections in 2006. Human influenza infections occurred throughout the year. Influenza A/H3, A/H1 and B caused 8, 7, and 7 deaths respectively. Six (27%) of deaths occurred in children

<10 years, 9 (41%) in patients aged 10-59 years, and 7 (32%) of deaths occurred in patients >60 years. Sixteen (73%) cases had at least one underlying illness. Five (22%) fatal cases were coinfected with bacteria including 2 *B. pseudomallei*, 2 *P. aeruginosa* and 1 *Staph. aureus* infections. **Conclusions:** We report 22 deaths due to laboratory-confirmed human influenza infection in Thailand during a 3-year period. These fatalities were identified only because they were initially suspected to be AI cases. Death from human influenza infection in Thailand is more common than previously appreciated.

Board 37. Use of Rapid Influenza Testing and Antiviral Agent Prescribing Practices Among Primary Care Physicians in Selected Geographical Areas - Connecticut, Minnesota, New Mexico, New York, 2006-07

C. Morin[1], K. Vick[1], R. Lynfield[1], M. Mueller[2], J. Baumbach[2], C. Long[3], R. Belflower[3], J. Palumbo[4], J. Meek[4], A. Laufer[4], D. Fazio[4], L. Kamimoto[5];

[1]Minnesota Department of Health, St. Paul, MN, [2]New Mexico Department of Health, Santa Fe, NM, [3]University of Rochester, Rochester, NY, [4]Yale University, New Haven, CT, [5]Centers for Disease Control and Prevention, Atlanta, GA.

Background: Use of antiviral agents within 48 hours of influenza-like illness (ILI) onset has been shown to shorten the course of influenza illness. As such, quick laboratory diagnosis of influenza can aid in clinical management. A survey of primary care physicians (PCPs) was undertaken in Emerging Infections Program sites to gain a better understanding of the attitudes and practices regarding influenza testing and antiviral agent prescribing practices. **Methods:** Physicians were identified using state-specific physician databases. Proportional, random sampling was performed among physicians in internal medicine, family practice, obstetric, and pediatric specialties. **Results:** Of 2,679 physicians surveyed, 1,262 (47%) responded, and 730 (58%) were considered PCPs, thus eligible for the study. Overall, 504 (69%) of 730 PCPs tested patients for influenza during the 2006-07 influenza season; 444 (61%) used rapid testing, 95 (19%) viral culture, and 32 (6%) serology. Among the 730 PCPs, 393 (54%) prescribed antiviral agents to patients with ILI. PCPs were asked to indicate antiviral agents they prescribed; 87% oseltamivir, 18% amantadine, 9% rimantadine, and 5% zanamivir. PCPs were less likely to "usually" order an influenza test for adult (47% vs. 26%) and pediatric (51% vs. 30%) patients as the influenza season progressed. PCPs were also more likely to prescribe antiviral agents to pediatric, adult, and high-risk patients presenting with ILI within 48 hours of onset of symptoms if they had a positive influenza rapid test than if they had no influenza test results. PCPs were also more likely to offer antiviral agents to those with conditions that increased a patient's risk of influenza complications. **Conclusions:** Results from this survey suggest that a majority of PCPs test patients for influenza. Among PCPs who test, most used rapid influenza testing and one-third performed rapid influenza testing on-site. Results of this survey also indicate that >50% of PCPs prescribed antiviral agents, and PCPs are more likely to prescribe antiviral agents to patients presenting within 48 hours of symptoms. Notably, amantadine and rimantadine were prescribed despite CDC recommendations to avoid these agents due to widespread resistance. Further education on antiviral agents should be targeted to PCPs.

New or Rapid Diagnostics

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

MONDAY

Board 38. Novel Method and Medium for Detecting and Identifying both Methicillin Susceptible (MSSA) and Methicillin resistant(MRSA) *Staphylococcus aureus*

S. C. Edberg;

Yale-New Haven Hospital, New Haven, CT.

Background: Currently, to detect MSSA or MRSA two pathways are available. The first uses semi-selective culture media; incubation 18-24h, then a series of tests for identification; subculture to a mec A inducing medium for an additional 18 to 24h. Accordingly, considerable skilled labor and time are required. The second pathway utilizes specific genetic amplification of the mecA gene for MRSA, and another amplification for MSSA. Each is quite costly in materials and equipment, thus precluding its use from all but the largest hospitals. A novel specific method and medium for detection of (MSSA) and (MRSA) [AureusAlert®, Pilots Point LLC] (AA) is presented. It requires no skilled labor, determines the presence of *S. aureus* (SA) within 4h, and differentiates MSSA and MRSA in an additional 12-16h, and costs 25% of PCR. **Methods:** The testing procedure first utilizes an enhanced plasma substrate. The specimen (e.g., nasal swab) is inoculated into this plasma substrate and incubated at 35C. If SA is present, in from 2 to 6 hours on average, a clot forms because of the detection of coagulase. Hence, the observation of the clot is specific for the presence of SA.. The clot is then dissolved, freeing the SA. An aliquot from the liquefied clot is added to a culture medium that promotes the growth of SA and also has cefoxitin to ascertain methicillin resistance. After incubation (8-18 h), growth, as evidenced by a color change, is specific for MRSA; no color change indicates the presence of MSSA. A total of 60 MSSA and 60 MRSA from patient nasal cultures were constructed to determine minimum SA sensitivity. In addition, 50 ICU patient samples were tested and compared to the mannitol salt agar (MSA) procedure. **Results:** From the 60 MSSA constructed, all were positive in 5 h; 49 in 4 h; 38 in 3 h; and 26 in 2. From the 60 MRSA constructed, all were positive in 6 h; 54 in 5h; 49 in 4h; 36 in 3h, and 24 in 2h. Detection limit in all were 10^{2-3}. From the 50 patients, there were no false positives. MSA and AA both detected MSSA in 9; AA alone in 2. For MRSA, both MSA and MRSA detected 13, MSA alone detected 1, and AA alone detect**ed 2. Conclusions:** AureusAlert® offers the prospect for all sized institutions at risk for SA a low cost, rapid means to detect both MSSA and MRSA utilizing unskilled labor. Widespread clinical evaluation is warranted.

Baord 39. Development of a Possible Screening Method for the Detection of *Norovirus* in Stool Samples

S. Snow;

CDC/APHL EID Fellow, Delaware Public Health Laboratory, Smyrna, DE.

Background It is estimated that Norovirus is responsible for approximately 90% of nonbacterial gastroenteritis cases. Recently it has been reported that Norovirus-like particles have agglutinated human red blood cell group antigens, notably antigens of the ABO and Lewis blood groups. In this experiment we looked at the ability of Norovirus-positive stool samples from outbreaks in Delaware from 2006-2007 to agglutinate human RBCs in an effort to establish

a screening test capable of quickly indentifying outbreaks. **Methods** Previously RT-PCR positive stool samples collected from outbreaks in late 2006 and early 2007 were gathered for testing. A 10% suspension of the stool samples were clarified and incubated with a 5% suspension of washed, pooled human RBCs at 4° for 75 minutes. After incubation the samples were spun down at 2500 rpm for 20 seconds. The cell buttons were gently re-suspended and assayed both macroscopically and microscopically for agglutination. **Results** Of the 30 previously positive and 5 previously negative samples screened, 29 /30 and 0/5 respectively were positive for agglutination. **Conclusions** The development of a quick and accurate screening test for Norovirus could prove very useful in both public health and clinical laboratories in the investigation of gastroenteritis outbreaks. In the initial investigation of these samples from the 2006-2007 outbreaks of Norovirus positive stools, agglutination was seen in 97% of previous positives and 0% of previous negatives. Our early results indicate this new methodology could have potential uses in preliminarily identifying outbreaks. In an effort to optimize this potential new method, future testing will be conducted using RBCs from a single donor that have been phenotyped for the ABO and Lewis Blood groups. Once optimized, this method will be used to screen all new stool samples submitted for Norovirus testing in conjunction with current methodologies.

Board 40. Rapid Detection of Animal Pathogens for Global Disease Surveillance

P. Naraghi-Arani;

Lawrence Livermore National Laboratory, Livermore, CA.

Background: Emerging infectious diseases and pandemics have historically presented specific challenges to response making rapid detection critical. We have developed four multiplexed RT-PCR assay panels that can rapidly screen for high priority agricultural pathogens, including Foot and Mouth Disease Virus and Avian Influenza in environmental and clinical samples. The use of bead-based liquid arrays has proven to be a well adapted and versatile technology that can be custom tailored to rapidly screen for both DNA and RNA in a single tube, as well as across a given signature cluster. Previously we had, in collaboration with the CDC, developed another panel for human biological threats. Our assays have been tested by researchers in multiple public health and USDA laboratories and proven robust. **Methods:** Multiplexed PCR assays are developed at LLNL through a proven technical process. This process involves the sequential process of sequencing, bioinformatics, and TaqMan screening, followed by multiplexed PCR assay development. For these panels, we have utilized the Luminex X-Map system for development of all panels. The process involves an end-point RT-PCR followed by hybridization to a mixture of probe-conjugated polystyrene beads that can be readily classified by flow-cytometry. Up to a maximum of 100 unique bead classes, and thus RT-PCR products can be identified using this system. **Results:** In collaboration with the USDA and multiple university partners, bead-based liquid arrays have been developed and fully optimized for multiplexed RT-PCR detection that is both sensitive and specific for the simultaneous of select biothreat agents. We have demonstrated that these multiplex assays are as selective as TaqMan assays with sensitivities in the range of 10-10000 genomes which compares well with other PCR-based methods. These assays have been tested for proficiency in the field and proven of value. **Conclusions:** Multiplexed assays provide many advantages over real-time PCR assays. In the event of a public health emergency, the use of these assays can provide rapid, sensitive, specific and cost effective means of handling high volumes of samples. Additionally, the rapid detection of agricultural pathogens is of great importance given the fact that most of the emerging infectious diseases have an agricultural origin.

Board 41. Establisment and Application of a Real-Time RT PCR for the Detection of Human Metapneumovirus in Children with Lower Respiratory Tract Infection in Taiwan

Y. Lin[1], J. Lin[2], S. Chiu[3], K. Lin[4];

[1]Departments of Medical Research, Pingtung Christian Hospital, Pingtung City, TAIWAN, [2]Research and Development Division, Central for disease control, Taiwan, Taipei City, TAIWAN, [3]Research and Development Division, Central for disease control, Taipei City, TAIWAN, [4]Department of Laboratory Medicine,Kaohsiung Medical University Hospital, Kaohsiung City, TAIWAN.

Background: Human Metapneumovirus (hMPV) was newly negative-sense RNA virus and has been assigned to the Metapnumovirus genus within the Paramyxoviridae family. The clinical manifestations of hMPV infection ranged from mild flu-like illness to severe pneumonia, and were difficult to distinguished between other respiratory viruses For the reasons of Severe Acute Respiratory Syndrome (SARS) outbreak in Taiwan in 2003 and several outbreaks of human avian influenza infection were reported in neighboring countries, currently, hence, the establishment of a rapid and effective diagnostic system to differentiate human metapneumovirus from other respiratory vireses is in urgent need. **Methods**: From Oct. 2006 to Feb. 2007, a total of 350 throat swabs from pediatric patients of Kaohsiung Medical University Hospital and Pingtung Christian Hospital, Taiwan were collected. Viral RNA was extracted from original sample or virus culture fluid with the QIAamp viral RNA mini Kit (QIAGEN). hMPV nucleoprotein region from NCBI database (Accession No. AY297748) was selected for primer and probe design. Phylogenetic analyses were done using Phylogeny Inference Package (PHYLIP, Version 3.573c). **Results**: Detection limit of this newly established system was 10 copies/ml. No cross-reaction to other common respiratory viruses (Flu A, Flu B, PIA 1, PIA 2, PIA 3,RSV, Adenovirus). hMPV was detected in 3 (0.86 %) of 350 specimens. Age distribution of the patients ranged from 1 months to 10 years old with a mean of 4.1±2.6 years. Phylogenetic analysis for the sequence of partial fusion protein, showed the existence of two groups among in our isolate. **Conclusions**: We establish a very sensitive and accurate real-time RT-PCR system to detect hMPV though the positive rate was very low in our samples. Phylogenetic analysis revealed that Taiwanese strains localized in each of the two major groups of the hMPV.

Board 42. An Integrated Molecular Platform for Detection, Isolation and Molecular Serogrouping of Shiga Toxin-Producing Escherichia coli (STEC)

M.W. Gilmour[1], L. Chui[2], G. Van Domselaar[1], L. Ng[1];

[1]National Microbiology Laboratory, Winnipeg, MB, CANADA, [2]Alberta Provincial Laboratory (MIcrobiology), Edmonton, AB, CANADA.

Background: The isolation of Shiga toxin-producing *Escherichia coli* (STEC) in clinical stool samples is problematic due to the predominance of non-pathogenic *E. coli* and a lack of differential culture media for all STEC serogroups. The development of molecular reagents capable of identifying both toxin and serogroup-specific genetic determinants holds promise for a more comprehensive characterization and isolation of STEC strains from stool samples. **Methods:** Clinical stool samples were enriched and STEC detected by conventional PCR and real-time PCR assays (HybProbe and LUX chemistries). Serogroup-specific assays provided preliminary characterization the STEC strain(s) prior to isolation, including a LUX real-time PCR assay targeting the O157 serogroup-specific fimbrial gene *lpfA*, and a microsphere suspension array targeting allelic variants of *espZ*. A template pooling technique

was developed to rapidly distinguish STEC strains from non-toxin producing strains after stool enrichment. PCR and DNA sequencing of the *gnd* locus was used to determine the O-serogroup of STEC isolates, and the '*E. coli* O-Typer' webtool was developed to assign serogroup classifications to *gnd* sequence data (www.corefacility.ca/ecoli_typer/). **Results:** The genetic profile of stool cultures was used to identify the presence of multiple STEC serogroups, and these data facilitated the isolation of the respective strains. These included samples that contained co-infections of both O157:H7 and O103:H2; O157:H7 and O26:H11; and O177:NM and O55:H7 strains. The allele profiles of *gnd* directly correlate to STEC O-serogroups, therefore allowing a molecular approach to serogrouping. The *E. coli* O-Typer webtool indicated the serogroup that is associated with that *gnd* allele, the number of strains examined to date (to provide confidence in the serogroup classification), Shiga toxin alleles associated with those strains, and an alignment between input and reference sequences. **Conclusions:** Molecular assays and a template pooling technique allowed for the detection and isolation of both O157 and non-O157 STEC strains in clinical stool samples, and the *E.coli* O-Typer webtool distributes to public health laboratories a complete platform for molecular serogrouping of STEC.

Nosocomial Infections

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 43. Cluster of Hepatitis B Infection Among Residents of an Assisted Living Facility - New York, 2007

K. L. Southwick[1], E. J. Clement[2], F. Konings[1], S. VanZetta[3], G. S. Johnson[2], J. K. Schaffzin[2];

[1]New York State Department of Health, New Rochelle, NY, [2]New York State Department of Health, Albany, NY, [3]Orange County Health Department, Middletown, NY.

Background: In April 2007, the New York State Department of Health (NYSDOH) and the Orange County Health Department investigated a cluster of hepatitis B virus (HBV) infections among elderly residents of an assisted living facility (ALF) in Orange County, New York. **Methods:** Acute infections were identified using standard surveillance. Newly identified cases or their families were interviewed using standardized instruments. Additional information was collected through medical record review. Screening was performed for all staff and epidemiologically-linked residents to determine serological status. ALF site visits were conducted to assess infection control and healthcare delivery. **Results:** Three acute infections were identified with onsets 2/27/07-3/9/07; all underwent finger-stick blood glucose monitoring (FSBGM). Eight of 10 diabetics undergoing FSBGM had serologic evidence of HBV infection. Of 23 diabetic residents who did not undergo FSBGM and were screened for HBV infection, two (9%) had serologic evidence of resolved infection, and none had current HBV infection (RR:9.2; 95%CI=2.4-35.8). One of 8 staff known to have assisted residents with FSBGM had current HBV infection. One of 9 (11%) non-diabetic roommates had evidence of past HBV infection; none had current infection. The site visit found that residents shared spring-loaded lancet holders and glucometers for FSBGM. The facility was not properly sanitizing FSBGM equipment after each use. No additional cases were identified after the ALF ceased the practice of sharing FSBGM equipment and implemented a FSBGM equipment sanitization policy. **Conclusions:** FSBGM was significantly associated with HBV infection among diabetic ALF residents. No additional cases were identified after the ALF stopped the practice of sharing FSBGM equipment. Transmission of communicable disease is a significant concern for these facilities. Education and outreach is essential to assure safe practices for FSBGM in ALFs.

Board 44. A Massive, Multi-hospital Outbreak of Surgical Infections Caused by a Rapidly-Growing Mycobacterium Previously Unreported in Brazil. Rio de Janeiro - Brazil, 2007.

M. H. Garcia[1], R. S. Duarte[2], J. R. Melo[1], R. C. Gomes[3], I. A. Nogeira[3], G. P. Oliveira[3], M. D. Samberg[3], G. S. Dimech[1], M. Dalcolmo[4], A. W. Barreto[4], M. C. Lourenço[5], M. M. Pereira[6], S. C. Leão[7], J. Sampaio[8], S. M. Gomes[9], J. Sobel[10], W. N. de Araujo[1];

[1]Programa de Treinamento em Epidemiologia Aplicada aos Serviços do SUS (EPISUS), Secretaria de Vigilância em Saúde (SVS), Ministério da Saúde (MS), Brasilia, BRAZIL, [2]Laboratório de Micobactérias da UFRJ, Rio de Janeiro, BRAZIL, [3]Núcleo de Vigilância Epidemiológica Hospitalar (NVEH), Secretaria Estadual de Saúde, Rio de Janeiro, BRAZIL, [4]Centro de Referência Professor Hélio Fraga (CRPHF), Secretaria de Vigilância em Saúde (SVS), Ministério da Saúde (MS), Rio de Janeiro, BRAZIL, [5]Laboratório de Micobactérias da FIOCRUZ/RJ, Rio de Janeiro, BRAZIL, [6]Laboratório Central Noel Nutels/RJ, Rio de Janeiro, BRAZIL, [7]Departamento de Microbiologia, Imunologia e Parasitologia da Universidade Federal de São Paulo – Escola Paulista de Medicina, Sao Paulo, BRAZIL, [8]Laboratório Fleury Medicina e Saúde, Sao Paulo, BRAZIL, [9]Agência Nacional de Vigilância Sanitária, Ministério da Saúde (MS), Brasilia, BRAZIL, [10]Office of Global Health, CDC, Atlanta, GA.

Background: Rapidly-growing mycobacteria (RGM) are ubiquitous in the hospital environment and are known to cause nosocomial infections. We investigated reports of nosocomial infections resistant to conventional antimicrobial therapies. **Methods**: We established active surveillance and conducted a descriptive study. A suspect case was defined as: a post-surgical infection unresponsive to routine antimicrobial therapy occurring between August 2006 - February 2007 in the greater Rio de Janeiro metropolitan area. A confirmed case was defined as a suspect case with positive AFB smear or isolation of non-tuberculous mycobacteria, or with granulomatous inflammation on a wound biopsy. Speciation was by PRA-hsp65 technique. **Results:** We identified 864 suspect cases in 64 hospitals and 7 townships. Median age was 45 years (range, 17-89) and 279 (82%) were female. The median incubation period was 32 days (range, 1-427). Confirmed cases totaled 196 (23% of all cases), and the most commonly identified species was *Mycobacterium abcessus* (98% of 133 isolates with identified species). Sequencing of the rpoB gene resulted in re-classification of 25 (19%) isolates as *Mycobacterium massiliense*. The descriptive study included 341 cases. Principal manifestations included: discharge (76%), granulomas (39%) and pain (33%). In 338 (99%) of surgeries, access was by videolaparoscope and 214 (70%) surgeries were cholecystectomies. Hospital sterilization units were not responsible for processing materials in 285 (84%) of the surgeries. In 204 (63%) surgeries disposable materials were reused and in 186 (57%) there was no validation of high-level disinfection for thermosensitive materials. Hospitals with reported cases were inspected by state regulatory authorities. A referral system with a guarantee of free treatment was established. **Conclusions**: This was the largest outbreak of post-surgical RGM infections ever reported in Brazil. Observed failures in disinfection of surgical supplies and involvement of a mycobacterial species and genotype not previously reported in Brazil may explain the outbreak. Systematic enhancement of disinfection in hospitals in the region is essential.

Board 45. Is The Epidemic Strain of Clostridium *difficile* NAP1 responsible for Community Acquired CDAD?

G. Dumyati[1], G. Hannett[2], D. Wroblewski[2], A. D. Thompson[3], B. M. Limbago[3];

[1]University Of Rochester, Rochester, NY, [2]New York State Department of Health, Albany, NY, [3]Centers for Disease Control and Prevention, Atlanta, GA.

Background: *Clostridium difficile* is an anaerobic gram positive bacillus that produces 2 pathogenic toxin types: toxin A and toxin B. Transmission of C. *difficile* occurs primarily in health care facilities (HCF). Over the past few years, several hospital and nursing home outbreaks have been attributed to the emergence of a new more virulent strain of C. *difficile* designated North American pulse-field gel electrophoresis type 1 (NAP1), toxinotype III. The strain produces a toxin called binary toxin and has an 18-bp deletion in the *tcdC* gene. Recently, several cases of serious CDAD have been reported in low risk populations such as healthy individuals living in the community without HCF exposure. **Methods:** In 2006, we conducted a CDC initiated pilot study, at Rochester General Laboratory, for enhanced surveillance of presumed community-acquired C. *difficile* (CA-CDAD). A case was defined as a patient with a C. *difficile* toxin-positive stool specimen collected as an outpatient or within 72 hours of admission, and with no evidence of HCF exposure in the preceding 3 months. Positive C. *difficile* stool specimens were cultured and isolates were tested for toxinotype, PCR for *tcdC* gene deletion and PFGE. **Results:** Over a 2 month period, 111 positive cases were reviewed, 24 (20%) were CA-CDAD. Information on antibiotic, proton pump inhibitors or H2 blocker intake in the 3 months preceding CDAD were obtained from electronic medical record or through a questionnaire sent to the patient's physician. The mean age was 50 years (range 8 months-89 years). 46% of patients were hospitalized but none resulted in severe disease (toxic megacolon, acute renal failure of shock) or death. Of the cases where information was available 92% had a history of recent intake of antibiotics. None were on H2 blockers or proton pump inhibitors. Sixty-one percent of the community acquired isolates were due to toxinotype 0 (most common hospital strain), 17% were due to the epidemic NAP1 strain and 9% were toxinotype III non-NAP1. **Conclusion:** CDAD is no longer limited to patients having contact with HCF. Disease is occurring in the community due known hospital stains and the newly described NAP1 strain. Further research is needed to study risks for disease acquisition and strain distribution in community settings.

Outbreak Investigation: Lab & Epi Response

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 46. Building Partnerships to Improve Outbreak Preparedness: the Establishment of an Emergency Vaccine Stockpile for Meningitis Epidemics

A. Fernandez, A. Costa, International Coordinating Group on Vaccine Provision;

WHO, Geneva, SWITZERLAND.

Background: Epidemics of meningococcal meningitis hit the African Meningitis Belt in periodic, but difficult to predict waves. The last major epidemic of 1996-1997 affected over 220,000 people in 10 countries. The WHO strategy for effective epidemic control in Africa includes: enhanced surveillance, appropriate case management and reactive mass vaccination with Polysaccharide (PS) vaccines. The characteristics of PS vaccines, together with their low prices and unpredictable demand, have made them an unattractive product. PS vaccine supply has further decreased with the development of conjugate vaccines. To minimize the impact of global vaccine shortages and ensure a coordinated and equitable access to PS vaccines, WHO together with UNICEF, MSF, and the IFRC established the International Coordinating group for Vaccine Provision (ICG) in 1997. **Methods:** The ICG set up a contingency stock of vaccine with funds raised by international appeals. To access this stockpile, a country facing an epidemic of meningitis must submit a request for vaccine to the ICG, through a standard form. The ICG members make a consensual decision based on pre-set epidemiological and operational criteria for outbreak response. This decision is communicated to the country within 2 working days of request submission. The vaccine stocks, held at the manufacturer's storage facilities are then released by the ICG. **Results:**

- Activity (1998-2007): over 32 million doses of vaccine shipped to countries facing outbreaks
- Performance of vaccine release mechanism (2003-2007)[1]: 48 out 50 approved requests fulfilled
- Timeliness of response 2006-2007[2]: 11 days from reception of vaccine request to arrival of vaccine at country level

Challenges:
- Improving communication between ICG and countries
- Building consensus among partners in decision making
- Ensuring and building continued engagement of partners
- Achieving financial sustainability

[1] Data not available before 2003
[2] Indicators established in 2006

Conclusions: The ICG has set up a mechanism to ensure rational access to vaccines in a shortage context. Working with its technical partners and their networks, the ICG strives to provide assistance and supplies to countries in need. However, many challenges should continue to be addressed to improve performance of this mechanism.

Board 47. A Legionnaire's Disease Outbreak Linked to Roof-Collected Rainwater Systems in New Zealand

C. N. Thornley[1], G. Simmons[1], S. Jury[1], D. Harte[2], J. Mohiuddin[1], M. Taylor[3];

[1]Auckland District Health Board, Auckland, NEW ZEALAND, [2]Institute of Environmental Science and Research Ltd, Porirua, NEW ZEALAND, [3]Ministry of Health, Wellington, NEW ZEALAND.

Background In February 2006, an outbreak of Legionnaires' Disease (LD) was identified in Beachlands, an isolated East Auckland suburb of 1400 households all supplied with drinking water from roof-collected rainwater systems. **Methods** Case finding was carried out to determine the scale of the outbreak. Risk factors for infection were investigated using a case-control study. Geographical clustering was determined using a Bernoulli model. Potential sources of infection were sampled, and molecular typing (using sequence-based typing (SBT) was undertaken on all *Legionella pneumophila* serogroup 1 (Lp1) isolates. **Results** Four cases were identified. Lp1 was isolated from the respiratory tract of one case, the roof-collected rainwater systems of five households (three associated with cases) and from a water blaster at a nearby marina. All isolates were indistinguishable, exhibiting the same SBT allele pattern. The four LD cases lived close to the water blaster and downwind in prevailing conditions. Twenty-three controls were recruited; cases were more likely to be male, elderly and to have chronic illnesses. Household water systems were less likely to have *Legionella* contamination if situated >650m from the water

blaster. Three of the four cases occurred in a statistically significant cluster (p=0.014). **Conclusions**: This is the first outbreak of LD in New Zealand linked to roof-collected rainwater supplies and the first isolation of *Legionella* from these systems in a temperate climate. Aerosols containing *Legionella* discharged to air by the marina water blaster may have infected some cases directly and may have seeded Beachland's roof-collected rainwater systems. Cases with *Legionella* contaminated water supplies may also have been exposed during showering. The water blaster was decontaminated and householders were provided with information about correct rainwater system maintenance. Roof-collected rainwater systems need appropriate design, careful cleaning and the maintenance of hot water temperatures at a minimum of 60°C to reduce the chances of multiplication of *Legionella*. Further research into the ecology of *Legionella* in roof-collected rain water systems is indicated.

Board 48. Identification of the Sources of Periodic Epidemics that Maintain the Cholera Bacteria in Ajegunle and Amukoko Districts (Ajeromi/Ifelodun Local Government Area - LGA) in Lagos State, Nigeria

C. E. Egbom[1], O. S. Badaru[1], E. Ademuson[1], E. B. Coker[2], A. Onoja[1], N. Njepuome[2], J. Scharff[3], P. Nsubuga[3], S. Gwarzo[4];

[1]Federal Ministry of Health, Lagos, NIGERIA, [2]Federal Ministry of Health, Abuja, NIGERIA, [3]Centre for Disease Control and Prevention, Atlanta, GA, [4]Centre for Disease Control and Prevention, Abuja, NIGERIA.

Background: Cholera is a severe diarrhoeal disease which causes alteration in the digestive system by the production of potent toxin called cholera toxin (CT), produced by a bacterium called *Vibrio cholerae* serogroup 01. It is endemic in areas where poor economic conditions, sanitary systems, public hygiene and safe drinking water are scarcely available. The sources of the endemicity or recurrent epidemics of the bacteria in Ajegunle/Amukoko districts of Ajeromi/Ifelodun Local Government Area (LGA) of Lagos State were investigated. **Methods**: A total of 27 stool and 24 water (from taps, wells and boreholes) specimens were collected at two health centres and 4 random geographical locations respectively in both Ajegunle and Amukoko districts of Ajeromi-Ifelodun LGA in Lagos State. Isolation of *V. cholerae* as well as biochemical, serological, chicken red blood cells agglutination and antimicrobial susceptibility tests were carried out. **Results:** Of the 27 human specimens collected, 11 (40.7%) had *V. cholerae* isolates while 12 (50%) of water specimens had same isolates. Both faecal and water specimens had the same serogroup 01 and similar strains by biochemical and other tests. Strains identification by plasmid profile and genetic characterization still need to be carried out to confirm the strains of cholera bacterium from the two sources. The presence of strains of *V. cholerae* serogroup 01 circulating in Ajegunle and Amukoko districts predicts an imminent danger of cholera outbreak in these areas at any point in time in future. Immediate control measure is to improve the quality of water and intensify efforts on public education about good sanitary practices. **Conclusions**: *V. cholerae* serogroup 01 has been isolated in stools of individuals and environmental water (taps, wells and boreholes) as the major sources of periodic cholera epidemics in Ajegunle and Amukoko districts of Ajeromi-Ifelodun LGA in Lagos State, Nigeria.

Sexually Transmitted Diseases

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 49. Prevalence of Sexually Transmitted Diseases and High Risk Behaviors among Female Sex Workers in Indonesia

L. R. Pasaribu, R. Rusli, L. Rif'ati, E. Rahardjo, S. Sihombing, K. R. Palupi, E. R. Sedyaningsih;

National Institute Of Health Research and Development, Jakarta, INDONESIA.

Background: Prevention of sexually transmitted infections is a high priority for the Ministry of Health in Indonesia. Promotion of condom use among persons with multiple sexual partners is a key strategy that has been used since 1990's. This study was conducted in November 2006 to April 2007 to measure the STI prevalence among female sex workers (FSWs) and to identify their sexual behaviors including condom use. **Methods**: After obtaining informed consent, 250 subjects were recruited randomly from the rosters of FSWs in known establishments of 7 major cities in Indonesia. Of the 1750 FSWs who agreed to participate, 1286 (73.5%) were direct and 464 (26.5%) indirect FSW. Trained interviewers collected the behavioral data in face-to-face interviews in a private room using standardized interview methods with a structured questionnaire. Clinical exam and standardized laboratory methods were used to identify STIs. **Results**: The prevalence of STIs was high and included 89.2% of subjects with cervicitis (Neisseria gonorrhoea, Chlamydia trachomaticum and other infections), 73% with Bacterial vaginosis, 24% Vaginal Candidiasis, 12.2% Syphilis, 5.3% Trichomoniasis, 2.1 % Condyloma, and 0.5% vaginal ulcers. Between cities, the prevalence of different STIs did not vary considerably with the exception of Syphilis where the prevalence ranged from 0.8% in Samarinda to 55.2% in Makassar. Gonnorhea, Syphilis, and Herpes simplex Virus-type 2 were more common in direct versus indirect FSW. Only 15.4% of FSWs reported always using condoms; 28.7% reported they never used condoms. FSW who reported not using condoms were more likely to have Cervicitis infection (PR = 1.44) and Chlamydia trachomaticum (PR = 1.76) infection. **Conclusion**: The prevalence of STIs among FSWs is high in Indonesia. There is considerable variation in the prevalence of Syphilis with widescale outbreaks in some cities. Greater efforts are needed to develop a behaviour change strategy among FSWs and their clients to promote condom use and lower transmission of STIs.

Surveillance: International and New Strategies

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 50. Differences in the Clinical Presentation of Confirmed Arboviral Infection in South America

M. S. Gipp[1], A. G. Lescano[1], C. Guevara[1], V. Suarez[2], L. Beingolea[3], J. Vargas[4], C. Madrid[5], A. Laguna[1], P. Pachas[3], S. Manock[6], M. Cespedes[7], J. Perez[1], D. L. Blazes[1], E. Gotuzzo[8], T. J. Kochel[1];

[1]US Naval Medical Research Center Detachment (NMRCD), Lima, PERU, [2]Instituto Nacional de Salud, Ministerio de Salud, Lima, PERU, [3]Direccion General de Epidemiologia, Ministerio de Salud, Lima, PERU, [4]Centro Nacional de Enfermedades Tropicales (CENETROP), Santa Cruz, BOLIVIA, [5]Hospital Naval de Guayaquil, Guayaquil, ECUADOR, [6]Hospital Vozandes Oriente, Quito, ECUADOR, [7]Instituto Nacional de Salud, Lima, PERU, [8]Universidad Peruana Cayetano Heredia, Lima, PERU.

Background Febrile illness is common in tropical developing countries, but lack of laboratory equipment and assays limit physicians' ability to identify infectious pathogens. A better description of the symptoms related to febrile pathogens could facilitate their accurate identification. We evaluated if the frequency of presenting symptoms differed between the five main arboviral causes of fever in three countries. **Methods** We analyzed data from an ongoing study of febrile disease conducted in 19 sites in Bolivia, Ecuador, and Peru since 2000. Patients >5 years old presenting with a febrile illness to local clinics were examined by a physician who recorded demographics and symptoms and drew a blood sample, which was sent to NMRCD in Lima for testing. Dengue fever, Venezuelan equine encephalitis (VEE), Group C virus, Mayaro and Oropouche fever were identified by immunofluorescence and polymerase chain reaction assays. We compared the occurrence of 34 different symptoms with each viral infection, excluding symptoms reported by <2% of patients. Differences in prevalence of symptoms between all viruses were first identified, then viruses were compared pair-by-pair. Differences of >10% ($p<0.05$) are reported. **Results** Samples from 18,938 subjects were analyzed, 85% from Peru. Subject's mean age was 27 years, 47% were female. Of all subjects, 2204 were confirmed infected with dengue virus, 102 VEE, 39 Mayaro, 27 Group C and 18 Oropouche. Vomiting was more frequent in subjects with VEE (49%) than with other viruses (13-31%), and also differed between Dengue and Mayaro (31% vs 13%). Prostration was more common with Mayaro (45%) than with Dengue, VEE, or Group C virus (19% to 23%). Malaise was more frequent with Dengue and VEE (98%) and Mayaro (100%) than with Oropouche (88%). Abdominal pain was more frequent with VEE and Mayaro (48% and 58%) than with Dengue (37%). Injected conjunctivae were more frequent with VEE (34%) than with Dengue (19%). **Conclusions** Arboviral pathogens had similar clinical presentations and definitive diagnosis could not be determined by the presence of a single symptom, however the frequency several symptoms differed between specific pathogens, some by >20%. Diagnostic algorithms developed using these results may be useful for clinicians without access to laboratory testing.

Board 51. Systematic Review of Surveillance Systems for Emerging Zoonotic Diseases

L. Vrbova[1], C. Stephen[1], N. Kasman[2], R. Boehnke[3], M. Doyle-Waters[4], B. Gibson[3], A. Chablitt-Clark[3], M. Brauer[1], M. Fitzgerald[4], D. M. Patrick[1];

[1]University of British Columbia, Vancouver, BC, CANADA, [2]York Region Health Services Department, Toronto, ON, CANADA, [3]Ontario Ministry of Health and Long-Term Care, Toronto, ON, CANADA, [4]Vancouver Coastal Health Research Institute, Vancouver, BC, CANADA.

Background: In response to a growing sense of urgency to prevent and control emerging infectious diseases (EIDs), EID surveillance systems are proliferating. There is a need to examine whether these systems are being developed and evaluated using evidence-based methods in order to properly interpret the early warning value of these systems and to recommend allocation of resources for their development and support. The purpose of this study was to conduct a systematic review of peer-reviewed literature published between 1992 and 2006 on surveillance systems for EIDs and their evaluation. **Methods:** A broad search was employed to search for peer-reviewed literature worldwide that described and/or evaluated EID surveillance systems, focusing on zoonotic EIDs. Preliminary results of the review were discussed by all authors at a one-day meeting intended to develop consensus on sources of information, inclusion/exclusion criteria, data extraction, and plan of analysis. **Results:** 209 articles were included in the review resulting in 225 emerging zoonosis surveillance systems. Many of the systems that were described as surveillance systems were misclassified as they did not include any time-sensitive response component, and were therefore either case detection systems or monitoring systems. More than half of the articles were published in the last quarter of the study (2003-6), suggesting many of the systems are still new. Only 17 of the 225 systems were evaluated, and only four of these used the evaluation results to support their claims that their systems were useful or not useful in identifying outbreaks or cases of disease. **Conclusions:** This systematic review has shown that many systems that claim to be surveillance systems for emerging zoonoses are in fact only monitoring or case detection systems, highlighting the common confusion regarding what constitutes 'surveillance'. Further, less than 10% of the systems have been evaluated, suggesting that they have not been developed using evidence-based methods. This lack of information makes it difficult for decision-makers to choose surveillance initiatives which have been proven effective.

Board 52. Development of Influenza Surveillance Networks in Korea

D. Kwon[1], J. Lee[1], W. Choi[1], N. Lee[1], M. Kong[1], J. Park[1], S. Kim[1], H. Jung[1], H. Jeong[2], H. Oh[1], H. Cho[1], C. Kang[1];

[1]Korea Centers for Disease Control and Prevention, Seoul, REPUBLIC OF KOREA, [2]Gyeongnam institute of health and environment, Gyeongnam Province, REPUBLIC OF KOREA.

Background: Korea has participated in Global Influenza Surveillance since Division of Influenza and Respiratory Viruses, National Institute of Health was designated as the National Influenza Center (NIC) in 1972. With the revision of the Communicable Disease Prevention Act in 2000, influenza was designated as a Class III National Notifiable Communicable Disease which needs to monitor. With this, Korea Influenza Surveillance Scheme (KISS) was established in 2000 and run by NIC to control influenza in Korea. To enhance current KISS we participated in five-year project which was managed by US CDC, and here we present the achievements of 3 budget years. **Methods:** The first budget year period of the project was from Sep. 15 2004 to Sep. 14 2005 and renewed annually. For three years we focused on three activities for the enhancement of KISS. These are the improvement of the capacity of all 17 Public Health and Environment Research Institues (PHERIs), the improvement of the capacity of NIC and, the cooperation with animal part for the establishment of active avian influenza surveillance. **Results:** For the improvement of the capacity of PHERIs, we performed on-site visit instructions for the quality control of facility and equipment. We performed proficiency test for RT-PCR by distributing panels for each type/subtype viruses. We held workshop to strengthen the collaboration between PHERIs and NIC and to increase the awareness about influenza surveillance. For the improvement of NIC capacity, We supplied reference reagents including viruses, cells, and genetic materials to all PHERIs before the beginning of influenza season. We established real-time RT-PCR methods recommended by US CDC and trained a laboratory staff for the diagnosis of avian influenza at US CDC. To strengthen international collaboration we sent influenza virus isolates to WHO CCs regularly. For the active surveillance of avian influenza, we collaborated with National Veterinary Research and Quarantine Service to develop the monitoring system for high-risk groups. **Conclusions:** With this project, we could enhance influenza surveillance system in Korea efficiently and upgrade and normalize the level of 17 PHERIs. And we could enhance the capacity of NIC

and contribute the global influenza surveillance for the preparedness of pandemic.

Board 53. Adherence to Perinatal Group B *Streptococcus* Prevention Guidelines: New York State, 2003-2004

N. L. Spina[1], G. L. Smith[2], J. B. Karr[2], S. M. Solghan[1], S. M. Zansky[1];

[1]NYS Dept. of Health, Albany, NY, [2]NYS Dept. of Health, Rochester, NY.

Background: Perinatal transmission of group B *Streptococcus* (GBS) is a leading cause of neonatal mortality. The 2002 CDC prevention guidelines recommend universal prenatal screening for maternal GBS colonization and intrapartum antibiotic prophylaxis (IAP) for carriers. The guidelines state that screening should occur within 5 weeks of delivery. Penicillin IAP should be administered if a GBS+ or unknown screen, and a vaginal delivery. If the mother is penicillin allergic, cefazolin should be used. In 2006 a review of maternal birth records was conducted by the Emerging Infections Program (EIP) to assess adherence to guidelines. Abstracted data from two NYS EIP areas (7 counties near Rochester and 8 near Albany) were compared. **Methods:** Using an algorithm, randomly selected birth records from 2003 and 2004 were reviewed using a data collection form. Maternal demographics, pre- and post-natal testing, antibiotic usage and labor and delivery information were abstracted. **Results:** In NYS, 804 birth records from 21 hospitals were reviewed (333 from Albany (A) and 471 from Rochester (R)). Pre-natal GBS testing was performed on 714 mothers (87% in A and 90% in R). Twenty percent (n=162) had a positive GBS screen with 17% not given IAP. There were 32 GBS+ newborns; 8 in A (rate 3.96/10,000 live births) and 24 in R (rate 9.72/10,000 live births). The mean number of weeks between GBS culture date and delivery of GBS+ infants was 4.8 in A and 6.8 in R compared to 5.0 for GBS- babies. Mothers with a GBS+ or unknown screening result delivered 14 GBS+ infants (4 A, 10 R). Antibiotic therapy was provided appropriately to 5 mothers who delivered GBS+ babies vaginally and were GBS+ or unknown. All mothers with a penicillin allergy, a positive or unknown GBS screen and delivered vaginally (n=22) were given inappropriate IAP (14 A, 8 R). **Conclusions:** The recommendation for universal screening and IAP when a GBS screen is positive or unknown was followed in most pregnancies in the two areas. Recommendations for screening within 5 weeks of delivery was more closely adhered to in Albany and may contribute to the higher rates of GBS+ infants born in the Rochester area. Treatment of penicillin allergic mothers was not appropriately followed in either area. Further study should be conducted to determine factors that may affect adherence to guidelines.

Board 54. Healthcare Utilization Practices for Influenza-like Illness and Severe Acute Respiratory Infection in Guatemala; Implications for Influenza Surveillance

A. J. Johnson[1], W. Clara[2], H. T. Jordan[1], W. Arvelo[1], N. Padilla[2], A. Fry[1], C. Friedman[1], L. Reyes[3], K. Lindblade[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Universidad del Valle de Guatemala, Guatemala City, GUATEMALA, [3]Guatemala Ministry of Public Health and Social Assistance, Guatemala City, GUATEMALA.

Background: The Pan American Health Organization (PAHO), in collaboration with Centers for Disease Control and Prevention, developed a standard protocol for influenza surveillance for its member states, which recommends surveillance for influenza-like illness (ILI) in sentinel outpatient clinics and for severe acute respiratory infection (SARI) in sentinel hospitals. We conducted a community healthcare utilization survey and estimated the proportion of ILI and SARI cases that would be captured using the PAHO protocol in Guatemala. **Methods:** The Department of Santa Rosa was selected for the study. Santa Rosa has one government-run hospital and 15 government-run outpatient clinics with physicians in attendance. Sixty populated areas were selected in a two-stage cluster sampling procedure with probability of selection proportional to size. Standardized questionnaires, requesting health histories of all members of the household, were administered to randomly selected households. Healthcare sought for all reported episodes of ILI (defined as fever and cough or sore throat) in the preceding month and probable severe respiratory illness (SRI; defined as cough and dyspnea for >2 days or physician-diagnosed pneumonia) in the preceding year were recorded. **Results:** Of 5356 individuals surveyed in 1,116 selected households, 697 (13%) had an episode of ILI during the past month and 327 (6%) had an episode of SRI during the past year. Among these, 467 (68%) and 247 (75%) persons sought some form of healthcare outside the home for ILI and SRI, respectively. Of those seeking care outside the home, 35% of ILI and 26% of SRI patients visited a government-run outpatient facility. Two percent of ILI and 13% of SRI patients visited a government-run hospital. Overall, 5% of SRI patients were hospitalized. Patients also sought care at pharmacies (28% ILI, 20% SRI), private hospitals (1% ILI, 3% SRI), and private clinics (19% ILI, 36% SRI). **Conclusions:** The majority of persons with ILI or SRI did not seek care at the government-run healthcare facilities in Santa Rosa. These results suggest that the PAHO protocol will need to be modified to accurately estimate the burden of ILI and SARI in this region. Including pharmacies and private clinics in surveillance efforts for ILI and SARI may provide more complete estimates.

Board 55. Impact of Phone Calls or Supervision Visits on Timeliness and Data Quality in an Electronic Disease Surveillance System in a Resource Limited Setting – Peru

M. A. Huaman[1], C. C. Mundaca[1], R. V. Araujo[1], G. M. Soto[1], J. M. Neyra[1], J. Quispe[1], V. Vallejos[2], M. Fernandez[2], D. L. Blazes[1];

[1]US Naval Medical Research Center Detachment, Lima, Peru, PERU, [2]Centro Medico Naval, Lima, Peru, PERU.

Background: Alerta DISAMAR is an electronic surveillance system for infectious diseases implemented in the Peruvian Navy, and covers a dispersed population in a resource-limited setting. Evaluation of surveillance systems is imperative to assess effectiveness. Data quality and timeliness are essential attributes of surveillance systems that are influenced by several factors. The objective of this study was to assess the effect of two monitoring strategies on the performance of the Alerta System. **Methods:** 40 Alerta units (18 clinics and 22 ships) were selected to participate in a 12-week prospective evaluation project. All units received a short refresher training course on the notification process and were then randomly assigned to one of three intervention groups: phone, visit or control. The phone groups were called 3 hours before the bi-weekly reporting deadline if they hadn't sent their reports. The visit groups received supervision visits on weeks 4 & 8, but no phone calls. The control groups were not contacted by phone or visit. Timeliness and data quality were assessed prior to and during intervention. Timeliness was measured through number of reports on time per total number of reports (ROTR) and Quality through number of errors per total number of reports (EPTR). **Results:** There were not significant differences between groups for ROTR or EPTR prior to the intervention. Timeliness in the phone cohort improved from 64.4% (IC95%: 56.2 - 72.4) to 84% (IC95%: 70.9 - 92.8) (p=0.01) in clinics, and increased from 46.4% (IC95%: 39.1 - 53.7) to 77.2% (IC95%: 67.2 - 85.3) in ships (p<0.001). Visit and control groups didn't show significant changes in timeliness. Differences in timeliness between groups during interventions were significant (ANOVA p<0.001). EPTR improved in the visit cohort

in 72% (IC95%: ↓14% -↓81%) among clinics (p=0.016) and 19% (IC95%: ↓58% - ↑97%) among ships (p=0.813). Phone and control groups didn't show improvement in data quality (ANOVA =0.8587). **Conclusions:** Regular phone reminders significantly improved the reporting timeliness in an electronic surveillance system, whereas regular monitoring visits caused a trend of improved data quality. Further investigations are needed to establish the cost-effectiveness and optimal use of each these strategies.

Board 56. Usefulness of Household-based Surveillance for Childhood Pneumonia in Rural Kenya

M. K. Van Dyke[1], A. Audi[2], G. Bigogo[2], B. Flannery[1], R. F. Breiman[3], D. R. Feikin[2];

[1]CDC, Atlanta, GA, [2]International Emerging Infections Program, CDC-Kenya, Kisumu, KENYA, [3]International Emerging Infections Program, CDC-Kenya, Nairobi, KENYA.

Background: Pneumonia is a leading cause of morbidity and mortality in children, yet accurate estimates of disease burden in Africa are lacking. Clinic-based surveillance may not be representative, and it underestimates incidence in populations with poor access to healthcare. Household-based surveillance can provide population-based estimates of pneumonia, although case definitions without radiologic confirmation or clinical examination may be nonspecific. **Methods:** We began active, clinic- and household-based surveillance for pneumonia in Lwak, Asembo Bay, Kenya in 2005. Biweekly household visits captured illness symptoms during the previous two weeks using a standardized questionnaire. We compared the symptom profile reported at the household with clinic information for surveillance participants diagnosed with Integrated Management of Childhood Illness (IMCI) severe pneumonia to develop a household-based case definition for pneumonia-like illness (PLI). We evaluated the sensitivity, specificity and incidence of the household-based PLI definition using the IMCI case definition for children presenting to the clinic as our gold standard. **Results:** Between July 1, 2006 and June 30, 2007, 85,520 household visits were conducted among 3,723 children aged < 5 years; respiratory illness was reported for 15,762 (18.4%) visits. During this period, there were 2,219 clinic visits with 246 episodes of IMCI severe pneumonia; 88% of pneumonia cases were linked with a household visit for the same illness episode. The household-based PLI definition that maximized the sum of sensitivity and specificity was cough or difficulty breathing and ≥ 1 of the following: inability to drink or breastfeed, lethargy, convulsions or chest indrawing. This definition was 49% (95% CI 36-62%) sensitive and 72% (95% CI 68-76%) specific for IMCI severe pneumonia. Accounting for specificity, there were 3,251 cases of PLI, and PLI incidence correlated with IMCI severe pneumonia for most months. The incidence of pneumonia in children aged < 5 years was 66 cases/1000 population at the clinic and 873 cases/1000 population at the household. **Conclusions:** Clinic-based surveillance underestimated pneumonia incidence. Household-based surveillance can better define the true burden of childhood pneumonia in this rural African setting.

Travelers' Health & Diseases Importation

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 57. Cutaneous Anthrax Associated with Drum-Making by Using Goat Hides from West Africa -- Connecticut, 2007

A. Guh[1], K. Glynn[1], A. Hoffmaster[1], K. Martinez[1], M. Guerra[1], S. Shadomy[1], T. Smith[1], C. Marston[1], J. Stratidis[2], D. Barden[3], K. Purviance[3], M. Cartter[3], J. Hadler[3];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Danbury Hospital, Danbury, CT, [3]Connecticut State Department of Public Health, Hartford, CT.

Background: In 2006, cases of inhalation anthrax were reported in two drum-makers - one in the U.S. - who had recently worked with untreated West African goat hides. In August 2007, the Connecticut Department of Public Health was notified of a suspect cutaneous anthrax case in a drum-maker working with goat hides from Guinea, and 2 days later, a suspect case in his child. We investigated to confirm the diagnosis, identify sources of exposure and extent of dissemination of *Bacillus anthracis* spores. **Methods:** The index patient and his wife were interviewed. Skin biopsy specimens from the two case-patients' lesions were obtained for diagnostic testing. Environmental testing using swabs, wipes, and vacuum sampling was conducted in the shed where the drum-maker worked, the house where the family lived, and the car used to transport recently purchased goat hides. All hides and drum tops in the shed were cultured. Skin biopsy specimens and extracted DNA from all isolates were sent to CDC for genotyping. **Results:** Biopsy specimens were *B. anthracis*-positive by PCR for both patients and also by immunohistochemistry for the child. Drum heads were made by soaking hides in water and stretching over the drum body, then scraping and sanding them. The index patient's routine practices minimized personal exposure (designated shoes, clothes, dust masks, gloves) and household cross-contamination (drums and work clothes not brought indoors). Two exceptions to these practices - once wearing short sleeves while sanding drums and once bringing shoes and clothes into the home - might account for exposure in the two cases. Positive cultures for *B. anthracis* were obtained from multiple skins and drum tops, the car trunk, 18/70 house samples, and all 16 shed samples, many with heavy growth. All isolates and *B. anthracis* DNA detected in the child's biopsy were genotype 1. **Conclusions:** This third recent case of anthrax in a drum-maker likely occurred from exposure while working on untreated goat hides from Guinea. Using personal protective equipment (PPE) might have prevented inhalation anthrax. The child was likely exposed from cross-contamination of the house. Drum-makers should be aware of the occupational risk of anthrax and the potential to expose others. Preventive methods include use of PPE and safer sources of hides.

Board 58. Screening for Influenza Infection in International Airline Travelers Arriving in New Zealand

P. Priest[1], L. Jennings[2], A. Duncan[3], C. Brunton[3], M. Baker[4];

[1]University of Otago Dunedin, Dunedin, NEW ZEALAND, [2]Canterbury Health Laboratories, Christchurch, NEW ZEALAND, [3]University of Otago Christchurch, Christchurch, NEW ZEALAND, [4]University of Otago Wellington, Wellington, NEW ZEALAND.

Background: Entry screening of air travelers is one possible component of border control that island nations may use to prevent or delay the entry of pandemic influenza. However, little is known about the entry of infectious diseases into countries by air, or about the likely effectiveness of this strategy. We investigated the feasibility of using a health screening questionnaire, throat swabs, and follow-up to measure the prevalence of seasonal influenza infection in airline travelers entering NZ. **Methods:** Questionnaires were distributed to passengers and crew on board 5 flights entering Christchurch International Airport in July 2007. Questionnaires were collected at the aircraft exit. Two groups of travelers were invited to provide a throat swab: those who reported one or more of fever, sore throat, cough, muscle aches, and chills, and randomly selected asymptomatic passengers. Follow-up data were collected three days after the arrival of each flight. **Results:** The number of staff required to collect questionnaires, identify respondents eligible for a throat swab and escort them through immigration was much greater than anticipated. Questionnaire response rates ranged from 40% to 70%, with 15% (55/359) respondents having one or more symptoms and 3 meeting an ILI case definition (fever plus sore throat or cough). Throat swabs were obtained from 47% of symptomatic respondents and 65% of 48 randomly selected asymptomatic respondents. Influenza B was recovered from 1 throat swab (from a symptomatic but non-ILI respondent). Permission for follow-up was provided by 161 of the 304 asymptomatic respondents. Contact was achieved with 121. At follow-up, 14 indicated they had developed one or more symptoms since arrival. Five of these consented over the telephone to provide a throat swab, but only 3 did so. **Conclusions:** It is feasible to use a voluntary screening questionnaire onboard aircraft to measure the prevalence of influenza in international airline travelers. Follow-up of respondents proved difficult even when they had agreed and provided contact details. A larger study is planned to measure the prevalence of symptomatic and asymptomatic influenza infection in arriving international air travelers, the predictive value of the questionnaire, and the resource requirements of routine entry screening.

Board 59. World Health Organization (WHO) Travel Recommendations During the 2003 SARS Outbreak: Lessons Learned for Mitigating Influenza Pandemic and Globally Emerging Infectious Diseases

A. D. Berro[1], N. Gallagher[2], E. Yanni[2], H. Lipman[2], A. Whatley[2], B. Bossak[2], R. Murphy[2], C. Pezzi[2], N. Marano[2];

[1]Centers for Disease Control and Prevention, San Francisco, CA, [2]Centers for Disease Control and Prevention, Atlanta, GA.

Background: Severe acute respiratory syndrome (SARS) is an emerging infectious disease caused by a novel coronavirus. From November 2002 through July 2003, SARS killed 774 persons in 11 countries. Mainland China, Hong Kong, and Taiwan reported the greatest number of cases. International travel contributed to the spread of SARS. In response, WHO issued recommendations to postpone nonessential travel to affected countries. This study evaluated the association between these travel recommendations and U.S. air travel to and from China, Hong Kong, and Taiwan. It also assesses travel recommendations as a mitigation tool for globally emerging infectious diseases. **Methods:** To coincide with the months in 2003 during which WHO posted travel recommendations for this region, data was analyzed on international passenger travel between the United States and China, Hong Kong, and Taiwan for April-June 2000-2006 using U.S. Bureau of Transportation Statistics. Data from 2003 were compared to data from the other years. A multivariable model was used to adjust for changes in 2000-2006 travel patterns. **Results:** In April-June 2003, the time period when WHO SARS travel recommendations were posted, the number of travelers between the United States and China, Hong Kong, and Taiwan was 59.8% (p<0.0001) lower than the number expected compared to the other years. This reduction in travel was due to a 71.7% (p<0.0001) decrease in travel between the United States and China, a 78.9% (p<0.0001) decrease in travel between the United States and Hong Kong, and a 46.7% (p<0.0001) decrease in travel between the United States and Taiwan. For China and Hong Kong, U.S. outbound travel was more affected than U.S. inbound travel. **Conclusions:** A statistically significant decrease in travel between the United States and China, Hong Kong, and Taiwan occurred during the months in 2003 when WHO posted SARS travel recommendations. Based on other studies showing that restricting travel reduces disease spread, the association in this study suggests that travel recommendations (among other tools and factors) may be an effective public health tool to limit the spread of an influenza pandemic and other emerging infectious diseases via global transportation networks.

Tropical Infections & Parasitic Diseases

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 60. High Complexity of the Glutathione Transferases Class III Gene in Malaria Vector *Anopheles gambiae*

L. Zhou, R. A. Wirtz, W. G. Brogdon;

Centers for Disease Control and Prevention, Chamblee, GA.

Background: The glutathione S transferase (GST) class III insecticide resistance gene has been shown to contribute to DDT resistance in *Anopheles gambiae*. This study explores sequence diversity in this gene in four strains of *An. gambiae* from the CDC Malaria Research and Reference Reagent Resource (MR4) vector program. **Methods:** We used PCR, cloning and sequencing techniques to describe haplotype diversity in the GST class III from strains relevant to study of insecticide resistance in *An. gambiae*: 1.G3, wild type susceptible; 2.ZAN/U, DDT resistant through increased GST activity; 3.RSP, resistant through possession of a serine-*kdr* allele plus, as we previously demonstrated, elevated beta-esterase and cytochrome P450 activity; and 4.VK, a hybrid strain multiply resistant through a novel serine TCT/*kdr*, and phe/*kdr*. **Results:** Extensive allelic heterogeneity has been observed within individual mosquito and between the strains evaluated at the gene locus GST Class III of *An. gambiae*. **Conclusions:** By applying cloning and sequencing procedures, the extensive heterogeneity of the GST Class III gene has been observed. These data have implications both for the flexibility with which *An. gambiae* can respond to insecticide selection and for the difficulties presented by this gene for the development of reliable molecular probes for detecting and assessing insecticide resistance in field populations. Thus, the GST gene shows similarity to the P450 and esterase insecticide resistance genes in possessing extreme diversity in allele sequences.

Board 61. Molecular profile of drug resistant mutations associated with *Pfcrt* and *Pfmdr*-1 genes in *Plasmodium falciparum* isolates from a malaria endemic region of Venezuela

L. M. Syphard[1], S. Sridaran[1], S. M. Griffing[1], T. Mixson[1], A. M. McCollum[1], L. Villegas[2], A. Escalante[3], V. Udhayakumar[1];

[1]CDC, Chamblee, GA, [2]Asociacion Civil Impacto Social, Tumeremo, VENEZUELA, [3]Arizona State University, School of Life Sciences, Tempe, AZ.

Background: Molecular markers such as single nucleotide polymorphisms (SNPs) and microsatellite (MS) markers have become valuable tools for monitoring the emergence of drug resistance in *Plasmodium falciparum*. Molecular surveillance data have shown that after removing drug pressure, there is a decline in the frequency of drug resistant genotypes in some populations, while in other populations the frequency of drug resistance has not changed. Recently, we reported that in an endemic part of Venezuela, sulphadoxine-pyrimethamine (SP) resistant parasites were fixed several years after SP was replaced with a combination therapy (artesunate plus mefloquine). Here we investigate the frequency and diversity of mutations in chloroquine transporter gene (*Pfcrt)* which has been linked to chloroquine resistance and a multi-drug resistance gene (*Pfmdr*-1) implicated in resistance to chloroquine and mefloquine in *P. falciparum* parasites in Venezuela. **Methods:** We used DNA from blood samples collected from 93 adults between June 2003 and May 2004 in Bolivar state, Venezuela. Direct sequencing was used to genotype *pfcrt* codons 72 to 76 and real time PCR was used to assess *Pfmdr-1* codon polymorphisms, including N86Y and Y184F. Microsatellite markers flanking *Pfcrt* and *Pfmdr*-1 genes were characterized. **Results:** All isolates had the SVMNT resistant genotype (mutations at codons 72 and 76) according to sequence analysis. For *Pfmdr*-1, all isolates tested were wild type at codon 86 and mutant at codon 184. Multiple closely related haplotypes were found for both *Pfcrt and Pfmdr*-1 genotypes. **Conclusions:** The frequency of the mutant *Pfcrt* and *Pfmdr*-1 genotypes suggest fixation of mutants in this study area of Venezuela. The lack of diversity in these mutant haplotypes supports the conclusion that both *Pfcrt* and *Pfmdr*-1 resistant genotypes appear to have derived from a common ancestral allele.

Board 62. Outbreak of Suspected Brazilian Purpuric Fever in Children with Antecedent Conjunctivitis, Para State, Brazil, 2007

E. A. Santana-Porto[1], A. A. Oliveira[1], W. N. de Araujo[1], D. Soares[2], C. Oliveira[3], M. L. Lopes[3], C. Silva[3], P. Vasconselos[3], A. Pinheiro[4], J. Sobel[5];

[1]Field Epidemiology Training Program, SVS, Brazilian Ministry of Health, Brasilia, BRAZIL, [2]Municipal Secretariat of Health of Anajas/State Secretariat of Health of Para, Anajas, BRAZIL, [3]Instituto Evandro Chagas, Belem, BRAZIL, [4]State Secretariat of Health and Epidemiologic Surveillance of Para, Belem, BRAZIL, [5]Office of Global Health, CDC, Atlanta, GA.

Background: Brazilian Purpuric Fever (BPF) is a rare, fatal systemic infection caused by *Haemophilius aegyptius* with antecedent conjunctivitis, last reported in 1990 and previously not detected in the Amazon region. Seven possible cases were reported in August-September 2007 from a remote town in Para State. **Methods**: We modified the CDC clinically-confirmed case-definition as follows: acute fever in a child aged 3 months to 10 years with abdominal pain and/or vomit, purpura, antecedent conjuntivitis, absence of meningeal symptoms, and exclusion of meningococcal infection. We defined a probable case as presence of any 5 of the above 6 symptoms. We conducted case-finding for BPF and conjunctivitis in the community and local schools. We conducted a case-control study for risk factors for death; a case was defined as death in a child within 24 hours of fever onset in August 2007. Controls were living children household members of cases. Due to the remoteness of the area, blood and conjunctival swabs for bacterial cultures were collected using available materials which lacked *H. aegyptius* selective growth agents, and were transported under precarious conditions. **Results**: Five of seven patients were clinically confirmed cases and one was a suspect case; 5 (83%) died within 24 hours of fever onset. Median age was 4 years (range, 2-8). The case-control study showed strong association of death with: eye pain (Odds Ratio [OR]=22.7, p=0.01; tearing (OR=13.5, p=0.03); eye redness and secretion (p= 0.004). Of 1,598 school children examined, 111 (7%) had conjunctivitis. Of 28 blood samples and 99 conjunctival swabs, none yielded *H. aegyptius*; screening for 19 arboviruses was negative. Serological and molecular test results are pending. Following institution of antimicrobial prophylaxis of contacts and conjunctival infections, and education of the population, no further BPF cases were detected. **Conclusions**: A clinically confirmed outbreak of BPF occurred in this remote Amazonian region, and was controlled by antimicrobial prophylaxis. Failure to isolate *H. aegyptius* from clinical samples was likely due to unavailability of proper culture materials and precarious transport conditions; pending serological and molecular tests may provide laboratory confirmation. Regional surveillance for BPF and conjunctivitis continue.

Board 63. Risk Factors for the High Mortality Observed in Visceral Leishmaniasis Patients Treated with Liposomal Amphotericin-B, Brazil, 2005-2006

A. L. Alencar Junior[1], W. A. Alves[2], M. L. Sousa-Gomes[2], A. N. Maia-Elkhoury[2], L. D. Costa[3];

[1]Brazilian Field Epidemiology Training Program (EPISUS), Secretariat of Health Surveillance, Ministry of Health, Brasilia, BRAZIL, [2]Coordenação de Doenças Transmitidas por Vetores e Antropozoonoses, , Secretariat of Health Surveillance, Ministry of Health, Brasilia, BRAZIL, [3]Centro de Ciências da Saúde, Universidade Federal do Piauí, Teresinha, BRAZIL.

Background: Visceral leishmaniasis (VL) is a public health challenge in Brazil and an important endemic disease worldwide. In view of rising mortality rates for VL in Brazil, the Ministry of Health has recommended in 2004 the use of liposomal amphotericin B in cases where compound pentavalent antimonials or colloidal amphotericin B deoxycholate are contraindicated. We describe the clinical and epidemiologic characteristics of VL patients treated with liposomal amphotericin B, and analyzed risk factors for death in patients treated with this agent. **Methods**: We conducted a case-control study using data from consultation forms and clinical progression forms. A case was defined as death in a VL patient who died after initiation of liposomal amphotericin B treatment. A control was a VL patient who improved on this therapy. **Results**: On report forms for 262 patients treated with amphotericin B, 78 (30%) patients were treated in 2005 and 184 (70%) in 2006. Age ranged from 4 months to 89 years, with predominance of adult males. Principal signs and symptoms included: splenomegaly, 234 (89%); fever, 228 (87%); palor, 218 (83%); hepatomegaly, 202 (77%); hemorrhage, 90 (34%); and edema, 89 (34%). Cure was reported in 167 (64%), and in 47 (18%) the outcome was not reported. Median time from symptom onset to initiation of therapy was 52 days (range 4-829 days). Mortality was 18% (48 of 262 patients). In the case-control study, risk factors associated with death were: generalized edema (Odds Ratio [OR]=2.5; 95%CI=1.3-5.2); elevated hepatic enzymes (OR=2.3; 95%CI=1.1-5.2) and cholestasis (OR=2.2; 95%CI=1.1-4.5). **Conclusions**: The delay from symptom onset to treatment and the high mortality in this group of VL patients underscores the need for training of healthcare professionals in the prompt diagnosis and treatment of VL. In VL patients treated with liposomal amphotericin B, clinical severity of presentation was associated with death. Standardized reporting forms are an important source of information for analysis of diagnosis, treatment and outcomes of VL in Brazil.

Vector-Borne Diseases

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 64. Precipitous Increase in the Incidence of Dengue Hemorrhagic Fever in Children: A New Challenge to Public Health in Brazil

G. E. Coelho[1], M. C. Mendes[1], G. H. Moraes[2], A. C. Simplicio[1];

[1]Secretariat of Health Surveillance, Ministry of Health, Brasilia, BRAZIL, [2]Secretariat of Health, Federal District of Brasilia, Brasilia, BRAZIL.

Background: Brazil reports 90% of the cases of Dengue Fever (DF) in the Americas; so far in 2007, over 440,000 cases have been reported. Dengue Hemorrhagic Fever (DHF) occurs in a small minority of cases but accounts for virtually all deaths. DF and DHF epidemiology is characterized by endemic areas of high incidence, simultaneous circulation of multiple virus serotypes, and predominance of adults among the ill. **Methods:** We analyzed data from the National Reportable Disease Surveillance System in 2005 and 2006 for changes in the age distribution of DHF cases. Case definitions for confirmed DHF were in accordance with Pan-American Health Organization guidelines. **Results:** Between January 2005 and December 2006, 1,395 cases of DHF were reported in Brazil. In 2005 the incidence in persons <15 years of age was 0.17/100,000 inhabitants. In 2006 the incidence of DHF in this age group rose to 0.52/100.000 inhabitant, an increase of 207%. The increase in incidence in this age group varied by geographic region. In the Northeastern region, the incidence increased 299%; the highest increase in incidence occurred in the states of Maranhão (1,666%), Alagoas (592%), Piauí (296%) and Rio Grande do Norte (221%). In the Southeast Region the incidence in this age group increased by 689%; the highest increase in incidence occurred in the states of Minas Gerais (394%) and Rio de Janeiro (542%). **Conclusions:** The precipitous increase in the incidence of DHF in persons <15 years old is highly unusual and was observed only once before, in Amazonas State in 2001. This phenomenon could be associated with successive exposures of affected populations to 3 different Dengue serotypes. Further investigations are needed to characterize risk factors for childhood dengue fever and explain the difference in the age distribution of DHF different regions of the country. The result of this investigation will be essential in orienting the actions of Ministry of Health, particularly in improving training for diagnosis and treatment of DHF patients of all ages.

Board 65. Evaluation of Five Formulations of *Bacillus Thurigiensis* for Dengue Control in The Municipality of João Pessoa - Pb

C. V. Assis-Pujol, F. G. Silveira, I. A. Braga, G. E. Coelho;

Ministry of Health, Brasilia - DF, BRAZIL.

Background: Detection of resistance of *Aedes aegypti* to organophosphates in Brazilian cities led the Ministry of Health (MS) to search for control alternatives. One of these options is the use of *Bacillus thurigiensis* sorovar *israelensis* (Bti). Even though the efficiency of this biolarvicide was confirmed in several studies, its application on large scale in dengue control programs is pioneering in Brazil, as an initiative of the MS, through the National Dengue Control Program (PNCD), in face of the need of insecticide substitution in the municipalities where resistance was detected. **Methods:** Five different commercial formulations were analyzed, herein designated as A, B, C, D e E. An area of approximately 6.000 premises, with occurrence of *Ae. Aegypti*, was selected. The total area was divided in five sub-areas. In João Pessoa Bti is not used in the routine program control, one of the subareas was treated with temephos. Formulations C and D were applied in the same sub-area since one is intended to treatment of human consumption water, while the other is used only for non-potable water. The House Index (HI) was assessed, prior to treatment, based on a larval survey of 30% of the study area premises. Each sub-area was treated with one of the tested larvicides. All water-filled recipients were inspected and treated according to PNCD's directives. All treated containers were tagged. In each sub-area blocks were selected with approximately 750 premises, of these 1/3 were weekly inspected during the two cycles of the test. The HI, Breteau Index (BI) and Recipient Index (RI) were used to evaluate the efficiency and persistence of each formulation. **Results:** Results revealed that the recipients treated with formulation A displayed a positivity of 0,0% in the eighth week of both cycles, the ones treated with formulation B showed 11,0% and 4,0% in the first and second cycle respectively, those treated with formulation C and D had 9,0% in the first cycle and 10,0% in the second cycle and the ones in which formulation E was applied showed 15,0% in the first and second cycle. **Conclusions:** The results indicate that formulation A is the one that showed the best persistence on field conditions.

Board 66. Primary Investigation on Arbovirus Distribution in China

G. Liang, S. Fu, X. Lv, X. Sun, H. Wang, Z. Lv, M. Li;

Institute For Viral Disease Control and Prevention,China CDC, Beijing, CHINA.

Background: Up to now, there are over 500 kinds of arboviruses in the world, 100 kinds of which may induce relevant diseases by infecting human beings and animals. Currently, infectious diseases caused by arboviruses are still epidemic all over the world, such as JE, dengue fever and West Nile encephalitis. However, the background of the arboviruses and relevant diseases are still unclear in China. A comprehensive systemic investigation on arboviruses and relevant diseases in China is imperative. **Methods:** Mosquitoes were collected both Yunnan and Xinjiang provinces in summer 2006. The samples were grinded and spin with a pool of 100 mosquitoes in 1ml of DMEM. The supernatant was inoculated to both C6/36 and BHK cell simultaneously. Suckling mice were inoculated of the positive isolates and observed daily. All of the virus isolates were identified by the methods of virology, morphologic, serology and molecular biology and some detection by specific antibody and primers of JEV, Flavivirus, alphavirus and bunyavirus. The PCR products were sequenced. **Results:** During the investigation, about thirty thousand mosquito samples were collected and forty-six virus isolates were isolated by tissue culture cell. Eighteen isolates were isolated from samples collected in Yunnan province and twenty-eight isolates were isolated from samples collected in Xinjiang province. The identification data showed that the virus isolates include Japanese encephalitis virus(JEV),Getah virus(GETV) and Bunyaviridae virus(BUN). In addition, among the forty-six isolates, twenty-eight strains are segmented double-stranded RNA virus (dsRNA), which include twenty-three strain Liaoning virus (LNV), one Banna virus (BAV) and four Kadipiro virus (KDV). **Conclusions:** Some studies have been reported that LNV and BAV can cause fever and viral encephalitis. In this investigation, 3 species of segmented dsRNA virus were isolated and identificated from mosquitoes samples in China. Our results indicated that LNV not only exist in Liaoning Province,where the virus was first isolated, north China, but also exist in Xinjiang, west China.The relationship between unknow fever and viral encephalitis occured in summer and newly arbovris isalates is being studied.

Board 67. Surveillance for Yellow Fever and other Arboviruses in Free-Ranging Primates in Southern Brazil: an Important Tool for Emerging Diseases Detection

M. A. de Almeida[1], E. Santos[1], D. F. Fonseca[1], M. A. Torres[1], J. C. Cardoso[1], L. L. Cruz[1], F. A. Paz[1], P. F. Vasconcelos[2], S. G. Rodrigues[2];

[1]Division of Environmental Health Surveillance (DVAS)/State Center of Health Surveillance (CEVS)/Rio Grande do Sul State Health Secretariat, Porto Alegre, BRAZIL, [2]Center for Arbovirus Reference and Research, Department of Arbovirus, Instituto Evandro Chagas/SVS/Ministry of Health, Belem, BRAZIL.

Background: In 2001 and 2002, after a 35-year hiatus, the Yellow Fever Virus (YFV) was identified in forest-dwelling monkey populations in Rio Grande do Sul State, Southern Brazil. At that time, two primates (Howler monkeys, genus *Alouatta*) died in forests in this state due to Yellow Fever (YF) infection, and YFV was isolated from mosquitoes (*Haemagogus leucoceleanus*) in the same area. These findings led the State Secretariat of Health in 2002 to initiate monitoring of YFV and 18 other arboviruses in free-ranging primates and mosquitoes. We sought to identify geographic risk areas for arbovirus occurrence based on the presence of primates and mosquitoes and virus circulation. **Methods:** Monkeys were captured through chemical immobilization (drug injection), using a CO_2 operated dart projector rifle. After drawing blood samples, taking biometric measurements and implanting a subcutaneous microchip, the monkeys were released. Mosquitoes were collected and preserved in liquid N_2. Isolation of arboviruses and serology by hemmaglutination inhibition (HI antibodies detection) and neutralization tests were attempted at the Center for Arbovirus Reference and Research, Department of Arboviruses, Evandro Chagas Institute. **Results:** Between 2002 and 2007, we conducted 34 field expeditions throughout the state. We captured 181 monkeys of two *Alouatta* species (*A. caraya* and *A. guariba clamitans*) and mosquitoes from two genuses (*Heamagogus* and *Sabethes*) capable of YF transmission. We detected immunity to Oropuche Virus in 1 monkey and immunity to Saint Louis Virus in 16 monkeys by neutralization tests. **Conclusions:** Although YFV was not found in the area, this is the first time Oropuche and Saint Luis viruses were identified in primates in Southern Brazil, suggesting that vector and reservoir surveillance should be strengthened, and that human arbovirus surveillance should be implemented.

Board 68. An Outbreak of Sylvatic Yellow Fever In Persons who had Refused Vaccination in a Yellow Fever Endemic Region, Brasil, 2007

A. Romano[1], Z. A. Guerra[1], S. Leal[1], R. C. Oliveira[1], R. P. Almeida[2], A. J. Rezende[2], M. Santalucia[2], B. R. Carvalho[3], M. A. Almeida[4], J. Sobel[5];

[1]Department of Vectorborne Diseases and Anthropozooses, Secretariat of Health Surveillance, Ministry of Health, Brasilia, BRAZIL, [2]State Secretariat of Health of Goiás, Goias, BRAZIL, [3]Municipal Health Secretariat, Jataí, BRAZIL, [4]State Secretariat of Health, Rio Grande do Sul, BRAZIL, [5]Office of Global Health, CDC, Atlanta, GA.

Background: Yellow fever (YF) vaccination is to recommend in high-risk areas only but offered anywhere at no cost. We investigated an outbreak of sylvatic YF in Jatai, Goias, an endemic area, in April 2007. **Methods:** We conducted a descriptive study with prospective case finding through the pulic health system in the affected area. Suspected cases and residents were interviewed and samples were collected for serology (MAC-ELISA). An environmental investigation included collection of serum from primates for serological testing (hemaglutination inhibition, (HI) and PRNT), and capture of vectors. Virus was sought in primate blood and vectors by means of inoculating C6/36 cells and RT-PCR. **Results:** Two cases of SYF were detected, with reactive IgM and positive immunohistochemistry. These case-patients were males, aged 23 and 54, rural laborers who refused vaccination during a recent campaign; both died. Indeterminant results were obtained on TGO:4170/5950 and TGP:4100/5840. Symptoms included: Fever, fatigue, headache, abdominal pain, vomit, diarrhea, hemorrhage, jaundice, and oliguria/anuria. In the probable area of infection we interviewed 14 persons with median age of 37 years (range, 10-64) of whom 9 (57%) were males, 10 (84%) had incomplete primary education , 9 (74%) had YF vaccination (5 (36%) were vaccinated after the interview). In the active case search, 6 suspect cases were identified: median age was 39 years (interval, 16-48), 4 (67%) were female, and none died. All had non-reactive IgM and were discarded as cases. On environmental investigation, 6 samples were collected from primates of *Cebus sp.* and 30 lots of vectors were captured at ground and tree canopy levels. Six (50%) primates had reactive serology by HI for *Flavivirus*; PRNT test results are pending. Among vectors, the causative virus of YF was isolated in *Sabethes glaucodaemon* captured in tree canopies. **Conclusions:** This YF outbreak occurred in an endemic area; mortality was 100%. Case-patients were poorly education and had refused vaccination; a substantial proportion of persons interviewed in the area were unvaccinated. *Cebus sp.* Primates and *Sabethes* genus mosquitos participate in the local sylvatic YF cycle. Intensification of education efforts among low-education populations in this and other endemic areas is essential.

Women, Gender, Sexual Minorities & Infectious Diseases

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 69. The Validation of a West Nile Virus Survey Among Women Living in the Deep South region of the United States

L. G. Yerby[1], M. Perko[2], J. Higginbotham[1];

[1]The University of Alabama School of Medicine, Tuscaloosa Campus, Tuscaloosa, AL, [2]The University of Alabama, Tuscaloosa, AL.

Background West Nile Virus (WNV) is now the most common arbovirus in the United States (US). Most at risk are persons over age 50 and the immunocompromised. There are also documented cases of WNV spreading from mother to child across the placenta and through breast-milk, possibly leading to neural defects or illness. Health education campaigns focused on personal protective behaviors are essential to prevent human illness from WNV, particularly given the nonexistence of a human vaccine. A review of the literature base revealed an absence of theoretically-driven US studies specific to the WNV prevention behaviors of women; thereby revealing a gender disparity in current vector-borne disease research. The purpose of this investigation was to modify and validate an existing International WNV survey based on the Health Belief Model (HBM) and administer among a population of women living in the Deep South region of the United States. **Methods** A multi-stage survey development process was used including literature review, expert panel review, focus groups, face-to-face interviews, central-location-intercept-interviews, instrument pilot study, and data analyses that included principal components factor analysis with varimax rotation. A final sample of 335 female

Southeastern community participants age 19 and older completed the survey either on paper or online. **Results** Qualitative results and expert feedback produced survey modifications that resulted in an instrument with high face-validity and documented participant comprehension. The final 28 Likert-scale survey items were found to be valid and reliable with a 6-factor model aligned according to the constructs of the HBM. This model explained 59.1% of the variance and yielded an overall Cronbach's alpha score of 0.698. **Conclusions** The validated WNV survey is a timely and effective health education tool to measure knowledge, perceptions and prevention behaviors of US women with regard to emerging infectious diseases while also reducing gender disparities in the study of vector-borne illness. Additionally, this instrument could be useful for needs assessment, conceptualization, and implementation of WNV prevention campaigns targeting women in the Deep South region of the United States.

Zoonotic & Animal Diseases

Monday, March 17
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 70. Efficacy of Chloramphenicol in the Treatment of a Hamster Model of Acute Leptospirosis

S. J. Becker, S. McCall, M. E. Griffith, C. K. Murray, D. R. Hospenthal;

BAMC, San Antonio, TX.

Background: Leptospirosis is a disease of worldwide importance which frequently occurs in developing countries. Chloramphenicol is an inexpensive medication which is widely available in the developing world. While in vitro studies suggest that chloramphenicol has limited activity against leptospirosis, there are few in vivo studies to confirm this. **Methods**: Female Golden Syrian hamsters were infected intraperitoneally with 1 x 10^5 organisms of *Leptospira* interrogans serogroup Canicola serovar Portlandvere. On days 2 through 6 after infection, groups of ten hamsters were treated daily with different intraperitoneal doses of chloramphenicol (25, 50, and 100 mg/kg). Control groups included a group of untreated hamsters and a group treated with doxycycline 5 mg/kg/day. The hamsters were monitored for survival for 21 days. Moribund animals were humanely euthanized. **Results**: All untreated hamsters died within nine days of infection. All of the doxycyline-treated controls survived to day 21. All of the hamsters treated with chloramphenicol 25 and 50 mg/kg died within nine days of infection, paralleling survival of the untreated control group. There was a trend toward longer survival among those animals receiving chloramphenicol at 100 mg/kg daily, but none of the hamsters in this group survived more than 12 days following infection. **Conclusion**: Chloramphenicol does not prevent death from leptospirosis in our animal model of acute leptospirosis. This study does not provide support for the use of chloramphenicol in the therapy of leptospirosis or when leptospirosis is suspected.

Board 71. Human Monkeypox in Sudan: Endemic or Introduced?

R. Levine[1], D. Carroll[1], P. Formenty[2], M. Muntasir[3], M. Reynolds[1], R. Regnery[1], I. Damon[1];

[1]Centers for Disease Control, Atlanta, GA, [2]World Health Organization, Geneva, SWITZERLAND, [3]Federal Ministry of Health, Khartoum, SUDAN.

Background: A model of the ecological niche of human monkeypox disease in Africa, generated in early 2005, suggested favorable area of distribution throughout most humid forests across Africa. In late 2005, WHO documented the first reported cluster of human monkeypox from Sudan, which fell in a southern region not predicted to have favorable disease ecology according to the ecological niche model (ENM). CDC confirmed monkeypox viral DNA signatures from Sudanese samples and performed genome-level DNA sequence analyses, which suggested that the virus was highly similar to monkeypox virus isolates obtained from the Congo Basin. A follow-up investigation conducted by WHO found evidence of other human monkeypox infections from the same region of southern Sudan in a similar timeframe as the original cluster. **Methods:** We re-created the human monkeypox ENM including 4 new Sudanese occurrence points of human infection to assist in formulating a robust hypothesis regarding whether the human monkeypox virus infections in Sudan were the result of either naturally circulating (endemic) virus or introduction events from a neighboring country coupled with human-to-human spread. **Results:** Inclusion of the Sudanese monkeypox cases in our ENM widened the predicted range of disease to include a trans-African belt extending from Sudan, north of the Congo Basin, to and including substantial areas of West Africa, as well as a wide corridor to the east of the Congo Basin continuing on toward much of coastal East Africa. The novel ENM encompassed territory in all 10 countries from which human monkeypox cases have been reported, as did the original ENM, but further included considerable tracts of favorable niche in a large number of additional countries from which human monkeypox has never been observed. **Conclusions:** The absence of reported human monkeypox cases from many of the geographic areas predicted by the ENM including Sudanese cases seems to support the hypothesis that virus was introduced to Sudan (as opposed to being endemic). However, this preliminary interpretation is predicated on lack of human monkeypox cases from many countries, which, in the absence of surveillance, is not known with confidence. The results of this exercise therefore point to a need for greater surveillance and awareness of human monkeypox in sub-Saharan Africa.

Board 72. *Mycoplasma* Species Isolated from California Sea Lions (*Zalophus californianus*)

D. V. Volokhov[1], H. Kong[1], A. A. Neverov[1], F. M. Gulland[2], M. Haulena[3], J. George[1], V. E. Chizhikov[1], M. K. Davidson[4];

[1]Center for Biologics Evaluation and Research, Food and Drug Administration, Rockville, MD, [2]The Marine Mammal Center, Sausalito, CA, [3]Vancouver Aquarium, Vancouver, BC, CANADA, [4]Center for Drug Evaluation and Research, Food and Drug Administration, Silver Spring, MD.

Background: Mycoplasmas are diverse microorganisms of the class *Mollicutes*, which are widely distributed in vertebrates. Although three species of mycoplasmas have been reported in harbor seals (*M. phocicerebrale*, *M. phocidae* and *M. phocirhinis*) and a new species *(M. zalophi*; Haulena M. et al. J. Wildl. Dis. 2006) has been recently described from California sea lions (CSL), the biodiversity of mycoplasmas in marine mammals has not been investigated. In the present study, we analyzed microbiologic and genetic characteristics of several clinical mycoplasma strains isolated from CSL, undergoing rehabilitation at The Marine Mammal Center (TMMC) in Sausalito, CA. (http://tmmc.org). **Methods:** Specimens from CSLs with purulent skin and soft tissue infections, as well as pneumonias, were subjected to bacteriological analysis. Mycoplasmas were initially cultured on tryptic soy agar with 5% sheep blood and A8 agars at 35°C in 5% CO_2 for up to 14 days. Mycoplasma isolates were sent to the *Mollicutes* Collection (Purdue University, IN) for detailed microbiological characterization and identification by serology and fluorescent antibody staining. The 16S rRNA, *rpoB*, *gyrB* genes and the 16S-23S rRNA ITS region were amplified and

sequenced. **Results:** 35 mycoplasma isolates from 14 CSLs were microbiologically and genetically analyzed. Finally, 34 isolates were identified as previously known mycoplasma species, *M. phocidae*, *M. phocicerebrale*, and *M. zalophi*. However, the reference rabbit antiserum to *M. phocidae* failed to recognize *M. phocidae* isolated from CSLs in the growth inhibition test. Phylogenetic analysis of *rpoB* and *gyrB* genes of *M. phocidae* isolates showed the existence of at least 4 divergent genogroups. One of 35 analyzed mycoplasma was found to be novel *Mycoplasma* species (CSL4779) affiliated to the *M. bovis*, *M. lipophilum*, *M. equigenitalium* phylogenetic cluster. This novel species was biochemically and genetically characterized and has been deposited in DSMZ (www.dsmz.de) and ATCC (www.atcc.org) under the proposed name *M. zalophidermidis* strain DSM19723. **Conclusions:** Interspecies diversity within *M . phocidae* was demonstrated. These data indicate that biodiversity of mycoplasmas in wildlife animals may impact *Mollicutes* taxonomy.

Board 73. Contrasting the Epidemiology of Evolutionarily Independent Strains of Rabies in a Common Host Species

S. M. Wisely, H. D. Barton, R. Davis;

Kansas State University, Manhattan, KS.

Background: Comparative approaches to molecular epidemiology permit inferences regarding evolutionary constraints and ecological underpinnings of disease transmission. Two evolutionarily independent strains of rabies occur in striped skunks (*Mephitis mephitis*) in the Midwest; the northern strain is derived from the world-wide terrestrial strain, and the southern strain is derived from New World bats. **Methods**: We characterized 516 bp of the N gene of the rabies genome and multilocus microsatellite (n=8) genotypes from the striped skunk genome from 89 brain samples of infected striped skunks collected from 2003-2006. Sampling occurred in a north to south transect from areas where only the northern strain occurred (n=30), through the zone of contact (n=29), and into the range of the southern strain (n=30). **Results**: The northern strain had substantially higher nucleotide (0.03±0.01 vs. 0.005±0.003) and haplotype (17.7±8.1 vs. 2.8±1.5) diversity than the southern strain. We found little geographic patterning in the northern strain, but southern strain had similar isolates clustered both in phylogenetic and geographic space. In the southern strain, viral population growth was pulsed with a greater overall number of infections than the northern strain. Striped skunk population genetics indicated high levels of gene flow from South Dakota through Nebraska to Kansas (F_{ST} = 0.01). **Conclusion**s: The low isolate diversity, strong geographic patterning, and high rate of infection found in the southern strain of rabies suggest that it may be more efficiently transmitted than the northern strain, but skunk population genetic data suggest that differences in the transmission properties of variants are not explained by regional host demography. The high level of admixture among skunk populations throughout the Midwest stands in contrast to the geographic structuring of rabies, suggesting that infected hosts have a reduced rate of dispersal compared to the overall population.

C1. Foodborne and Waterborne Diseases I

Monday, March 17
1:15 PM – 2:45 PM
Centennial I

Outbreaks Associated with Frozen, Stuffed, Pre-browned, Microwaveable Chicken Entrees in Minnesota: Implications for Labeling and Regulation

C. Medus[1], S. Meyer[1], D. Boxrud[1], K. Elfering[2], C. Braymen[2], R. Danila[1], K. Smith[1];

[1]Minnesota Department of Health, St. Paul, MN, [2]Minnesota Department of Agriculture, St. Paul, MN.

Background In 1998, a *Salmonella* Typhimurium outbreak (33 cases) associated with eating Brand A chicken Kiev, a frozen, stuffed, pre-browned, microwaveable chicken product occurred in Minnesota (MN). Microwave cooking and consumer perception that the product was pre-cooked were contributing factors. One production date of product that tested positive was recalled. Brand A stuffed chicken product labels were changed to include longer cooking times. During 2005-2006, 3 more *Salmonella* outbreaks associated with the same type of product were identified in MN. **Methods** Outbreaks were identified by routine interviews of all reported *Salmonella* cases coupled with real-time pulsed-field gel electrophoresis (PFGE) subtyping of all *Salmonella* isolates. Intact products from case households and retail stores were cultured for *Salmonella*, and isolates subtyped by PFGE. **Results** Four *S.* Heidelberg cases associated with eating Brand B chicken broccoli and cheese were identified during January-March 2005. Brand B product labels were modified and cooking instructions verified. An *S.* Enteritidis outbreak resulting in 27 cases in MN and 14 cases in 9 other states occurred during August 2005-July 2006. Cases ate multiple brands of product from 3 manufacturers. One production date of Brand A product was recalled in March 2006. During April-June 2006, different varieties of Brand B product were implicated in a *S.* Typhimurium outbreak (3 cases). Several product samples tested positive for the outbreak serotype and subtype in all 3 outbreaks. Press releases were issued in all the outbreaks. Most cases in all outbreaks cooked the products in the microwave; none took the internal temperature of the product. Following these outbreaks, the National Advisory Committee for the Microbiological Criteria for Foods issued guidelines for labeling these products: 1) microwaving raw poultry from frozen is not advisable unless instructions ensure the 165ºF endpoint; and, 2) the label's principal display panel should warn that the product is raw. **Discussion** The cooked appearance of these products, inadequate labeling, and microwave cooking led consumers to undercook the products. Press releases were ineffective. Microwave cooking for these raw products is still allowed; whether the new label requirements will prevent outbreaks is unknown.

A Point-Source Outbreak of Guillain Barre Syndrome (GBS) Associated With Consumption of City Water, ShuangYang District, Changchun, Jinlin, China, 2007

R. Feng[1], Z. Lei[1], L. qun[2], M. Huilai[1], R. Fontaine[3];

[1]Chinese Field Epidemiology Training Program(CFETP), BeiJing, CHINA, [2]Emergency Response Office, Chinese CDC Beijing, China, BeiJing, CHINA, [3]Chinese Field Epidemiology Training Program(CFETP);United States Centers for Disease Control and Prevention, Atlanta, GA, USA, BeiJing, CHINA.

Background: The acute motor axonal neuropathy (AMAN) type of Gullain Barre Syndrome (GBS) affects hundreds of persons throughout the Far East each year. *Campylobacter jejuni* (CJ) infection may be a precipitating cause. In July 2007 we investigated a GBS outbreak in ShuangYang District (100,000 population) to identify risk factors of this outbreak and recommend appropriate control measures. **Methods**: We defined a GBS case as subacute onset from June 1 to July 31 2007 of bilateral flaccid weakness (on neurological examination) or paralysis in a resident of or person working in Shuangyang. We searched for GBS cases in all Changchun hospitals. We selected control persons through a random selection from all households within 100 m of GBS-households. We compared previous diarrhea and exposure to city water of all 36 cases to 165 controls. We also detected CJ infection by culture and serologic testing. **Results**: We identified 36 GBS (attack rate = 36/100,000) among residents of (33) or visitors to (3) Shuangyang. GBS -patients were widely dispersed throughout Shuangyang. Onset of all GBS occurred from June 21 to July 6 (16 days). On June 11 (from 10 to 35 days earlier) the pumps for the city water system failed and water pressure was restored on June 12 without first flushing the mains. Of GBS-patients 94% reported drinking un-boiled tap water from the city water system compared to 55% of control-persons OR =12 (95%CI=2.7-52). Of GBS-patients 61% reported having diarrhea since June 1 compared to 32% of control persons (OR = 3.4; 95% CI=1.4-8.4). After adjusting for drinking un-boiled water the OR for diarrhea was 2.7 (95%CI=1.2-6.5). CJ with the same PFGE and MLST type was isolated from 1 GBS-patient and 3 of 51 family contacts or neighbors. We found anti-CJ IgG in 61% of GBS-patients and anti-CJ IgM in 27% of GBS-patients. In comparison, 29% of family contacts and neighbors had anti-CJ IgG and 12% had anti CJ IgM. **Conclusions**: Drinking city water during a failure of the pumping system probably led to this point-source GBS outbreak. The weak association with diarrhea and the low isolation rate of CJ contrast with the high anti-CJ IgG prevalence to suggest that exposure only or asymptomatic infection with CJ initiated the development of GBS. We recommended regular surveillance of the city water supply for standard indicators of drinking water safety.

Oyster-associated *Vibrio* Infections in the United States, 1998-2006

M. Iwamoto, P. Yu, D. Swerdlow, J. Painter;

CDC, Atlanta, GA.

Background: Several *Vibrio* species are pathogenic and associated with clinical syndromes including gastroenteritis, wound infection, and septicemia. Foodborne infection usually occurs after eating raw or undercooked seafood, particularly oysters. CDC collects reports of *Vibrio* infections submitted by health departments. Regulatory efforts to address the threat of seafood-associated vibriosis have focused on prevention and surveillance for *V. vulnificus (Vv)* and *V. parahaemolyticus (Vp)* illnesses. **Methods:** We examined data on non-cholera vibriosis identified during 1998-2006. A case was defined as isolation of *Vibrio spp*. other than toxigenic *V. cholerae* from a clinical specimen. Transmission was classified as foodborne based on clinical information, specimen source, and patient exposures. Cases were considered oyster-associated if the case was foodborne and the patient consumed oysters within the 7 days before illness onset. To examine annual trends, we performed Wilcoxon-rank sums tests on year-to-year changes in incidence. **Results:** Of 4,364 non-cholera *Vibrio* infections reported from 49 states and territories, 3,090 (71%) were foodborne. Of patients with reported food histories, 1,519 (67%) reported eating oysters in the week before illness; among oyster-eaters, 83% reported eating them raw. Most oyster-associated infections (65%) were caused by *Vp*; other frequently reported species were *Vv* (18%), and *V. cholerae* non-O1, non-O139 (6%). Among oyster-eating patients, 484 (32%) were hospitalized and 139 (9%) died. No significant trends in the incidence of *Vp* or *Vv* oyster-associated cases were noted. The annual incidence of *Vp* varied greatly, with the largest number of cases reported during years coinciding with large outbreaks, most notably 1998 and 2006. **Conclusions:** Oysters continue to be an important source of foodborne vibriosis and deaths. To date, prevention efforts have been ineffective at reducing oyster-associated vibriosis. Industry and regulatory agencies have recently instituted control measures aimed at reducing the prevalence of vibrios in shellfish. Continued coordinated surveillance is necessary to monitor whether these efforts lead to a reduction in illness.

Large Outbreak of Beribéri Possibly Related to Consumption of Mycotoxin-contaminated Rice, Maranhão, Brasil, 2007

H. A. Lima[1], E. A. Santana-Porto[1], A. F. Santelli[1], G. Carmo[1], R. S. Alves[2], L. R. Queiroga[3], S. M. França[4], A. A. Siqueira[1], J. Sobel[5], R. P. Marins[6];

[1]Field Epidemiology Training Program, SVS, Brazilian Ministry of Health, Brasilia, BRAZIL, [2]COVEH/SVS, Brazilian Ministry of Health, Brasilia, BRAZIL, [3]Department of Heath, Imperatriz -Maranhao, BRAZIL, [4]Department of Epidemiologic Surveillance, Imperatriz - Maranhao, BRAZIL, [5]Office of Global Health, CDC, Atlanta, GA, [6]Division of Transmissible Diseases, SVS, Ministry of Health, Brasilia, BRAZIL.

Background: The accepted cause of beriberi is thiamine deficiency. Alcohol consumption, physical activity and high carbohydrate diets are known aggravating factors. Early 20th Century epidemics in Japan were attributed to rice contaminated by citreoviridin (CTV) mycotoxin, which produces a beriberi-like illness in animal models, possibly by disruption of thiamine metabolism. In 2006-7, 471 cases of suspected beriberi were reported from Maranhao State, Brazil. Previously reported data from this outbreak showed that rice samples from local rice processors and patient homes yielded *Penicillum citreonigrum*, *Fusarium spp*, and *Aspergillus spp*, and that all cultures produced CTV. We investigated risk factors for illness, including rice exposure. **Methods:** We conducted a 1:1 neighborhood-matched case-control study for risk factors of illness, defining a case as a clinically compatible illness in a resident of Maranhao reported with a diagnosis of beriberi. We collected samples of rice from case and control households. **Results:** Of 90 case-patients, 73 (80%) were male; the median age was 29 years (median, 9-73 years). Case-patients and controls reported low thiamine intake (0.7mg/day, 0.6 mg/day, respectively, p=NS). On multivariate logistic regression analysis, factors independently associated with illness were: male sex (matched Odds Radio [mOR]=2.4, 95%CI=1.0-5.6, p<0.035); alcohol intake (mOR=7.8, 95%CI=3.2-19.o, p<0.01); intensive physical labor (mOR=4.2, 95%CI=1.5-11.9, p=0.01), medical co-morbidities (mOR=2.7, 95%CI=1.1-6.5, p=0.02), and consumption of locally grown rice from subsistence farming (mOR=3.2, 95%CI=1.5-7.1, p≤0.01). Fungal cultures and assays for mycotoxin presence are pending. **Conclusions:** This study showed an association between beriberi and multiple risk factors, including consumption of locally produce rice, compared with rice from other sources. Previously reported data showed that locally produced rice was contaminated with CTV mycotoxin-producing fungi. In combination, these findings suggest that in a thiamine-deficient population, CTV mycotoxin may have contributed to development of beriberi. Culture and mycotoxin testing of rice samples from case-patient and control households, currently underway, may confirm this association.

Salmonella Montevideo Infections Associated with Exposure to Poultry from Mail-order Hatcheries - United States, 2007

U. Sharapov[1], C. Barton Behravesh[1], E. Hedican[2], J. Goplin[3], A. Garvey[4], K. Smith[2], S. Jawahir[2], C. A. Perry[1], M. Sotir[1];

[1]CDC, Atlanta, GA, [2]Minnesota Department of Health, St. Paul, MN, [3]North Dakota Department of Health, Bismarck, ND, [4]Iowa Department of Public Health, Des Moines, IA.

Background *Salmonella* infections from poultry contact are a public health problem. This report documents a multi-state outbreak of *S.* Montevideo infections, including three septic pediatric cases in siblings, associated with exposure to mail-ordered poultry. **Methods** On June 15, 2007, the Minnesota (MN) Department of Health reported to PulseNet (National Molecular Subtyping Network for Foodborne Disease Surveillance) a cluster of human *S.* Montevideo isolates with indistinguishable pulsed-field gel electrophoresis (PFGE) patterns (outbreak strain). Patients reported exposure to young poultry before illness. State health departments and PulseNet identified additional patients, who were interviewed using a questionnaire assessing poultry exposure and sources. **Results** Fifty-six persons with isolates indistinguishable from the outbreak strain were identified from 16 states; 45% were MN residents. Twenty-one (39%) were female; median age was 24 years (range: 2 months-84 years). Illness onsets occurred from March-September, 2007. Of 31 patients with available clinical information, all reported diarrheal illness and eight (26%) were hospitalized. Three cases of septic salmonellosis were reported in children from a North Dakota (ND) family; illness onsets occurred on the same day and all 3 patients were hospitalized. Twenty-three (70%) of 33 patients reported young poultry exposure during the 5 days before illness onset; 11 (48%) acquired birds at retail feed stores, and 8 (35%) ordered birds by mail. Poultry and environmental samples from bird enclosures at patient residences in MN and ND tested positive for the outbreak strain. Source hatcheries were identified for eighteen patients: 5 hatcheries from 3 states were identified as sources of implicated birds. Investigation of the hatcheries revealed multiple egg suppliers and outsourcing of hatching to smaller firms. **Conclusions** Young live poultry remain an important source of human *Salmonella* infections, with children at risk for severe illnesses. Distribution of birds through feed stores or by mail order directly to consumers occurs with minimal oversight. The mail-order hatchery industry can facilitate transmission of bird-associated human pathogens, including *Salmonella*, and poses an important challenge to the public health community.

An Investigation Points Towards Contaminated Mud as the Source of a *Campylobacter jejuni* Outbreak Associated with a Mountain Bike Race, British Columbia, Canada, June-July 2007

T. L. Stuart[1], J. Sandhu[2], R. Stirling[1], B. Wong[3], P. Martiquet[2], E. Galanis[3];

[1]Canadian Field Epidemiology Program, Public Health Agency of Canada (PHAC), Ottawa, ON, CANADA, [2]Office of the Chief Medical Health Officer, Vancouver Coastal Health Authority, Vancouver, BC, CANADA, [3]British Columbia Centre for Disease Control, Vancouver, BC, CANADA.

Background: One of the largest reported *C. jejuni* outbreaks in Canada occurred in June 2007 in a small community in British Columbia. It was associated with a 67 km mountain bike race that took place in wet and muddy conditions. There were 785 individuals who raced. **Methods**: Case definitions were developed. A retrospective cohort study was conducted to test hypotheses regarding potential exposures. Race participants were invited to complete an online questionnaire. Samples of mud and water from the race course were collected and tested for *Campylobacter*, generic *Escherichia coli* and total coliform counts. **Results**: Of race participants who responded, 25 (5%) met the laboratory-confirmed case definition, 200 (36%) the clinical definition, and 312 (57%) the well case definition. Although individuals who drank cups of water from official stations had an increased risk of developing illness (relative risk (RR) = 2.04, 95% confidence interval (CI) 1.44-2.88), no association between refilling personal water supplies at stations and illness was seen. Drinking water samples tested negative for *Campylobacter* and 25 racers were ill despite not drinking water from official stations. Racers who reported inadvertently consuming mud had a RR of illness of 2.11 (95% CI 1.50-2.97). After stratifying by consumption of cups of water, the relationship between mud exposure and illness remained. Mud samples tested negative for *Campylobacter*, but most were positive for generic *E. coli*, with coliform counts in some samples exceeding 24,192/100mL. **Conclusions**: Mud contaminated with human or animal feces was the likely source of *Campylobacter*. As *Campylobacter* is difficult to isolate from the environment, it is not surprising that samples taken three weeks after the race were not positive for the organism. The presence of *E. coli* and high coliform counts along the trail suggests that fecal contamination was present. The association between water consumption and illness was likely due to contamination of the water with mud from racers' hands, lips and faces. Recommendations include the use of fenders to decrease splashing and hoses at water stations to clean water bottles, gloves and faces. The race course should be surveyed to remove visible animal feces and racers educated on potential risks associated with accidental mud ingestion.

C2. Influenza I

Monday, March 17
1:15 PM – 2:45 PM
Centennial II

Influenza Testing Practices in the Emergency Department: Correlation with Laboratory-Confirmed Influenza Hospitalization Rates, Emerging Infections Program, 2006-2007 Influenza Season

M. Mueller[1], J. Baumbach[1], P. Daily Kirley[2], D. Aragon[3], K. Gershman[3], J. Palumbo[4], J. Meek[4], K. Openo[5], M. Farley[5], K. Martin[6], R. Lynfield[6], R. Bellflower[7], C. Long[7], N. Spina[8], M. Vandermeer[9], A. Thomas[9], B. Barnes[10], L. Kamimoto[11];

[1]New Mexico Department of Health, Santa Fe, NM, [2]California Emerging Infections Program, Oakland, CA, [3]Colorado Department of Health, Denver, CO, [4]Connecticut Emerging Infections Program, New Haven, CT, [5]Georgia Emerging Infections Program, Atlanta, GA, [6]Minnesota Department of Health, St. Paul, MN, [7]University of Rochester, Rochester, NY, [8]New York State Health Department, Albany, NY, [9]Oregon Public Health Division, Portland, OR, [10]Tennessee Emerging Infections Program, Nashville, TN, [11]Influenza Division, CDC, Atlanta, GA.

Background: The Emerging Infections Program (EIP) has performed active surveillance for pediatric lab-confirmed influenza (flu) hospitalization since 2003. Because the surveillance case definition requires a positive flu test, variation in emergency department (ED) testing practices might explain differences observed among state rates. In addition, the availability of a flu test result may affect the clinical management and treatment of influenza. **Methods**: ED providers working in EIP surveillance area hospitals during the 2006-07 flu season were surveyed in 9 states (CA, CO, CT, GA, MN, NM, NY, OR, TN). Age-adjusted flu hospitalization rates ranged from 3.7 to 23.1 per 100,000 persons <18 years. Web-based and mailed surveys were collected from May

to September 2007 and described the following: flu testing and antiviral prescription practices, practice variations throughout the flu season, and hospital testing and treatment policies. Correlation and Poisson regression analyses were performed to identify which factors most affect the state-specific rates of pediatric influenza hospitalization observed during the 2006-07 flu season. **Results**: A total of 1,055 (48%) ED providers responded. Providers were a mean of 11.4 years (median 9.0) since training, and 52% worked in community medical centers. The percentage of ED providers who reported they test for flu varied across states (range 54-100%, p<0.0001). The pediatric flu hospitalization rate was correlated with the percentage of providers who test for flu, the percentage who test in the beginning of the season, mean years since training, and whether results were available while a patient was still in the ED (p<0.05 for all). Poisson regression analyses show that increasing the testing rate by 10% could result in a 13.9% (95% C.I. 10.5-17.6%) increase in the flu hospitalization surveillance rate. Bivariate analysis showed a significant positive association between rate of testing and antiviral prescription rate (p<0.001). **Conclusions**: The variability of pediatric flu hospitalization rates among EIP sites is correlated with influenza testing practices among their ED providers. Increased influenza testing in the ED setting may provide more accurate surveillance estimates of the burden of influenza and also increase appropriate antiviral treatment.

The Burden of Human Influenza In East And Southeast Asia: A Review of The Scientific Literature

J. M. Simmerman[1], T. M. Uyeki[2];

[1]CDC/NCID/International Emerging Infection Program, APO AP, THAILAND, [2]CDC/NCID/VR, Atlanta, GA.

Background: While human infections with avian influenza A/H5N1 viruses have prompted concerns about an influenza pandemic, the burden of human influenza in East and Southeast Asia has received far less attention. An understanding of available scientific data is needed to guide future research and inform development of influenza control strategies. **Methods**: We searched English language articles on influenza in 18 countries in East and Southeast Asia indexed on PubMed and published from 1980 to 2006. Articles that described laboratory-confirmed human influenza among outpatients or hospitalized patients, influenza-associated deaths, or influenza-associated socioeconomic costs were reviewed. **Results**: The PubMed search criteria returned 1652 records for consideration. An analysis of titles and abstracts revealed 56 articles relevant to this analysis and 35 articles from 9 countries met the inclusion criteria. Significant heterogeneity was noted in case definitions, sampling schemes and laboratory methods. Early studies relied on tissue cell culture, reported problems with specimen handling practices, and a low burden of disease. The recent addition of PCR testing greatly increased the proportion of respiratory illness diagnosed with influenza. More recent studies reported that 11-26% of outpatient febrile illness and 6-14% of hospitalized pneumonia cases were laboratory confirmed influenza infections. **Conclusions**: The scientific literature on influenza disease burden from East and Southeast Asia is limited but expanding. Early studies likely underestimated the burden of disease due to limitations in study design and laboratory methods. Recent studies using improved laboratory testing methods and indirect statistical approaches report a substantial burden of disease similar to that of Europe and North America. Current increased international focus on influenza coupled with unprecedented new funding for surveillance and research, provide a unique opportunity to describe the burden of human influenza in the region and to utilize this knowledge to guide control programs.

A Comparison of Clinical and Epidemiological Characteristics of Human Infections with H5N1 versus Human Influenza Viruses in Thailand, 2004-2006

V. Shinde[1], D. Areechokechai[2], W. Hanshaoworakul[2], U. Narueponjirakul[2], W. Sanasuttipun[3], S. Kaewchana[3], A. Fry[1], K. Ungchusak[2], M. Simmerman[3];

[1]Centers for Disease Control and Prevention, Atlanta, Georgia, USA, Atlanta, GA, [2]Thailand Ministry of Public Health, Bureau of Epidemiology, Bangkok, THAILAND, [3]Thailand-US CDC Collaboration, Bangkok, THAILAND.

Background In response to an epizootic of avian influenza among poultry, Thailand initiated national surveillance for human H5N1 cases. Suspected cases included persons with influenza-like illness (or ILI: defined as fever *and* cough or sore throat) and any exposures to sick or dead poultry. Between January 2004 and December 2006, 11,641 suspected cases were tested for influenza viruses; 2076 (18%) cases of human influenza (H1N1, H3N1, and B) and 25 cases of H5N1 were detected. These data presented an opportunity to conduct the first direct clinical and epidemiologic comparison of human versus avian influenza virus infections in one surveillance population. **Methods** A retrospective chart review was conducted of all 25 hospitalized human H5N1 cases, all 22 fatal hospitalized human influenza cases, and a sample of 405 hospitalized, non-fatal human influenza cases from 29 provinces. We compared all H5N1 cases to all hospitalized human influenza cases. **Results** Similar proportions of H5N1 and human influenza cases presented with ILI (96% vs. 93%) and had at least one chronic condition (16% each). A higher proportion of H5N1 cases compared with human influenza cases consumed (28% vs. 3%, p<.001), directly touched (64% vs. 24%, p<.001), or had diseased poultry in the household (64% vs. 36%, p=.04). Fewer H5N1 cases (8%) compared to human influenza cases (25%) had no reported poultry exposures (p=.05). At presentation, higher proportions of H5N1 versus human influenza cases had dyspnea (61% vs. 20%, p<.001), vomiting (48% vs. 10%, p<.001), abdominal pain (16% vs. 2%, p<.001), and diarrhea (20% vs. 1%, p<.001). Among cases with chest X-rays, H5N1 cases were more likely to have radiographic evidence of pneumonia (60% vs. 35%, p=.02). H5N1 cases versus human influenza cases demonstrated higher mean serum AST and ALT (269 vs. 82 U/L and 131 vs. 36 U/L respectively, both p<.01). Among the entire surveillance population, 17 (68%) of 25 H5N1 cases and 22 (1%) of 2076 human influenza cases died. **Conclusions** Human H5N1 cases were more likely to have lower respiratory and gastrointestinal tract involvement and fatal illness compared with human influenza cases. More H5N1 cases had high risk poultry exposures compared with human influenza cases. These surveillance data may provide important guidance for refining H5N1 screening recommendations.

Comparison of Robust Regression Models for Estimating Influenza-Associated Deaths Using the CDC 122 Cities Mortality Reporting System Data

P. Cheng, W. Thompson, E. Weintraub, L. Brammer, L. Blanton, R. Dhara, J. Bresee, D. Shay;

CDC, Atlanta, GA.

Background: The Centers for Disease Control and Prevention (CDC) 122 Cities Mortality Reporting System (122 CMRS) currently provides the most timely data source for estimating influenza-associated deaths in the US. In this system, the percentage of all deaths due to pneumonia and influenza (P&I) are compared with a seasonal baseline calculated from previous respiratory seasons. A robust regression technique has been used to generate the baseline and threshold for decades. In this study, we compare results obtained from the current statistical model with results from

several different robust regression models using both the 122 Cities data and the National Centers for Health Statistics death data. We also compare the results with those obtained from a Serfling ordinary least squares regression model. **Methods**: Weekly numbers of P&I deaths and all-cause deaths from the 122 Cities data for the years 1972-2005 were extracted for data analysis. Three robust regression models (Andrews, Bi-square, and Huber weight functions) and a Serfling ordinary least squares regression model were used to estimate the influenza-associated deaths and the number of epidemic weeks. **Results**: For the Andrews model, an annual average of 1,383 (95% CI: 915 - 1,804) P&I deaths were associated with influenza from 1972/73 through the 2005/2006 seasons using the 122 CMRS. The average length of the influenza seasons was 9 weeks. The Bi-square and Huber weight function estimated slightly lower annual estimates and fewer epidemic weeks compared to the Andrews model. Similarly, the Serfling regression model estimated an annual average of 1,651 influenza-associated P&I deaths and an average of 6 epidemic weeks. Using the percentage of the standard error over the parameter estimates, the results indicated that the Andrews model was the best fitting robust regression model. Using these results to project national estimates, the Andrews model estimated an annual average of 3,763 P&I (1.54 P&I deaths per 100,000 person years) were associated with influenza. **Conclusions**: Robust regression techniques can be used to provide timely estimates of weekly number of P&I deaths associated with influenza. These methods are particularly useful for prospectively generating baselines to monitor both influenza epidemics and pandemics.

Emerging Trends In Adamantane Resistance: 2006-07 Influenza Season

V. M. Deyde, R. Garten, T. Sheu, A. Foust, A. Balish, J. Barnes, X. Xu, M. Shaw, A. Klimov, L. Gubareva;

Centers for Disease Control and Prevention, Atlanta, GA.

Background: Influenza A viruses are important human pathogens. Understanding the mechanisms behind the emergence and spread of drug resistance remains a challenging task. In 2003, over-usage of adamantanes may have contributed to emergence of resistance in Asia. Recent studies showed that gene reassortment within the H3N2 subtype could have facilitated the global dominance of adamantane resistant viruses in 2005-06 that belong to the 'N'-lineage (Simonsen et al., 2007). Here, we investigate the changes in genomes of H3N2 viruses resulting in a significant decrease in adamantane resistance among viruses circulating in some geographic regions in 2006-07. We also provide an update on resistance in H1N1 viruses. **Methods:** Influenza A viruses of H3N2 and H1N1 subtypes (n=2240) collected globally during 2006-07 season were tested for presence of markers of adamantane resistance using pyrosequencing. For phylogenetic analysis, the hemagglutinin (HA) and matrix (M) genes of 65 H3N2 and 100 H1N1 as well as the entire genomes of 20 representative H3N2 viruses were sequenced. **Results:** Resistance in H3N2 viruses (n=1348) remained high (72%), although, a significant reduction was observed in several countries compared to the previous season (2005-06). Phylogenetic and antigenic analyses indicate co-circulation of 4 distinct genotypes. Their HA, a major surface antigen, appear to have evolved from the HA of the drug resistant 'N'-lineage. Phylogenetic analysis of their internal genes provided evidence of reassortment. For instance, the resistant viruses from the 2006-07 season contained M and PB1 genes closely related to those of the 'N'-lineage. In contrast, the sensitive viruses contained M and PB1 from 2 distantly related groups of viruses circulating prior to the spread of the 'N'-lineage. Another trend was a rise in adamantane resistance to 100% in H1N1 viruses isolated in several Asian countries; while in the US, it remained relatively low (<6%). The phylogenetic analysis of HA and M of H1N1 viruses isolated in 2006-07 showed reassortment between the two major clades, 1 and 2. **Conclusions:** Resistance to adamantanes remains high among influenza H3N2 viruses and is rising in H1N1 viruses. Our results suggest that genome reassortment events play a prominent role in the evolution of drug resistance.

High Prevalence of Influenza in Hospital Surveillance in Bangladesh

R. Zaman[1], A. Alamgir[2], E. S. Gurley[1], M. Rahman[2], A. W. Brooks[1], T. Azim[1], J. Hossain[1], M. Rahman[1], S. P. Luby[1];

[1]ICDDR,B, Dhaka, BANGLADESH, [2]IEDCR, Dhaka, BANGLADESH.

Background: Bangladesh, the most densely populated large country in the world, has a large domestic poultry population that often lives in close proximity to humans. Since March 2007, 19 out of Bangladesh's 64 districts have reported outbreaks of H5N1 in poultry. We initiated hospital based human influenza surveillance to identify individuals and clusters of people presenting to hospitals with life threatening influenza virus infections and to characterize the diversity of influenza strains circulating in Bangladesh **Methods:** Surveillance began in April 2007 and gradually involved 6 government and 6 private hospitals across the country. Every morning surveillance physicians monitor patients and review medical records to identify clusters of patients, health care workers or poultry workers with severe acute respiratory illness. To characterize the diversity of circulating strains throat and nasal swab specimens are collected once monthly from hospitalized patients with severe acute respiratory illness and persons attending outpatient facilities with influenza-like illness. Swabs are analyzed at ICDDR,B virology laboratory using real time RT-PCR influenza assays. **Results:** Between Arpil and October 2007 specimens have been collected from 589 patients; of whom 237 (40%) had live poultry exposure in the preceding week. Out of 228 specimens tested thus far 81 (35 %) were influenza A or influenza B positive. Among the influenza positive samples, 43 (53%) were influenza A and 38 (47%) were influenza B. Hemagglutinin subtyping was performed on 36 influenza A positive samples; 21 (58%) were H1 and 15 (42%) were H3 subtypes. No clusters of severe acute respiratory illness have been identified. **Conclusions:** Patients presenting to Bangladeshi hospitals with respiratory symptoms commonly suffer from influenza infections; the strains of influenza virus circulating are diverse. Persons infected with influenza virus frequently have exposure to live poultry increasing the opportunity for reassortment. Bangladesh is a high risk setting for the emergence of new strains of influenza.

C3. Surveillance: International

Monday, March 17
1:15 PM – 2:45 PM
Centennial IV

Aetiology of Encephalitis in England: An On-going Multi-centre Prospective Study

J. Granerod[1], H. E. Ambrose[1], J. P. Clewley[1], A. Walsh[1], D. Morgan[1], R. Cunningham[2], M. Zuckerman[3], K. J. Mutton[4], D. W. Brown[1], N. S. Crowcroft[1], UK Aetiology of Encephalitis Study Group;

[1]Health Protection Agency, London, UNITED KINGDOM, [2]Derriford Hospital, Plymouth, UNITED KINGDOM, [3]King's College Hospital, London, UNITED KINGDOM, [4]Central Manchester and Manchester Childrens University Hospitals NHS Trust, London, UNITED KINGDOM.

Background Encephalitis is a devastating neurological illness. Yet, in England the cause remains unknown in 60% of cases. The combination of an increasing number of viruses known

to cause encephalitis in humans and the spread of West Nile virus across Europe, has given added impetus to establish the cause of encephalitis in more UK patients. **Methods** The Health Protection Agency, together with colleagues in the National Health Service, has embarked on a prospective cohort study of encephalitis. Patients are being recruited over a 2-year period from 24 hospitals located in the South West, North West and London areas of England. Samples collected as part of good clinical practice are being tested for an array of different organisms, beyond those screened routinely. Innovative pathogen discovery techniques are being developed and will be used on samples from patients where the aetiology remains unknown to assess the possibility of new and emerging infections. In parallel, research nurses are collecting extensive clinical information on presentation and outcome in the patients who participate. **Results** To date, 161 patients have consented to take part, including 86 (53%) males and 75 (47%) females. Sixty-seven percent are adults, 26% are children aged between one and 16 years, and 7% are infants below the age of one. Of the first 100 cases, the commonest confirmed agent of encephalitis is herpes simplex virus (30%). Other causes include varicella zoster virus, enteroviruses, *Mycoplasma pneumoniae*, human herpes virus 6, and post-infectious encephalitis. Thirty-five percent of cases remain of unknown aetiology. **Conclusions** The proportion of cases of unknown aetiology so far in our study (35%) is less than that previously described in England (60%), probably due to the systematic application of modern molecular diagnostics in a prospective study. The largest category however, remains that of unknown aetiology. It is possible that undetected, new or emerging infections may be contributing to these cases. The methods in development for pathogen discovery will help shed light on this, and will be applicable to other enigmatic and emerging infections.

Active Population-Based Surveillance for Emerging Infectious Diseases in Resource-Limited Settings: An Evaluation of Pneumonia Surveillance in Thailand

O. W. Morgan[1], D. Areechokchai[2], H. Baggett[3], S. Thamthitiwat[3], P. Prapasiri[4], S. Chunsutiwat[5], K. Ungchusak[2], R. Prasarnthong[2], S. Henchaichon[6], S. Naorat[7], A. Fleischauer[1], S. Olsen[1], S. Maloney[6];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Bureau of Epidemiology, Nonthaburi, THAILAND, [3]International Emerging Infections Program, Thai MOPH - US CDC Collaboration, Nonthaburi, THAILAND, [4]International Emerging Infections Program, Thai MOPH - US CDC Collaboration, Nakhon Phanom, THAILAND, [5]Department of Disease Control, Nonthaburi, THAILAND, [6]3. International Emerging Infections Program, Thai MOPH - US CDC Collaboration, Nonthaburi, THAILAND, [7]3. International Emerging Infections Program, Thai MOPH - US CDC Collaboration, Sa Kaeo, THAILAND.

Background Information regarding true incidence and etiology of pneumonia, the leading global cause of infectious disease mortality, is limited. We evaluated the performance of an active population-based surveillance system for pneumonia in Thailand, a resource-limited setting. **Methods** The surveillance system includes all 20 hospitals in Sa Kaeo and Nakhon Phanom provinces (population 1.2 million). Surveillance officers review admission records daily for any 60 diagnoses indicative of pneumonia and upload patient data to a central database. We calculated the positive predictive value (PPV) of the 60 admission diagnoses compared to a clinical pneumonia case definition (evidence of acute infection and respiratory symptoms). We also compared pneumonia incidence estimated from this system with the national reportable passive disease surveillance system. We conducted semi-structured interviews with key healthcare stakeholders to assess the system's complexity and acceptability. **Results** In 2006, 12,203 pneumonia patients were identified by the active surveillance system. 67% of patients with one of the 60 admission diagnoses met the clinical case definition for pnuemonia (PPV). Approximately 90% (n=11,026) of all pneumonia patients were identified through 17 admission diagnoses. Pneumonia incidence estimated from the active system was up to 6 times higher than the national passive surveillance system. Both surveillance systems identified peaks in March and July/August and the highest age-specific incidence among children under 5 years and adults over 60 years. Major strengths of the active system include the ability to estimate true pneumonia incidence, determine pneumonia etiology, and identify novel respiratory pathogens. The main limitations are the complexity of data collection, data management and analysis, and the operating cost (approximately $150,000 per province annually). **Conclusions** Active population-based surveillance can improve pneumonia incidence estimates. Although relatively complex and expensive, experience in Thailand suggests that investment in active surveillance systems provides crucial data, which can guide health policy, target programs, and measure the impact of interventions, such as vaccines, to prevent pneumonia in resource-limited countries.

Epidemiology and Incidence of Viral Severe Pneumonia in Population-based Surveillance Among Children Younger Than Five Years in Rural Western Kenya, 2006-2007

M. O. Ope[1], K. Njenga[2], G. O. Bigogo[3], P. O. Muluare[3], B. Aura[3], W. Rose[3], H. Burke[2], D. Erdman[4], R. F. Breiman[2], D. R. Feikin[2];

[1]field Epidemiology And Laboratory Training Program, Cdc, Kisumu, Kenya, [2]international Emerging Infections Program, Centers For Disease Control And Prevention, Atlanta, Ga, [3]centre For Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya, [4]division Of Viral Deseases, Centers For Disease Control And Prevention, Atlanta, Ga.

Background: Severe pneumonia remains a leading cause of morbidity and mortality in African children. The burden of viral etiologies of severe pneumonia is not well known since testing for viruses is not routinely done. **Methods**: As part of a population based enhanced passive surveillance for infectious diseases among 25,000 persons in rural Western Kenya, parents were encouraged to bring all sick children to a centrally-located referral clinic. Data were collected at sick child visits (SCVs) using a structured questionnaire. For children under 5 years meeting a WHO clinical definition of severe pneumonia, combined nasopharyngeal and oropharyngeal swabs were collected and tested for viruses associated with respiratory diseases using real-time reverse transcription polymerase chain reaction assays. Incidence rates were calculated using the midyear population of children less than 5 years in the surveillance area (N=3322). **Results**: From September 2006 - August 2007, 2,391 SCVs were made; 1,934 (81%) had cough or difficulty in breathing and 308 (13%) met the WHO severe pneumonia definition. The mean age was 26 months, and 29.3% were less than 1 year. The annual incidence of SCVs for severe pneumonia was 92.7 (95% CI 82.3-102.6) per 1000 children. Among the 308 severe pneumonia patients, 162 (53%) had swabs taken, of which 119 (73%) have been tested to date. The two leading viral pathogens detected were RSV (12.6%), and adenovirus (9.2%); others included parainfluenza 1 virus (1.7%) , parainfluenza 2 virus (0.8%), influenza B virus (0.9%) and human metapneumovirus (2.2% among the 45 swabs tested for this pathogen). Influenza A virus was not detected. RSV and adenovirus resulted in the greatest number of hospitalizations (85.7% and 33.3% hospitalized, respectively). No deaths occurred in hospital. The minimum incidence of SCVs with severe pneumonia due to RSV and adenovirus were 11.7 (95% CI 8.0-15.3) and 8.6 (95% CI 5.4-11.7) per 1000 children respectively. **Conclusions**: Children have high hospitalization rates due to severe pneumonia caused by RSV and adenovirus in rural western Kenya. Whether adenovirus is the causative agent of severe pneumonia in this

setting needs further clarification. Although RSV vaccine is still not available, its use has the potential of reducing morbidity in this setting.

Global Surveillance for Infectious Disease Deaths in Active Duty United States Military Personnel

R. N. Potter[1], L. M. Pearse[1], C. T. Mallak[1], J. C. Gaydos[2];

[1]Office of the Armed Forces Medical Examiner, Rockville, MD, [2]Global Emerging Infections Surveillance System, Silver Spring, MD.

Background: Deaths from infectious agents account for only a small number of all active duty deaths. However, these cases are important as they may signal an outbreak, an emerging infectious agent, or a biological attack. Consequently, a near real-time global mortality surveillance system that can detect infectious disease deaths is an important component of public health surveillance within the Department of Defense. **Methods:** The Mortality Surveillance Division (MSD) of the Armed Forces Medical Examiner System began tracking the medical cause of death in all military personnel worldwide in 1998. Prompt reporting of all deaths to our office allows us the opportunity to coordinate appropriate laboratory testing in most suspected infectious deaths. **Results:** From 1998 to September 30, 2007, there were 140 deaths due to a primary infectious disease. These accounted for 1.1% of the 13,187 active duty military deaths during that time frame. Of the 140 deaths, 44 (31%) were respiratory, 26 (19%) were due to myocarditis, 20 (14%) were due to meningitis/encephalitis and 18 (13%) were due to sepsis. Causative agents were identified in only 85 (61%) of the 140 deaths. Agents in the 85 deaths included: *S. aureus* (13%), *S. pneumoniae* (11%), Grp A Strep (11%), hepatitis C (9%), Neisseria species (8%) and adenovirus (7%). An agent was identified in 73% of the 37 pneumonia deaths, most commonly adenovirus, influenza, *S. pneumoniae*, and *S. aureus*. Agents were not identified in any cases of ARDS or myocarditis. As a result of this finding, pathologists in the Armed Forces Medical Examiner System now routinely save a section of frozen (non-formalin fixed) heart tissue for diagnostic evaluation. **Conclusions:** Because many military personnel die in non-military facilities, close relationships with civilian pathologists, hospitals and laboratories are vital. Key elements for successful surveillance for deaths from infectious diseases include: rapid notification of deaths, standardized protocols for testing and routine communication with pathologists. Specifically, pathologists need to know that there is a need for etiologic testing, the specimens that are required for optimal testing, and the laboratory and shipment information for processing.

International Circumpolar Surveillance Of Invasive Non-typeable *Haemophilus influenzae*, 2000-2006

T. Zulz[1], M. G. Bruce[1], T. Tam[2], D. Parks[1], A. J. Parkinson[1];

[1]Centers for Disease Control, Anchorage, AK, [2]Public Health Agency of Canada, Ottawa, ON, CANADA.

Background: The International Circumpolar Surveillance system conducts population-based surveillance of invasive bacterial diseases caused by *Haemophilus influenzae* (Hi) in Northern Canada (N Can) and in the U.S. Arctic (Alaska [AK]). **Methods:** We defined invasive Hi as an isolate from a normally sterile site drawn from a surveillance region resident. Isolates were forwarded to reference laboratories in AK and N Can for confirmation and serotyping. Serotyping was performed by slide agglutination except for cases in Quebec (QC) where polymerase chain reaction (PCR) was utilized. Isolates in AK were tested for antimicrobial resistance. Clinical and demographic information were collected on standardized surveillance forms. Data reported are for the years 2000 through 2006. **Results:** A total of 172 Hi cases were reported (AK=95, N Can=77). 167 isolates were serotyped; of those, 54 (32%) were non-typeable either by PCR [QC=8 of 12 (67%)] or slide agglutination [AK=34 of 91 (37%), rest of N Can=12 of 64 (19%)]. Isolates serotyped by PCR were more likely to be determined non-typeable than by slide agglutination (p=0.002). Age adjusted rates of invasive disease caused by non-typeable Hi (NT-Hi) were 1.1/100,000 (AK) and 4/100,000 (N Can). Case ages ranged from newborn to 80 years. Age distribution differed between countries; 65% of AK cases were > 40 years compared with 30% in N Can (p=0.02). In all ages, pneumonia was the most common clinical presentation [AK (41%) and N Can (45%)]. Of pneumonia cases, 50% in AK had chronic lung disease compared to 11% in N Can; all chronic lung disease occurred in adults > 35 years old. Seven fatal cases in AK occurred in two children less than 1 year old and five adults ranging 46-80 years old. The one fatality in N Can occurred in a 71 year old. There were no significant differences in case fatality ratios between AK and N Can when stratified by age. Isolates in AK were susceptible to ceftriaxone and chloramphenicol (100%), cotrimoxazole (82%) and ampicillin (79%). **Conclusions:** The variability in proportions of NT-Hi from areas using different typing methods should be further evaluated. Cases are more likely to occur in older persons in AK and young children in N. Can; age distribution differences warrant further study. Chronic lung disease is commonly associated with cases presenting with pneumonia in AK.

Forecast and Outbreak of Rift valley fever in Sudan, 2007

A. Anyamba[1], J. Chretien[2], J. Small[1], C. J. Tucker[1], P. Formenty[3], J. Richardson[4], K. Earhart[5], E. Pak[1], S. C. Britch[6], D. C. Schnabel[7], R. L. Erickson[2], K. J. Linthicum[6];

[1]NASA Goddard Space Flight Center, Greenbelt, MD, [2]Department of Defense Global Emerging Infections Surveillance & Response System,, Division of Preventive Medicine, Walter Reed Army, MD, [3]World Health Organization, Department of Epidemic and Pandemic Alert and Resp, SWITZERLAND, [4]U.S. Army Medical Research Unit –Kenya, Department of Entomology & Vector-borne Disease, KENYA, [5]U.S. Naval Medical Research, Unit 3, EGYPT, [6]USDA-ARS, Center for Medical, Agricultural, & Veterinary Ent, FL, [7]U.S. Army Medical Research Unit –Kenya, Nairobi, KENYA.

Background: Rift Valley fever (RVF) outbreaks occur during heavy rainfall in various sub-Saharan countries including Kenya, Somalia, and Tanzania and more recently in Saudi Arabia and Yemen. Given the wide geographic and ecological range of RVF virus, it is necessary to monitor large areas for conditions that may trigger the emergence of mosquito vectors that could spread RVF. **Methods:**The Department of Defense Global Emerging Infections System (DoD-GEIS) coordinates epidemiologic surveillance and epidemic response through a global network of laboratories and public health professionals. In Africa/Middle East, DoD-GEIS, with NASA, also uses satellite indicators (normalized difference vegetation index [NDVI], outgoing longwave radiation [OLR], rainfall, others) to provide early warning of RVF activity. Monthly continental-scale maps flag high-risk areas. The DoD-GEIS hubs in Egypt (NAMRU-3) and Kenya (USAMRU-K) transmit RVF alerts through regional networks. **Results**:Satellite monitoring (June-September 2007) showed focal positive NDVI anomalies and negative OLR anomalies over most of central Sudan suggested unusually heavy rainfall, and generated RVF risk warnings for central and southern Sudan in July-Septemner. In late October, RVF outbreaks were reported by WHO in humans in Sudan in White Nile, Sinnar, and Gezira states, and by early November 2007, 329 human cases, including 96 deaths were reported. The cases being reported in Gazeera State are in an area close to irrigation canals and are linked to naturally occurring cycles involving livestock and mosquitoes which are abundant in the irrigation zone. **Conclusions:**Validated RVF forecast models may provide early warning (~3 months) for RVF epidemics in Africa. Model performance, integrated with

epidemiologic and environmental surveillance systems, should be assessed systematically for RVF and other mosquito-borne diseases using historical epidemiologic and satellite data.

C4. Zoonotic & Animal Diseases I

Monday, March 17
1:15 PM – 2:45 PM
Centennial III

Investigating Disease Emergence from Wildlife - a Transdisciplinary Approach

H. E. Field;

Biosecurity Queensland, BRISBANE, AUSTRALIA.

Background: Nearly 75% of all emerging infectious diseases that impact or threaten human health are zoonotic. The majority have spilled from wildlife reservoirs, either directly to humans or via domestic animals. The emergence of many can be attributed to predisposing factors such as global travel, trade, agricultural expansion, deforestation/habitat fragmentation, and urbanization; such factors increase the interface and/or the rate of contact between human, domestic animal, and wildlife populations, thereby creating increased opportunities for spillover events to occur. **Methods:** Disease emergence can be regarded as primarily an ecological process, with emergence precipitated by a change in the ecology of the host or the agent or both. The epidemiologic investigation of emerging diseases associated with wildlife requires a comprehensive transdisciplinary approach that includes an understanding of the ecology of the wildlife species, and an understanding of human behaviors that increase risk of exposure. Nipah virus and SARS emergence provide good case studies. **Results:** The emergence of Nipah virus was (in part) associated with the encroachment of commercial pig farms into forested areas. Once the virus spilled from its natural bat host into the immunologically naïve pigs, high pig and farm densities facilitated the rapid dissemination of the infection locally. The movement of pigs for sale and slaughter in turn led to the rapid spread of infection to southern peninsular Malaysia, where the high-density, largely urban pig populations facilitated transmission to humans. Identifying the factors associated with the emergence of SARS in southern China in 2003 requires an understanding of the ecology of infection both in the natural reservoir and in secondary market reservoir species. A necessary extension of understanding the ecology of the reservoir is an understanding of the trade, and of the social and cultural context of wildlife consumption. **Conclusions:** Meeting the challenges and complexities of understanding and managing the risk of emergence of infectious diseases from wildlife requires skills from a range of disciplines (both 'hard' and 'soft' sciences) working collaboratively towards a common goal.

Anticipating the Next Monkeypox: Trends in Rodent Importation, 1999-2006

B. Schroeder[1], J. McQuiston[1], R. Marquis[2], G. Galland[1], N. Marano[1];

[1]Division of Global Migration and Quarantine, Centers for Disease Control and Prevention, Atlanta, GA, [2]Office of Law Enforcement, U.S. Fish and Wildlife Service, Arlington, VA.

Background: Rodents are becoming increasingly popular as pets for families. Rodents, commercially bred or trapped in the wild, may be infected with a number of zoonotic infections, including *Salmonella*, lymphocytic choriomeningitis virus (LCMV), Machupo virus hemorrhagic fevers, murine typhus, tularemia, and plague. A 2003 outbreak of monkeypox resulting in 71 human infections was traced to a shipment of wild-caught African rodents imported to the US. This outbreak led to a June 2003 ban on importing rodents of African origin. The objective of this study was to assess the effect of the African rodent ban on overall rodent imports. **Methods:** We queried the Fish and Wildlife Service's Law Enforcement Management Information System (LEMIS) for imports from 1999 to 2006 whose species code fell under the Order Rodentia. The common names, uses, and historical region of origin were identified for each listed species. **Results:** According to LEMIS data, the total number of rodents imported increased from 53,068 before the ban (1999-2003) to 171,421 after the ban (2004-2006). However, the number of rodent species being imported decreased from 77 (1999-2003) to 53 (2004-2006). The species that showed the greatest decline in imports since the ban were of African origin: fat-tailed gerbils (from 703 to 0), striped grass mice (from 508 to 0), and African dormice (from 510 to 0). The species that showed a large increase in the number imported since the ban included Mongolian jirds (from 0 to 1500) and dwarf hamsters (from 18,581 to 120,346), both of which are of Asian origin but currently bred throughout the world. An increase was also observed in chinchilla imports (from 8708 to 21,641), which are of South American origin. **Conclusions:** The 2003 importation ban on African rodents was effective in reducing the number of African rodent species coming to the US; however, the observed 200% increase in the overall number of rodents being imported to the US after the ban suggests a replacement for the market that African rodents once supplied. Rodents may also be reservoirs for emerging diseases not currently recognized, or introduce foreign animal diseases into the United States. Because the risks to public health are high, regulatory changes should be considered to better manage the health threats posed by imported rodents.

Risk Factors for Brucellosis in Siziwang County, Inner Mongolia, China,2007

Y. Wenwu[1], D. Fengman[2], S. Hui[1], F. Mengguang[3], C. Buyun[1], P. Dongri[1], L. Qun[1], F. Zijian[1];

[1]China CDC, Beijing, CHINA, [2]CFETP, Beijing, CHINA, [3]Inner Mengulia CDC, Huhehot, CHINA.

Background: Brucellosis has reemerged since 1992 in China,epicially in Inner Mongolia of China. To identify risk factors for brucellosis, we conducted a case-control study in Siziwang County of Inner Mongolia with high prevalence in August,2007. **Method:** We defined brucerllosis case as fever, fatigue, sweats, myalgia, arthralgia, headaches, and serum tested positive (SAT 1:100 or above) in a resident during August 1 2006 to August 1 2007. The control persons were randomly selected from the same family or neighbors, with no symptom and negative serum tested. We interviewed them with questionnaire on exposures to livestock and its products. We compared exposures between 86 brucellosis cases to 385 controls with univariate analysis. Signicance risks were identified with forward stepwise selection for logistic regression. **Results:** Multivariate analysis indicated that brucellosis was associated with exposure to aborted livestock (OR = 2.4; 95% CI= 1.3--4.4). OR increased from 2.1 (95%CI=1.1-3.7) in 1-6 exposure group to 9.3 (95%CI=2.2--39) in more than 6 exposure group. **Conclusions:** Contacting aborted livestock with no personal protective measure is high risk factor for brucellosis. Veterinary services should eliminate sick livestok. We recommended that gloves should be weared when dealing with abortion.

A Fatal Case of Inhalation Anthrax in Scotland associated with West African Goat Skin Drums

C. Ramsay;

Health Protection Scotland, Glasgow, UNITED KINGDOM.

Background: A 50 year old male, living in rural Scotland, died from a sudden short duration septicaemic illness. Blood culture

later confirmed growth of *Bacillus antharcis*. Cutaneous or inhalation exposure routes were considered possible. An investigation was mounted to clarify the route of infection and identify possible sources. He was a woodworker and musical instrument maker and was also involved in animal rescue work, gardening and other country pursuits. Social activities included drumming. Uncertainties regarding the timeline for the potential incubation period and initial exposure route to anthrax lead to the use of chemoprophylaxis on a precautionary basis. **Methods:** Review of the clinical and autopsy findings was undertaken by colleagues in the UK Health Protection Agency and the US CDC. Specialist immunohistochemistry analysis was carried out on PM tissue samples. Investigation of potential sources included sampling at the case home residence, workplace, vehicles and locations where West African drums were used or stored were. Sample analysis was carried out at the Novel and Dangerous Pathogens Laboratory (NADP), Porton Down, UK. **Results:** Inhalation Anthrax was confirmed by CDC finding evidence of *Bacillus anthracis* antigens in lung tissue. No anthrax contamination was found at the home, workshops or vehicles used by the case. Anthrax spores were identified from imported Djembe drums used at events attended by the case and one unused goat skin hide, intended for use as a drum head. Spores were identified from three locations where Djembe drums had been used or stored prior to the case's illness. **Conclusions:** On the balance of probabilities, the source of infection was concluded to be inhalation of *Bacillus anthracis* spores liberated from anthrax contaminated goat skin used on West African Djembe drums at a venue in rural Scotland. All sites in Scotland where contamination with spores was confirmed were subsequently successfully decontaminated using gaseous Chlorine Dioxide, with US specialist assistance. Contaminated drums were decontaminated by the HPA NADP, UK using formaldehyde. Drums and goat skins imported from West Africa pose a potential infection hazard to drummers and others working with them. This is the fourth documented case worldwide of anthrax infection associated with this source.

Oral Rabies Vaccination: Implications for Zoonosis Prevention, Control and Elimination

D. Slate[1], C. E. Rupprecht[2], R. B. Chipman[3], D. Donovan[4], E. Oertli[5];

[1]USDA, APHIS, Wildlife Services, Concord, NH, [2]Centers for Disease Control and Prevention, Atlanta, GA, [3]USDA, APHIS, Wildlife Services, Castleton, NY, [4]Ontario Ministry of Natural Resources, Peterborough, ON, CANADA, [5]Department of State Health Services, Austin, TX.

Background: Oral rabies vaccination (ORV) has been used to eliminate rabies in red foxes in several Western European countries. In North America, it has been applied toward elimination of red fox rabies in southern Ontario and to eliminate canine rabies in coyotes from south Texas, leading to the declaration of canine rabies free status in the U.S. Attaining elimination of rabies in additional carnivore reservoirs in the U.S., such as the raccoon, should facilitate a comprehensive focus on bat rabies control issues, the greatest challenge facing pubic health. We discuss the successes and challenges in rabies control in carnivores and development of a North American Rabies Management Plan to enhance international collaboration to better achieve goals. **Methods:** ORV is an adjunct to conventional rabies prevention and control, independently or integrated with methods such as trap-vaccinate-release. Public health surveillance has been complemented with enhanced, real-time systems to improve ORV decisions. ORV campaigns have also been tiered to natural and human-made features to enhance "barriers." Evaluation is based on serologic and biomarker indices, and the distribution of rabies variant-specific cases relative to ORV zones. **Results:** In 2000, elimination of canine rabies in coyotes in Texas from a high of 166 cases in 1994 reinforces that ORV may be used effectively to target specific reservoirs. Progress has also been made in containing rabies in gray foxes in Texas and raccoons in the eastern U.S. Post-ORV seroconversion (mean 30±11%) and the frequency of contingency actions to support established ORV zones targeting raccoon rabies point to the need for a better understanding of: the timing, pattern and density for baiting; habitat preferences of raccoons and nontarget competitors for baits; the potential for translocations; and the contribution of natural and human-made features to the ORV "barrier effect." Field performance of the available oral vaccine and baits underscore the need for improvements, while exploration and development of effective new vaccines and baits continues. **Conclusions:** ORV shows potential for eliminating specific variants of rabies in carnivore reservoirs in the U.S. Achieving rabies management goals will hinge on collaborative efforts with our North American partners.

C5. Methicillin Resistant Staphylococcal Infections

Monday, March 17
1:15 PM – 2:45 PM
Regency VI

Trends in Invasive Infection with Methicillin-resistant *Staphylococcus aureus* (MRSA) in Connecticut, 2001-2006

S. Petit[1], Z. Fraser[1], M. Mandour[2], J. L. Hadler[1];

[1]Connecticut Department of Public Health, Hartford, CT, [2]Connecticut Department of Public Health Laboratory, Hartford, CT.

Background. In 2007, CDC published an article that described the epidemiology of invasive MRSA infections in 2004-05 in 9 sentinel sites, including Connecticut (CT). The CT system has been in place since 2001 and provides an opportunity to examine trends in the 3 major groupings of MRSA by place of onset and relationship to healthcare: hospital-onset (HO) vs. community-onset but healthcare- associated (HA) or community-associated (CA) MRSA. **Methods.** Cases identified from laboratory reporting of MRSA isolates from normally sterile body sites were classified after medical record review as HO (isolate >2 days after hospital admission), HA (hospital admission, surgery, dialysis, or long-term care facility stay in the past year, a history of MRSA, or an indwelling device); or CA (by exclusion). A systematic sample of blood isolates were typed by pulsed-field gel electrophoresis (PFGE). **Results.** In 2001-2006, 5464 cases of invasive MRSA were reported; 34.5% HO, 58.9% HA and 6.6% CA. Annual incidence overall (26.2 per 100,000) and of HA-MRSA (15.4) was stable. However, incidence of HO-MRSA decreased (10.0 to 7.6) while CA incidence increased (1.1 to 2.8, $p<0.01$ for each trend). By site, blood isolates were most common for HA-MRSA (92%), followed by HO (88%) and CA (81%, $p<0.01$ vs HA and vs HO). By contrast, joint isolates were most common for CA (14%) and less common for HA (5%) and HO (2%, $p<0.01$ for CA vs HA and CA vs HO). CA cases were younger compared to HO and to HA cases (54 vs. 65 and 69 years, $p<0.01$ for each) and were more likely to be susceptible to clindamycin, fluoroquinolones, and erythromycin ($p<0.01$ for each). Characterization of isolates by PFGE indicated that 4% of 89 HA and 2% of 48 HO isolates were community related PFGE types (USA 300, 400 or 1000). By contrast, 24% of 17 CA isolates were these types ($p=0.02$). **Conclusions.** Two MRSA problems with different epidemiology are occurring in CT. Incidence of HO-MRSA has decreased overall while CA incidence is increasing. Persons with CA-MRSA differ from their HO and HA counterparts by having

younger age and a higher percentage of joint infections. Continued surveillance of MRSA infections by setting is needed to monitor trends and evaluate ongoing efforts to identify the most effective HO prevention strategies. Identification and implementation of CA prevention strategies is needed.

Short-term Mortality Associated With Methicillin-Resistant and Methicillin-Susceptible *Staphylococcus aureus* Infections Among Veterans Administration Medical Center (VAMC) Patients

C. Lexau[1], C. Lees[1], R. Lynfield[1], J. Nyman[2], G. A. Filice[3];

[1]Minnesota Department of Health, St. Paul, MN, [2]University of Minnesota, Minneapolis, MN, [3]Veterans Affairs Medical Center, Minneapolis, MN.

Background: Healthcare-associated *Staphylococcus aureus* (SA) infections are a major cause of infectious disease morbidity. Among VAMC patients with infections caused by methicillin-resistant (MR) or methicillin-susceptible (MS) SA, we assessed whether death from any cause and death due to SA infection were independently associated with methicillin resistance. **Methods**: Minneapolis VAMC patients with SA infections identified from January 2004 to June 2006 were enrolled in a study of costs associated with methicillin resistance. Clinical and healthcare utilization data were collected for each patient for the 6 month period after onset of the SA infection. The Charlson Index (CH-IND), which quantifies number and severity of co-morbidities, was calculated for each patient. **Results**: Of 725 patients, 335 had an initial infection caused by MRSA, and 390 by MSSA. Patients in the group with MRSA infections were older than those with MSSA infections (median 67 vs. 63 years, P =.049, Wilcoxon) and had greater CH-IND scores (median 4 vs. 3, P <.0001, Wilcoxon). More patients with MRSA infections than with MSSA infections had ≥ 1 hospitalization (80%, [268/335] vs. 63% [245/390], P <.0001) and had ≥ 2 infections (33%, [110/335]) vs. 23% [88/390], P =.002) respectively. There were twice as many deaths during the 6-month follow up period among patients with MRSA infection (24%, 79/335) as among patients with MSSA infection (12% 45/390, OR 2.4, 95% CI 1.6-3.5, P < .0001). After adjustment for age and CH-IND, this difference remained significant (OR 1.9, 95% CI 1.2-2.9, P =.005). There was clinical evidence that SA infection caused or clearly contributed to death in 28% (35/124) of all deaths; 7% (25/335) among those with MRSA infection and 3% (10/390) among those with MSSA infection. After adjustment for age, those with MRSA infection were almost 3 times more likely than those with MSSA infection to die of SA disease (OR 2.8, 95% CI 1.3-6.0, P =.007). **Conclusions**: In this patient population, methicillin resistance was associated with a greater risk of death attributable to SA disease and to death from any cause. MRSA infections were more common among those with chronic illnesses. Optimal methods of prevention and treatment of healthcare-associated SA, particularly MRSA infections, are urgently needed.

Transmission of Methicillin-Resistant *Staphylococcus intermedius* between Animals and Humans

E. van Duijkeren[1], D. Houwers[1], A. Schoormans[1], M. Broekhuizen-Stins[1], R. Ikawaty[2], A. Fluit[2], J. Wagenaar[1];

[1]Faculty of Veterinary Medicine, Utrecht University, Utrecht, THE NETHERLANDS, [2]Department of Medical Microbiology, University Medical Center Utrecht, Utrecht, THE NETHERLANDS.

Background *Staphylococcus intermedius* is a commensal and a pathogen in dogs and cats, but is rarely isolated from humans. However, *S. intermedius* in humans has been associated with dog bite wounds, bacteraemia, pneumonia and ear infections. In the Netherlands, the prevalence of canine and feline infections with methicillin-resistant *S. intermedius* (MRSI) is increasing and therefore also the risk of their zoonotic transmission. **Methods** At Utrecht University MRSI were cultured from infected surgical wounds of five dogs and one cat which had undergone surgery at the same veterinary clinic (clinic A). Samples were taken from the nose of the surgeon, from six technicians and from the nose and coat of two healthy dogs living at the clinic in order to identify the source. In addition, 22 environmental samples were taken from several sites at the clinic. *S. intermedius* was identified in these samples using standard techniques. Antimicrobial susceptibilities were determined by an agar diffusion method. The *mec*A gene was detected by PCR. The isolates were genotyped by PFGE using *Sma*I as restriction enzyme. Four epidemiologically unrelated MRSI isolates from patients at other veterinary clinics were also included. **Results** MRSI was cultured from the nose of the surgeon, three technicians, one healthy dog and four environmental samples. The isolates were resistant against ampicillin, amoxicillin with clavulanic acid, cephalexin, ceftiofur, ceftazidime, enrofloxacin, gentamicin, kanamycin, chloramphenicol, lincomycin, clindamycin, tetracycline and trimethoprim/sulphamethoxazole and susceptible to fusidic acid and rifampicin. This was the same resistance pattern as the initial isolates from the six patients. All isolates were *mecA* positive by PCR. The PFGE profiles from the MRSI isolates from clinic A were all indistinguishable and differed from the profiles of the isolates from other clinics. **Conclusions** Together, these data suggest transmission of MRSI between animals and humans. To our knowledge, this is the first report on the transmission of MRSI between humans and animals. People working at veterinary clinics should be aware of this risk for their own and their patients' sake.

Community-Associated (CA) Methicillin-Resistant *Staphylococcus aureus* (MRSA) in Affected Households: Prevalence of Colonization and Incidence of Subsequent Infections

J. M. Buck[1], R. Gorwitz[2], R. Lynfield[1], K. Harriman[3];

[1]Minnesota Department of Health, Saint Paul, MN, [2]Centers for Disease Control and Prevention, Atlanta, GA, [3]California Department of Public Health, Richmond, CA.

Background: MRSA has emerged as a community pathogen over the last decade. Several reports indicate that CA-MRSA infections can occur among multiple household members (HHMs). We describe MRSA colonization prevalence and subsequent infection incidence among children with CA-MRSA infections and their HHMs. **Methods**: MRSA infections in children <18 years-of-age lacking healthcare MRSA risk factors were identified through sentinel surveillance at 12 Minnesota hospitals from May 1, 2005 through April 2006. Three home visits to enrolled households (HHs) were conducted over a one-year period to collect nasal swabs and information on possible MRSA transmission risk factors and subsequent MRSA infections from case-patients (CPs) and HHMs. *S. aureus* isolates were screened for oxacillin resistance. **Results**: 119 HHs were enrolled during the study period. 67% (80) of HHs composed of 335 study participants (80 CPs and 255 HHMs) completed all three home visits. 15% (12), 11% (9), and 6% (5) of CPs and 8% (20), 6% (15) and 8% (19) of HHMs were colonized at the 1st, 2nd, and 3rd home visits, respectively. 28% (22), 20% (16) and 23% (18) of HHs had at least one HHM colonized during the 1st, 2nd, and 3rd home visits, respectively. One CP and 3 HHMs remained colonized during all three home visits. Participants sharing soap ($p = 0.03$), towels ($p < 0.001$) or balms/ointment/lotion ($p < 0.001$) with colonized HHMs at the 1st visit were more likely to be colonized with MRSA at the 2nd visit. Participants reporting use of antibacterial hand soaps at the 1st visit were less likely to be colonized at the

2nd visit (p = 0.03). 31% (25) of HHs (16 CPs and 16 HHMs) reported subsequent MRSA infections. Participants who reported use of mupirocin (at least BID x 5 days) were not less likely to be colonized with or have subsequent infections due to MRSA after use (p > 0.05). **Conclusions**: The prevalence of MRSA colonization in affected HHs did not decrease during the study period; over 20% of HHs had at least one colonized HHM one year after initial CP infection. Use of mupirocin did not appear to affect long term MRSA colonization or infection in HHs. Behavior modifications (e.g. not sharing personal items) may be more important in reducing MRSA transmission. Additional strategies to prevent CA-MRSA infection and transmission in HHs should be evaluated.

Detection of Community Acquired Methicillin Resistant *Staphylococcus aureus* Associated with Nosocomial Infections

S. M. Tallent, D. M. Toney;

Virginia Division of Consolidated Laboratory Services, Richmond, VA.

Background: *Staphylococcus aureus* is a human commensal that has emerged as a significant pathogen due to the production of a variety of virulence factors and acquisition of numerous antimicrobial resistant genes. Methicillin resistant *S. aureus* (MRSA) is an antimicrobial resistant strain traditionally associated with hospital infections, but is now increasingly associated with illness in typically healthy individuals outside healthcare facilities. Pulsed-field gel electrophoresis (PFGE) genotyping of staphylococcal isolates by the CDC categorized MRSA strains into two groups, community-acquired methicillin resistant *S. aureus* (CA-MRSA) and hospital-acquired methicillin resistant *S. aureus* (HA-MRSA). The two groups clustered into ten lineages which were designated as pulsetypes USA100-USA1100. More recently, distinctions between HA-MRSA and CA-MRSA have become less apparent, presumably due to recombination events giving rise to new MRSA strains that differ from the USA pulsetypes. **Methods**: *S. aureus* isolates from previous hospital and community outbreaks occurring in Virginia as early as 1997 were subjected to PFGE genotyping, generating a DNA fingerprint database at the Division of Consolidated Laboratory Services (DCLS), the Virginia state laboratory. Archived isolates from 2005-2007 (N=258) were compared to the prototype USA fingerprint patterns and classified based on pattern similarities. Clusters of isolates possessing ≥80% similarity to the USA pulsetypes were further evaluated. **Results**: Forty percent of the 258 MRSA isolates examined clustered with USA100, the most common HA-MRSA pulsetype. Of these strains, 23% were associated with community outbreaks not hospital infections based on epidemiologic investigations. In contrast, 22% of the 258 isolates clustered with USA300, the most common CA-MRSA pulsetype. Of these, 88% were previously determined to be associated with nosocomial infections. **Conclusions**: This study has identified a subset of MRSA strains designated as outliers based on PFGE pulsetype patterns and epidemiology. Additional molecular characterization is ongoing to understand these findings, determine if this is a representative trend in Virginia and whether the most invasive form of MRSA has become endemic to Virginia's healthcare facilities.

C6. Vectorborne Diseases

Monday, March 17
1:15 PM – 2:45 PM
Regency VII

Long-term Clinical Sequelae and Rates of Recovery Following Infection with West Nile Virus

K. O. Murray, M. Sierra, M. Resnick, V. Miller;

The University of Texas Health Science Center at Houston, Houston, TX.

Background: West Nile virus (WNV) is an important emerging pathogen, with the long-term clinical outcomes continuing to be defined. **Methods:** Following the introduction of WNV to Houston in 2002, we began enrolling clinical cases identified through surveillance into a longitudinal prospective study. In this study, 108 patients were evaluated every 6-months for up to 5 years to determine the subjective and objective clinical outcomes and rates of recovery following WNV infection. **Results:** Of the 108 patients, 54 (50%) presented with encephalitis, 32 (30%) with meningitis, and 22 (20%) with uncomplicated fever. Persistent symptoms from WNV were reported by 60.1%, 46.4%, 40.6%, 38.9%, and 41.9% at 1, 2, 3, 4, and 5 years post-onset, respectively. Most commonly reported symptoms include fatigue, weakness, depression, personality changes, difficulty walking, and memory deficits. Survival analysis showed a significant difference in rates of recovery between those presenting with encephalitis when compared to meningitis and fever cases. The majority of those who reported full recovery resolved their symptoms in the first year following infection. Objective measurements revealed significant differences in both the cognitive functioning and physical functioning between encephalitis patients and those who presented with meningitis or fever. At the one-year follow-up, new onset depression was reported by 31% of cases, with 75% having CES-D scores indicative of mild to severe depression. Among a subset of 50 patients with neurological exams, the diagnosis of WNV encephalitis was significantly associated with an abnormal neurological examination when compared to the diagnosis of WNV meningitis, even after adjusting for age. WNV encephalitis patients had numerous neurological abnormalities, particularly muscle weakness and gait impairment. **Conclusions:** WNV infection can result in significant long-term clinical sequelae and cognitive and functional impairment, particularly in those who present with encephalitis. This study provides us with a better understanding of the clinical aspects of a virus that is likely to continue to be an important global emerging pathogen.

The Changing Epidemiology of Malaria in Brazil: National Surveillance Data and Environmental Correlates, 1990-2006

A. F. Santelli[1], J. Sobel[2], E. V. Rossetto[1], J. L. Ladislau[3];

[1]Malaria National Control Program, Secretariat of Surveillance in Health, Ministry of Health, and Field Epidemiology Training Program, SVS, Brazilian Ministry of Health, Brasilia, BRAZIL, [2]Office of Global Health, CDC, Atlanta, GA, [3]Malaria National Control Program, Secretariat of Surveillance in Health, Ministry of Health, Brasilia, BRAZIL.

Background: Brazil reports more malaria cases than all other countries in the Americas combined. We present the first comprehensive review of national malaria surveillance data, 1990 to 2006, and correlate regional rates with environmental data. **Methods**: Descriptive study using data from the Malaria National Surveillance System, national health information systems, and the Brazilian Institute of Geography and Statistics. **Results**: Between 1990 and 2006, smear-confirmed malaria cases remained stable at

about 550.000/year but incidence declined from 32/1,000 to 23/1,000. Malaria deaths diminish by 93%, from 664 to 64 cases/year, and hospitalizations declined by 67%, from 28,456/yr to 9,470/year. *Plasmodium falciparum* caused 45% of cases in 1990 and 26% in 2006. The burden of malaria increased in the western Amazon region during this period; municipalities with higher incidence coincided with areas covered by rain forest (Acre, Amazonas, Amapá and Rondônia states) and with specific locations where the government subsidized fish-farming in open water tanks. Incidence dropped in savanna-dominated regions of southern Brazil while agriculture and cattle ranching extended (Maranhao, Mato Grosso and Tocantins states). In 2006, 2.4 million persons (10% of the Amazon region population) resided in municipalities with incidence ≥50 /1,000 inhabitants; some had incidence as higher as 1500/1,000. About 86% of case-patients reside in rural areas: 12% in newly settled areas, 6% in indigenous areas and 2% in mining areas. Peripheral zones of two major metropolitan areas presented high malaria incidence coincident with 50% increase population. In 2006 among municipalities reporting ≥100 cases, 52 (6%) had an increase of more ≥30% in malaria case compared with 2005. **Conclusions**: In Brazil, national malaria incidence has decreased since 1990, but specific areas in the Amazon region have experienced intensified transmission, correlating with ecological changes and urbanization. Consistent surveillance of confirmed cases allows identification and monitoring of high-incidence areas, outbreak detection and application of control measures. Massive population shifts and ecological changes are underway in Brazil's endemic Amazon region.

Pneumonic Plague Mortality and Transmission Potential in the United States

A. F. Hinckley, K. S. Griffith, P. S. Mead;

Centers for Disease Control and Prevention, Fort Collins, CO.

Background: *Yersinia pestis* (YP), the cause of plague, has been designated a Category A bioterrorism agent based in part on its potential for airborne, human-to-human transmission. To help guide rational distribution of antibiotic prophylaxis following an intentional release of YP, we developed a model to quantify the transmission potential of pneumonic plague in the U.S. population using historical data. **Methods:** We reviewed data for all primary pneumonic plague cases reported in the U.S. from 1900 through 2007. We evaluated the transmission potential of pneumonic plague in the pre-antibiotic era (<1944) by calculating the average number of secondary cases per primary case (R_0). To obtain the R_0 estimate, we fitted probability density functions to our data by maximizing the log-likelihood function for probability and frequency of individual transmission events. **Results:** A total of 60 primary pneumonic cases were reported before the introduction of antibiotics in 1944. Of these, at least 85% were due to human-to-human transmission, and 92% were fatal, with an average time from symptom onset to death of 4 days (range 2 to 14). From 1944 to 2007, 14 primary pneumonic cases were reported. Of these, 100% were due to animal or laboratory exposures and 36% were fatal; average time from symptom onset to death was 8 days (range 2 to 27). Among those who received antibiotics within 2 days of illness onset, 89% survived; after 2 days only 25% survived. For 15 cases where data were available, the average time from onset to diagnosis was 4.7 days (range 0 to 14). Using pre-antibiotic era data to estimate transmission potential, the negative binomial distribution gave the best fit model with an estimated R_0 of 0.77 and variance of 7.6. **Conclusions:** Previous transmission models of pneumonic plague have relied on data from large outbreaks occurring abroad. These models do not account for individual occurrences of primary pneumonic plague or standards of care in the US. Our findings suggest that the risk of human-to-human transmission of pneumonic plague is far lower than previously assumed, even in the absence of any antimicrobial prophylaxis. Current plans for utilization of the Strategic National Stockpile may benefit from reevaluation in light of these new findings.

Molecular and Epidemiologic Analysis of *Francisella Tularensis* Subsp. *Tularensis* AI And AII in Humans and Animals

K. J. Kugeler, J. M. Petersen, J. E. Staples, K. A. Kubota, L. Chalcraft, A. M. Janusz, P. S. Mead;

Centers for Disease Control and Prevention, Fort Collins, CO.

Background: Two subspecies of *Francisella tularensis* cause human tularemia, *F. tularensis* subsp. *tularensis* (type A) and *F. tularensis* subsp. *holarctica* (type B). Molecular subtyping studies have further divided type A isolates into two distinct subgroups, AI and AII, which correlate with differences in geography and illness outcome. To further define epidemiologic differences between and within the AI and AII subgroups, we evaluated a large sample of type A isolates from humans and animals. **Methods:** Type A isolates from humans (n = 205) and animals (n = 96) submitted to or cultured at CDC between 1964 and 2005 were analyzed. Pulsed-field gel electrophoresis (PFGE) with *Pme*I was performed on all isolates, and patterns compared in the BioNumerics software program. Statistical analyses were performed using SAS. Multivariable logistic regression was performed using all variables significant at $p<0.05$ with univariate analyses. **Results:** PFGE pattern analysis divided all 301 type A isolates into two subgroups, AI and AII. Among human infections where illness outcome was known, case fatality rates differed between those caused by AI (14/108; 13%) and AII (0/53; 0%)($p<0.01$). PFGE analysis of AI isolates identified two additional clusters, AIa and AIb. Case fatality rates differed for human infections caused by AIa (2/55; 4%) and AIb (12/48; 25%)($p<0.003$). 67% of AIb strains were recovered from blood, lung or cerebrospinal fluid, as compared to 44% of A1a strains ($p<0.02$). Logistic regression modeling of risk factors for fatality among humans with AI infections revealed that infection caused by AIb strains and isolation of the organism from an invasive site are important contributors to fatality. **Conclusions:** Our analysis confirms previously reported differences between AI and AII isolates and reveals additional clusters among AI isolates, AIa and AIb, which correlate with differences in invasiveness and mortality in humans. AI infections are associated with higher human mortality when compared to AII infections, with only a subset of AI isolates (AIb) accounting for most fatal infections. Further studies are needed to identify molecular or ecologic differences which may account for mortality differences among infections caused by AII, AIa and AIb.

Clinical Features of *Zika* Virus Infection During an Outbreak on Yap Island, Federated States of Micronesia, 2007

T. Chen[1], M. Duffy[2], W. T. Hancock[3], J. Kool[4], M. Pretrick[5], M. Bel[3], S. Holzbauer[1], C. Dubray[1], E. Hayes[2], M. Fischer[2];

[1]Epidemic Intelligence Service Field Assignments Branch, Centers for Disease Control and Prevention, Atlanta, GA, [2]Arboviral Diseases Branch, Centers for Disease Control and Prevention, Fort Collins, CO, [3]Wa'ab Community Health Center, Yap State Department of Health Services, Colonia, MICRONESIA (FEDERATED STATES OF), [4]Western Pacific Regional Office, World Health Organization, Suva, FIJI, [5]FSM Department of Health, Education and Social Services, Palikir, MICRONESIA (FEDERATED STATES OF).

Background: Zika virus (ZIKV) is a mosquitoborne flavivirus. Serologic evidence of human ZIKV infection has been documented in Africa and Asia. Fewer than 20 patients with symptomatic disease caused by ZIKV have been reported in the literature, including a case series of seven febrile hospitalized patients from Indonesia in 1977-1978. We describe the clinical features of symptomatic ZIKV infections that occurred during an outbreak on the island of Yap. **Methods:** We performed surveillance during March 1-July 31, 2007 at all five medical facilities on Yap, including one hospital and four

outpatient clinics. A case was defined as a Yap resident or visitor with a clinically compatible illness and laboratory evidence of recent ZIKV infection. A clinically compatible illness was defined as acute onset of (1) generalized macular or papular rash, (2) arthritis or arthralgia, or (3) nonpurulent conjunctivitis. We interviewed patients by using a standardized questionnaire. Variables collected included patient demographics, clinical signs and symptoms, duration and severity of illness, and outcome. **Results:** Clinical information was obtained for 31 (72%) of the 43 patients identified with laboratory-confirmed ZIKV infection. Of these 31 patients, 19 (61%) were female. The median age was 33 years (range: 2-58 years), and 23 (74%) were aged ≥18 years. The most common clinical symptoms reported included rash (90%), arthritis/arthralgia (61%), and conjunctivitis (61%); 25 (81%) patients had two or more of these findings. Other symptoms reported included myalgias (42%), headache (39%), retro-orbital pain (32%), edema (26%), and vomiting (10%). Of the 20 (65%) reporting subjective fever, 12 patients had temperature documented and none had fever ≥100.4°F. Median duration of rash and arthralgia was 5.0 days (range: 2-14 days) and 3.5 days (range: 1-14 days), respectively. No associated hospitalizations, hemorrhagic manifestations or deaths were reported. **Conclusions:** During this outbreak, symptomatic ZIKV illness was acute, self-limited, and primarily reported among adults. Rash, conjunctivitis, and arthralgia were the most common clinical findings. None of the Yap patients was hospitalized, and fever was often absent or low-grade.

Japanese Encephalitis in Bangladesh

M. Hossain[1], E. S. Gurley[1], S. Montgomery[2], L. Petersen[2], J. Sejvar[3], M. Fisher[2], L. Davis[2], N. Nahar[4], A. Uddin[4], M. Rahman[5], A. Ekram[6], S. P. Luby[1], R. F. Breiman[1];

[1]ICDDR,B, Dhaka, BANGLADESH, [2]CDC, Ft. Collins, CO, [3]CDC, Atlanta, GA, [4]Dhaka Medical College Hospital, Dhaka, BANGLADESH, [5]Mymensingh and Sylhet Medical College Hospitals, Mymensingh and Sylhet, BANGLADESH, [6]Rajshahi Medical College Hospital, Rajshahi, BANGLADESH.

Background: Following the detection of Japanese Encephalitis (JE) in Bangladesh during an outbreak in 1977 it has not been reported there since, although it is routinely reported in bordering countries. We conducted a study to characterize the etiology of encephalitis in four tertiary government hospitals in Bangladesh from June 2003-July 2005. This report describes our findings on JE. **Methods:** Every fourth patient with fever, evidence of acute brain pathology, and indication for lumbar puncture was eligible for enrollment. Patient information and sera were collected at recruitment and 4-6 weeks after discharge for surviving patients. Acute- and convalescent-phase sera were tested for JE virus - specific IgM and IgG antibody at CDC. Patients with IgM antibodies in acute serum or CSF (collected during acute-phase only) OR ≥4 fold rise in JE neutralizing antibodies from acute to convalescent sera were classified as probable JE cases and patients with both characteristics were defined as confirmed JE. **Results:** Five hundred forty six patients were enrolled and tested for JE; 23 (4%) patients had evidence of JE-- 10 were confirmed and 13 were probable cases. Two (9%) patients with evidence of JE died. Probable or confirmed cases were identified from all age groups_3 (13%) were <5 years old, 6 (26%) were 5-10 years old, 3 (13%) were 11-17 years old and 11 (48%) were >17 years old. No cases were identified between January to April and 87% occurred between May and October. Most of the cases were identified from the northwestern part of Bangladesh. Patients with JE presented with altered consciousness (96%) (most with loss of consciousness), convulsion (87%), and stiff neck (48%). Six patients had prolonged sequelae including focal weakness, paresis and paralysis. Nineteen patients were seen 4-6 weeks after discharge and at that time 8 (42%) were experiencing cognitive difficulties (thinking/reasoning). **Conclusions:** Our findings suggest that JE is an important cause of encephalitis in Bangladesh, especially in the north. Population-based studies to quantify the burden of disease would be useful to assess the appropriateness of a vaccine program for prevention.

D1. Foodborne and Waterborne Diseases II

Monday, March 17
3:00 PM – 4:30 PM
Centennial I

Prognosis of Salmonellosis and Brucellosis: One Year Follow-up of a Population-based Surveillance in Fayoum Governorate, Egypt

S. A. Afifi, Sr.[1], F. G. Yousef, Sr.[1], M. Saeed, Sr.[2], E. Kilbane, IV[1], R. Hajjeh, Sr.[3];

[1]US Naval Medical Research Unit #3, Cairo, EGYPT, [2]Egyptian Ministry of Health and Population, Cairo, EGYPT, [3]Centers for Disease Control and Prevention, Atlanta, GA.

Background: Brucellosis and salmonellosis are the most commonly reported causes of acute febrile illness in Egypt. More than 70% of patients seek care in primary health facilities, where laboratory diagnosis is unavailable. Little is known about prognosis of both diseases. We studied the clinical outcome of the laboratory diagnosed cases of brucellosis and salmonellosis in Fayoum, Egypt. **Methods**: Cases were identified during population-based surveillance in Fayoum, Egypt, 2003. Salmonellosis cases were confirmed by positive blood culture, and brucellosis cases were confirmed by positive blood culture or tube agglutination, titer ≥ 1: 160. Patients' households were visited 12 months after diagnosis. Either the patient or a family member was interviewed using a standardized questionnaire to assess complications, relapses, treatment and disease outcome. Treatment received was compared to recommended WHO treatment for brucellosis (doxacillin, streptomycin, rifampin, trimithprim sulpha (TMX), ciprofloxacin) and for salmonellosis (amoxicillin, TMX, choramphenicol, ceftriaxone, ciprofloxacin). Data were compared using chi^2 and t-test. **Results**: A total of 141 (76%) of brucellosis cases and 144 (87%) of salmonellosis cases were interviewed. Median age of brucellosis cases was 30 years (range 6-70), 65% were males, relapse rate (RR) was 12% and complication rate (CR) was 33%. Median age of salmonellosis cases was 11 years (range 3-54), 53% were males, RR was 5% and CR 10%. Case-fatality rates in both groups were 1.4%. Among salmonellosis cases, RR and CR were significantly lower (3/116 vs 4/28, 11/116 vs 7/28, $p<0.05$) in patients treated with WHO recommended antibiotics than those who were not. Among brucellosis cases, RR was lower in cases treated with the WHO regimen than in cases receiving other treatment (12/121 vs 5/21, p=0.05). **Conclusions**: High RRs and CRs occurred in laboratory confirmed cases of brucellosis and salmonellosis. Patients treated with WHO recommended antibiotics had a significantly better outcome. Laboratory confirmation should be used to direct clinicians to use WHO recommended treatment and improve patient outcomes.

Analysis of *Listeria* Case Report Forms Among Non-Pregnant Cases: FoodNet Sites, 2004-2006

S. M. Hurd[1], R. Marcus[1], S. Zansky[2], M. Soeters[1], D. Vugia[3], S. Cosgrove[4], M. Tobin-D'Angelo[5], C. Medus[6], P. McCarthy[7], K. Jackson[8], M. Iwamoto[8], E. Scallan[9];

[1]Connecticut Emerging Infections Program, Yale University, New Haven, CT, [2]New York State Department of Health, Albany, NY, [3]California Department of Health Services, Berkeley, CA, [4]Colorado Department of Public Health and

Environment, Denver, CO, [5]Georgia Department of Health, Atlanta, GA, [6]Minnesota Department of Health, St. Paul, MN, [7]FDA, Center for Food Safety and Applied Nutrition, College Park, MD, [8]National Surveillance Team/Enteric Diseases Epidemiology Branch, CDC, Atlanta, GA, [9]Enteric Diseases Epidemiology Branch, CDC, Atlanta, GA.

Background Listeriosis, caused by *Listeria monocytogenes* (LM), is a rare bacterial infection that affects primarily pregnant women, the elderly, and the immunocompromised. Listeriosis has a high case fatality rate and is generally acquired through consumption of contaminated food. In 2003, the Council for State and Territorial Epidemiologists (CSTE - position statement ID-01) and CDC recommended prompt interviewing of all patients with culture-confirmed listeriosis using a standardized *Listeria* Case Report Form (CRF) to facilitate investigation of LM outbreaks. We describe the case-patient data collected from non-pregnant cases in FoodNet (FN) sites from 2004-2006. **Methods** FN conducts active laboratory surveillance for foodborne pathogens, including LM, in 10 states (15% of the US population). LM cases interviewed with the CRF were entered into a central database at CDC. Demographic characteristics, illness severity, and food consumption patterns were analyzed. Cases associated with pregnancy were excluded from this analysis. **Results** Nationally, approximately 19% (447/2375) of all listeriosis cases reported to CDC from 2004-2006 had a CRF completed and submitted; 72% (321/447) were from FN catchment. Overall CRF submission within FN was 82% (321/393). Of the 282 (88%) non-pregnancy associated cases, 52% were male. The median age was 67 years. The most common clinical manifestations were fever (76%), chills (54%), headache (41%), and diarrhea (41%). Eighty-two percent of cases had septicemia/bacteremia; 89% were hospitalized and 13% died. Analysis of food history data indicated that case-patients reportedly "ate or likely ate" the following high-risk food items in the month before their illness: hot dogs (40%), turkey deli meat (38%), and Mexican-style soft cheese (10%). **Conclusions** Listeriosis is a serious life threatening illness among non-pregnancy associated cases, the majority of whom are elderly and immunocompromised. Case patients continue to consume a variety of common foods known to be associated with LM contamination. Continued educational efforts, often directed at pregnant women, should also be directed toward those who treat and interact with the elderly and immunocompromised. Use and completeness of the standardized questionnaire should be evaluated.

The Impact of Sodium Dichloroisocyanurate Treatment on Household Drinking Water Quality and Health in Peri-Urban Ghana: a Randomized Placebo-Controlled, Double-Blinded trial

E. M. Blanton[1], S. Jain[1], O. K. Sahanoon[2], A. Schmitz[1], T. S. Imoro[2], M. Hoekstra[1], R. E. Quick[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]New Energy, Tamale, GHANA.

Background: Diarrhea causes 1.8 million deaths a year. Consumption of fecally contaminated drinking water is an important contributor to diarrheal diseases. Sodium dichloroisocyanurate (NaDCC), a proven water treatment chemical, has been used in tablet form in emergencies for years and was recently approved for daily household use. The impact of daily NaDCC water treatment on health has not been established. **Methods**: We conducted a randomized, placebo-controlled, double-blinded trial to determine the health impact of NaDCC tablets in Tamale, Ghana from August to November 2006. We conducted a baseline survey, distributed water treatment or placebo tablets and 20-liter safe water storage containers with taps to all study households, and initiated twice weekly active diarrhea surveillance home visits over a 12-week period. We tested stored water for residual chlorine at each visit and analyzed 20% of water samples for *E. coli* using Colilert®. **Results**: We enrolled 240 households with 3,240 individuals (median 12 persons; range 2-42). Median age of individuals was 18 years (range 1 month-95 years); 1,647 (51%) were female and 682 (21%) were children ≤5 years old. Intervention household residents had 1.27 diarrhea episodes per person-year of observation compared to 1.13 episodes per person-year among control household residents (P=0.7). Detectable free chlorine residuals were found in stored water samples from 88% of intervention and 10% of control households; 93% of households used tap water. At baseline, *E. coli* contamination was found in stored water in 96% of intervention households and 88% of control households (P=0.24) with median *E. coli* counts of 88 per 100ml (range 0-173,290) and 22 per 100ml (range 0, 24,196), respectively. At the end of the study, *E. coli* contamination was found in stored water samples in 8% of intervention households and 50% of control households (P=0.003); the median *E. coli* count of contaminated control water samples was 8 (range 1, 54). **Conclusions**: Diarrhea incidence rates were very low and similar between intervention and control groups. Stored water quality improved in both study groups. In the control group, safe storage containers may have helped protect water quality and reduced waterborne disease risk. Further research is needed to determine the health impact of NaDCC tablets.

Foodborne Disease Outbreaks Associated with Leafy Greens, 1973-2006

K. M. Herman, T. L. Ayers, M. Lynch;

Centers for Disease Control and Prevention, Atlanta, GA.

Background: Several recent large outbreaks have been associated with leafy green foods in the United States, such as *Escherichia coli* O157:H7 infections due to spinach; however, the characteristics of all reported outbreaks due to leafy greens have not been described. The Centers for Disease Control and Prevention conducts surveillance for foodborne disease outbreaks (FBDO) investigated by local and state health departments in the United States. **Methods**: We reviewed data from the FBDO surveillance system for 1973-2006. A leafy green-associated FBDO is defined as two or more illnesses due to the consumption of a single leafy green food item (lettuce, cabbage, mesclun mix, spinach) or a salad item containing one or more leafy greens. These data were compared with U.S. leafy greens per capita availability, a proxy for leafy green consumption. **Results**: Among 10,421 FBDO reported during 1973-2006, 502 (4.8%) outbreaks, 18,242 (6.5%) illnesses, and 15 (4.0%) deaths were associated with leafy greens. Among leafy green-associated FBDO with a confirmed etiology, Norovirus was responsible for 196 (58.3%) outbreaks, followed by *Salmonella*, 35 (10.4%) outbreaks, and *Escherichia coli* O157:H7, 30 (8.9%). The median size of leafy green-associated outbreaks (18 illnesses) was twice the median size of non-leafy green-associated outbreaks (9). During 1986-1995, U.S. leafy green consumption increased 17.2% from the previous decade. During the same period, the proportion of all FBDO due to leafy greens increased 59.6%. Likewise, during 1996-2005 leafy green consumption increased 9.0% and leafy green-associated outbreaks increased 38.6%. In 296 (69.4%) outbreaks, leafy greens were served at a restaurant; 11 (2.2%) involved cases in multiple states. **Conclusions**: Leafy greens are an important cause of FBDO and may transmit pathogens with human or animal reservoirs. The proportion of FBDO due to leafy greens has increased, and cannot be accounted for completely by an increase in leafy green consumption. Contaminated leafy greens may cause restaurant-associated or widespread outbreaks. Efforts by local, state, and federal agencies to control leafy green outbreaks should span from the point of harvest to the point of preparation

Eight Years of National Botulism Surveillance in Brazil: What We Know Now

G. Carmo[1], R. S. Alves[2], C. P. Dimech[1];

[1]EPISUS/COVEH, Secretariat of Health Surveillance, Ministry of Health, Brasilia, BRAZIL, [2]COVEH, Secretariat of Health Surveillance, Ministry of Health, Brasilia, BRAZIL.

Background: Botulism entails potentially fatal flaccid paralysis by action of toxins of *Clostridium botulinum*. Foodborne botulism is due to consumption to toxin-contaminated food. A case was defined as detection of botulinum toxin in clinical samples or food consumed by a person with compatible illness, or compatible illness in a person epidemiologically linked to a laboratory-confirmed case. An outbreak was defined as one or more epidemiologically linked cases. National surveillance for botulism in Brazil was initiated in 1999. **Methods:** We reviewed botulism data reported to the National Foodborne Diseases Surveillance System of the Brazilian Ministry of Health from 1999 to 2006. **Results:** During the study period, a total of 32 outbreaks of foodborne botulism were reported. Patients' median age was 21 years (range: 6 - 76 years); the case-fatality rate was 31% (10/33). The median number of cases per outbreak was 1 (range 1-4 cases). The cases occurred in the following States: São Paulo (8 cases), Bahia (5), Ceará (4), Mato Grosso (4); Goiás (4), Minas Gerais (3), Rio Grande do Sul (2); Rio Grande do Norte (1) and Pernambuco (1). The foods types associated with 32 foodborne botulism outbreaks were: pork products, 15 (47%); canned palm hearts, 13%; chicken pie, 4 (13%); tofu 4 (13%), and unknown, 5 (16%). In 27 outbreaks for which data was available, foods were homemade in 18 (67%), industrially produced in 5 (19%), and bakery-produced in 4 (15%). Of the 15 outbreaks caused by foods of swine origin, 80% were related to "tinned meat," a home preparation method involving frying meet and storing it under fat; 13% were caused by pork liver patê that was either homemade or industrially produced; and 7% by industrialized cured salami. Laboratory confirmation was obtained in 27 (84%) of reported outbreaks. Of these, type A toxin caused 21 (78%) and type B caused 3 (11%) of outbreaks; toxin type was not identified in three outbreaks. **Conclusions:** Most outbreaks and cases of botulism in Brazil are caused by contaminated home-canned foods, especially "tinned meat." Botulism mortality may be lowered by improved diagnosis and timely antitoxin administration. Educational efforts should be directed at populations known to consume the highest risk foods.

Prevalence of Noroviruses in Hospitalized Kenyan Children: Comparison of Realtime RT-PCR and Enyme-linked Immunoassays.

M. A. Widdowson[1], N. Gregoricus[1], C. O'Reilly[1], V. Omballa[2], J. Tate[1], C. Bopp[1], B. Ochieng[3], D. Feikin[2], K. Njenga[2], R. Breiman[2], E. Mintz[1], J. Vinje[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Centers for Disease Control and Prevention, Nairobi, KENYA, [3]KEMRI/Centers for Disease Control and Prevention, Kisumu, KENYA.

Background: Noroviruses (NoVs) are the most common cause of infectious diarrhea in developed countries. Very few data exist in developing countries, where most diarrhea deaths occur, largely because of lack of simple diagnostic assays. Even when rotavirus testing and bacterial culture are available, an etiology is not identified in most diarrheal episodes.. We investigated the prevalence of norovirus among hospitalized children in western Kenya and compared realtime reverse-transcription-polymerase chain reaction (rRT-PCR) with a simple commercial enzyme immunoassay (EIA). **Methods**: From 31 June 2005 to 1 July 2006, we enrolled 571 children under five years of age hospitalized with diarrhea (≥3 stools in 24 hours) at two district hospitals. We collected whole stool and administered a questionnaire for demographic and clinical data. Stools were tested for *Salmonella spp*, *Shigella* spp and *Campylobacter* spp by standard culture methods, rotavirus by EIA (Rotaclone™) and norovirus by both rRT-PCR with primers for GI and GII genogroups and by EIA (IDEIA™). **Results**: Noroviruses were detected by rRT-PCR in 47 (8%) of 571 stools. Of these, 10 were positive for GI strains, 35 for GII and 2 for both GI and GII. Rotaviruses and bacteria were also detected in 5 (11%) and 10 (21%) NoV positive stools respectively. Norovirus symptoms included bloody stools [2/47 (4%], vomiting [25/47 (53%)] and fever [22/47 (47%)]. The median duration of illness before hospitalization was 5 days (range 1-7 days). Intravenous rehydration was administered in 64%. By EIA, 24/571 (4%) stools were positive for norovirus, of which only 8 were also positive by rRT-PCR (6 GII, 1 GI and one mixed GI+GII), for a sensitivity of EIA versus rRT-PCR of 17% (8/47) and a specificity of 97% (508/524). **Conclusions**: Noroviruses may be an important cause of severe childhood diarrhea in rural Kenya, but further studies are needed to test stools from control subjects and to understand the potential contribution of norovirus infection to diarrrheal mortality. Based on our results, this EIA assay needs further development before reliable use to detect norovirus in sporadic cases of diarrhea.

D2. Influenza II

Monday, March 17
3:00 PM – 4:30 PM
Centennial II

Swine Influenza in a Child with Remote Exposure, Iowa, 2006

D. L. Dufficy;

Centers for Disease Control and Prevention, Des Moines, IA.

Background: The Centers for Disease Control and Prevention (CDC) recieves approximately one report of human swine influenza every 2 years; the majority of cases are associated with discrete swine exposure. Person-to-person transmission of swine influenza rarely occurs and was last reported in 1988. In November 2006, a female aged 4 years was hospitalized and tested positive for influenza. Iowa's public health laboratory identified the virus as a non-human influenza A virus. CDC characterized the virus as a triple reassortant swine influenza (H1N1). An investigation was conducted to determine the mode of transmission. **Methods:** Immediate family members and seven community contacts were interviewed. Active hospital laboratory surveillance was initiated. Environmental investigations of the patient's home, preschool, child care center, grandparents' home, great-grandparents' swine farm, and mother's meat-processing plant workplace were conducted. Serum samples were collected from eight family members and from a convenience sample (10/240) of the great-grandparents' unvaccinated swine. Antibodies to swine influenza were determined by using hemagglutination inhibition (HI) assay. **Results:** Influenza-like-illness (ILI) was present in at least one of the great-grandparents' swine in September. The grandfather experienced ILI 10 days after a farm visit in early September, and the grandmother had ILI 9 days after a farm visit in late September. The patient's cousin experienced ILI 7 days after contact with the grandmother, and the patient had ILI 6 days after contact with her cousin. No other family members were ill. Sera from 10 swine tested positive by HI for IgG antibodies to a 2001 swine influenza H1N1 strain and to the patient's swine influenza virus. HI testing of human sera was inconclusive. Enhanced surveillance did not reveal additional cases. **Conclusions:** Since no direct swine contact occurred, the source of swine influenza infection for this patient may have been from an ill relative or an environmental source. Given the dynamic nature

of influenza viruses through both shift and drift, all cases of novel influenza A infection should be thoroughly investigated for early identification of sources for infection and to assess the risk of human to human transmission and the virus's pandemic potential.

Pandemic Influenza in the Australian Army of World War I

G. D. Shanks[1], A. MacKenzie[2], R. Mclaughlin[2], M. Waller[2], J. F. Brundage[3];

[1]Army Malaria Institute, Enoggera, AUSTRALIA, [2]Centre for Military and Veteran's Health, University of Queensland, Brisbane, AUSTRALIA, [3]Army Medical Surveillance Activity, Silver Spring, MD.

Background: Improved understanding of the epidemiology of the 1918-19 influenza pandemic could provide useful insights into a future worst-case pandemic scenario. **Methods:** Prospectively collected demographic and disease information from the medical / administrative records of Australian Army soldiers of 1914-19 were entered into a database using cause of death as reported by medical officers at the time. **Findings:** Influenza / pneumonia mortality during Oct 1918 - Mar 1919 in nearly identical infantry units ranged from 0 to 48/1000. Overall, the median time from illness onset to death was 7 days. Hospitalization for respiratory illness in May-Jun 1918 substantially protected soldiers (OR=0.44, 95% CI 0.32-0.61, p<.001) against death due to influenza/pneumonia during Oct 1918-Mar 1919; in contrast, hospitalization for respiratory illness (including "purulent bronchitis") during the epidemic of Nov 1916-May 1917 was not protective (OR=1.00, 95% CI 0.73-1.37, p=0.98). There was no relationship between an infantry battalion's (n=60) influenza/pneumonia mortality during 1916-17 and its subsequent mortality during 1918-19. **Interpretation:** During the influenza pandemic of 1918-19, the heterogeneity of mortality across comparable military units and the relatively long times from illness onset to death suggest significant roles for secondary bacterial infections. Respiratory infection early in 1918 protected soldiers from mortality during the main influenza pandemic suggesting that the May-Jul 1918 wave of the pandemic created cross-immunity to H_1N_1. That such cross-protection was not seen during the "purulent bronchitis" epidemic of 1916-17 could either indicate that the earlier epidemic was caused by another pathogen or that infection with a poorly-transmitted highly-lethal influenza virus caused few oligo-symptomatic infections.

Pandemic Influenza Policy Model, a Web-Based Tool for Military Planners

B. H. Feighner[1], J. P. Chretien[2], J. C. Gaydos[2], S. P. Murphy[1], J. F. Skora[1], M. J. Mabee[3], M. L. Sikes[1], J. S. Coberly[1], S. L. Lewis[1], J. S. Lombardo[1];

[1]Johns Hopkins University Applied Physics Laboratory, Laurel, MD, [2]DOD Global Emerging Infections System, Silver Spring, MD, [3]Fort Leonard Wood MEDDAC, Ft. Leonard Wood, MO.

Background: A pandemic involving a novel respiratory pathogen is a significant, credible threat not only to the health of our nation, but also to the operational effectiveness of the military forces defending our nation. Computer disease simulations allow planners to evaluate the effects of public health interventions in a quantifiable and reproducible manner, with all assumptions open to discussion. We believe the mission-oriented nature and the structured social composition of military installations may result in public health intervention strategies that differ from those appropriate for civilian populations; indeed, the strategies may differ significantly between military installations. **Methods:** The Pandemic Influenza Policy Model (PIPM) is a web-based, user-configurable, installation-specific, quick-response model created by DOD-GEIS, JHU/APL, and Fort Leonard Wood, MO public health officials. The PIPM allows military planners to evaluate the effect of various intervention strategies in the face of a respiratory pandemic. The structure of the PIPM is that of two independent, yet interrelated, components. First, a dynamic social network simulates the population's daily interactions relevant to disease transmission. A disease model then estimates individual disease progression and disease propagation through the community using a Susceptible-Infected-Recovered model. Public health interventions in the PIPM are divided into three basic types, 1) those which decrease opportunities for disease transmission, 2) those which decrease efficiency of disease transmission, and 3) those which decrease the severity of disease given infection. **Results:** The PIPM is operational for Fort Leonard Wood, MO. Innovations in the PIPM include expanding on the mathematics of prior stochastic models using social network epidemiology, a user-friendly graphical user interface, utilization of DOD personnel data bases to more accurately characterize the population at risk, and the incorporation of possible interventions, e.g., pneumococcal vaccine, not examined in previous models. **Conclusions:** The PIPM is a web-based pandemic influenza modeling system for military planners. Further work is underway to extend the PIPM to additional military installations.

Case Report: Dual Infection of *H5N1 Avian Influenza* and *H3N2 Human Influenza* in Jakarta Indonesia, April 2007

V. Setiawaty;

Center for Biomedical and Pharmaceutical R&D, Jakarta, INDONESIA.

Background: Human influenza A viruses are transmitted year round in Indonesia with a higher frequency detected among patients with influenza-like illness during the rainy season. In 2005, the Ministry of Health established a referral system for patients with avian Influenza A virus (H5N1) infection and identified 113 patients with laboratory-confirmed disease between 2005 and 2007. We are reporting a case-report of a patient with simultaneous infection with avian (H5N1) and human influenza A (H3N2) virus infection. **Methods:**In April 2007, a 16 year old female patient was hospitalized with respiratory illness at a referral hospital in Jakarta. A case investigation form was used to collect clinical and epidemiologic data and clinical samples were collected for hematological profile and as well as acute and convalescent antibody titers for H1, H3, and H5 antigen using HAI assays. Throat & nasal swab specimens were collected on the 6th day of onset, when she visited NIHRD laboratory and tested with real-time and gel-based RT-PCR for H1, H3 and H5 at NIHRD-MOH. Patient was hospitalized after results showed H5N1 positive infection. Specimens were sent to the Eijkman Institute for confirmation of PCR results and genetic sequence analysis. **Results:** The patient presented with moderate symptoms of fever > 38°C, sore throat, cough, rhinitis, headache and myalgia, but no dyspnoea. The leucocytes counts were 4,700-5,800 cells/mm^3, lymphocyte 31 - 44.7%. no thrombocytopenia, X ray and CT scan of thorax showed no pneumonia. PCR results were positive from throat and nasal swabs for influenza A/H3N2 and H5N1 by real-time and gel based RT-PCR. These results were confirmed by repeat testing at Eijkman. HAI antibody titers were negative for H3N2 and 1:10 for H5N1 from sera that was collected 6 days after onset of illness. HAI antibody titers from convalescence sera were 1:640 for H3N2 and negative for H5N1. **Conclusions:** This is the first case-report of a human with both influenza A/H5N1 and H3N2 co-infection. Such infections are of great concern due to the possibility of genetic reassortment leading to the emergence of a H5N1 strain that is more easily transmitted human to human and emphasizes the importance of advanced laboratory-based surveillance in geographic regions where both human and avian influenza viruses are co-circulating.

Pilot Findings of a Cluster Randomized Trial of Non-Pharmaceutical Interventions for Influenza Prevention in Households in Hong Kong

B. J. Cowling[1], K. Y. Cheng[1], R. O. Fung[1], V. Fang[1], C. L. Lam[1], L. M. Ho[1], K. H. Chan[1], W. H. Seto[1], R. Yung[2], T. M. Uyeki[3], P. M. Houck[4], J. S. Peiris[1], G. M. Leung[1];

[1]The University of Hong Kong, Hong Kong, HONG KONG, [2]Centre for Health Protection, Hong Kong, HONG KONG, [3]Influenza Division, CDC, Atlanta, GA, [4]Division of Global Migration and Quarantine, National Center for Preparedness, Detection and Control of Infectious Diseases, CDC, Seattle, WA.

Background: There are sparse data on the efficacy of non-pharmacological interventions for prevention of influenza virus transmission. We implemented a pilot study of the feasibility and efficacy of masks and hand hygiene to reduce transmission in Hong Kong households (February to September 2007) as part of a larger community trial planned for 2008. **Methods**: We conducted a cluster randomized controlled trial of households (composed of at least 3 members) where an index subject presented with influenza-like-illness of <48-hour duration. After confirmation as influenza by the QuickVue Influenza A+B rapid test, the household was randomized to 1) control group or 2) surgical masks or 3) hand hygiene. Households were visited within 36 hours, and again 3, 6 and 9 days later. Nose and throat swabs were collected from index subjects and household contacts at each home visit and tested by viral culture. The primary outcome measure was laboratory confirmed influenza in a household contact; secondary outcome was clinical influenza (by self-reported symptoms). **Results**: We randomized 198 households and completed follow up home visits in 128 households. There were 23 household contacts with laboratory confirmed influenza and 41 with clinical influenza, corresponding to secondary attack ratios of 4% and 8% respectively. The secondary attack ratios did not significantly differ across the intervention groups. In multivariable regression models, history of influenza vaccination and younger age of the corresponding index subject were associated with lower risk of secondary infection, but were not statistically significant at the 0.05 level. **Conclusions**: The secondary attack ratios were lower than anticipated, and lower than in previous studies in Western settings, perhaps due to differing patterns of susceptibility, lack of significant viral strain drift, and/or issues related to the symptomatic recruitment design.

Initial Results from the First Comprehensive Influenza Surveillance Activity in Kenya

D. Schnabel[1], W. Bulimo[1], J. Goy[2], R. Achilla[1], J. Wangui[1], S. Bedno[3], S. Martin[1];

[1]US Army Medical Research Unit - Kenya, Nairobi, KENYA, [2]McMaster University School of Medicine, Hamilton, ON, CANADA, [3]Walter Reed Army Institute of Research, Silver Spring, MD.

Background: Continuous, global influenza surveillance is critical for the detection of viral antigenic drift and shift. No consistent influenza surveillance has been conducted in east and central Africa despite strong evidence of frequent ILI within this population. **Methods:** To address this surveillance gap, the US Army Medical Research Unit - Kenya (USAMRU-K) in collaboration with the Kenya Medical Research Institute (KEMRI) and CDC-Nairobi developed an influenza surveillance network in Kenya. 8 hospital study sites were selected from the major population centers. ILI cases were recruited by dedicated clinicians. Identification was performed by real time PCR and viral isolation at the refurbished Kenya National Influenza Center. **Results:** During the first year of testing (July 2006 - 07), 576 of 2081 specimens (28%) tested positive for influenza A and 200 (10%) for influenza B by PCR. 36 influenza isolates were obtained and shared with the WHO. The majority were similar to the 2006 Southern Hemisphere influenza A (H3N2) and influenza B (Malaysia-like) vaccine strains. Two H3N2 viruses isolated from Nairobi slum residents were unique drift variants of the vaccine strain. An increase in H3N2 infections occurred during the cold season in all regions (peak of 207 cases in June). Influenza B infections occurred at a steady, low rate at most sites throughout the year except for a spike in cases (n=58) in Mombassa from January - March. Significantly more influenza B cases (25%) were over 16 years of age (p<001). **Conclusions:** Though generally neglected as a cause of morbidity or mortality, influenza is a significant cause of respiratory disease in Kenya with 776 (37%) detected cases of influenza. Vaccination with the Southern Hemisphere vaccine strain is supported by our data. The discovery of two unique drift variants demonstrates the potential for reassortment in the overcrowded, under-resourced urban areas of Kenya. A sustained ILI surveillance effort will assist the Kenyan MoH in monitoring and responding to epidemics, provide isolates for vaccine selection, and benefit the global influenza surveillance effort in a previously under-studied part of the world. The close interagency cooperation between USAMRU-K, KEMRI, and the CDC is a significant and successful new model for conducting challenging surveillance in Africa.

D3. Surveillance Domestic

Monday, March 17
3:00 PM – 4:30 PM
Centennial IV

Incidence of Staphylococcal Toxic Shock Syndrome, 2000-2006

A. DeVries, L. Lesher, R. Danila, R. Lynfield;

Minnesota Department of Health, St. Paul, MN.

Background: The incidence of Staphylococcal toxic shock syndrome (STSS) among young women decreased significantly from 1980-1986 (approximately 13 to 1.5 per 100,000 in Minnesota). Infections with community-associated methicillin-resistant Staphylococcus aureus (CAMRSA) have widely increased in Minnesota since 2000, and cases of STSS have been reported associated with CAMRSA. We were interested in determining whether the incidence of STSS has changed during this period. **Methods:** Retrospective surveillance was established among all 24 hospitals in the seven-county Minneapolis-St. Paul area (MSP) (population 2,642,056). All hospitalizations receiving the ICD-9 code for STSS (040.82 or 040.89) from every MSP hospital from January 1, 2000-December 31, 2006 was reviewed for the STSS CDC surveillance definition. **Results:** 194 hospitalizations received the STSS ICD-9 code and all hospitalizations were reviewed. Significant variability occurred in the frequency of the STSS code (range 18 to 39 per year). Forty-two STSS cases (26 menstrual, 16 nonmenstrual) were identified. Three cases had MRSA isolated (9% of culture positive cases); with one confirmed as USA400, a known CAMRSA genotype. Averaged over 2000-2006, the yearly incidence per 100,000 persons for all STSS was 0.2, for all nonmenstrual was 0.1, and for all menstrual was 0.4. Yearly incidence of menstrual STSS among women aged 12-24 years for 2000-2006 was 0.0, 0.9, 2.1, 2.5, 1.7, 1.7, and 0.8 per 100,000 respectively. Incidence of menstrual STSS among ages 25-54 years was 0.6, 0.5, 0.3, 0.2, 0.2, and 0.0 per 100,000 respectively. **Conclusions:** Menstrual STSS is most common among young women with the highest incidence in 2003, but decreasing incidence from 2004-2006. There was a similar decrease in incidence among menstrual cases aged >25 years. Based on a prior MDH study, use of the specific STSS ICD-9 code can underestimate the number of cases by up to 50% of nonmenstrual STSS, but 18% of menstrual STSS. However, it does not appear that the emergence of CAMRSA is associated with significant changes in the incidence of STSS.

Rapid Identification of Divergent and Novel Viruses From Previously Untypable California State Department of Public Health Pathogen Surveillance Program Samples

J. G. Victoria[1], A. Kapoor[1], K. Dupuis[2], D. P. Schnurr[2], E. L. Delwart[1];

[1]Blood Systems Research Institute, San Francisco, CA, [2]Viral and Rickettsial Disease Laboratory, Division of Communicable Disease Control, California State Department of Public Health, Richmond, CA.

Background: Public surveillance of bacterial and viral infections is critical in detecting and preventing new outbreaks of known viruses. Occasionally, identification of a specific causative agent using all available serological, histology and genetic tests fails. Six such untypable samples collected between 1963 and 1980, three from homogenized insect tissues inoculated by intracerebral injection of fetal mouse brain and three derived from human tissues in cell culture inoculations, were targeted for viral discovery. **Methods**: Viral particles were purified from cells and cellular debris by 0.45µm filtration. Following digestion of all non-encapsidated nucleic acid with DNase and RNase, protected viral RNA and DNA was amplified using sequence independent reverse transcription and random amplification. Products were cloned, sequenced and analyzed using BLAST. **Results**: In all 6 cases a single viral agent was rapidly identified by limited sequencing (between 42-108 clones) and labeled as VRDL-1 through VRDL-6. Initial sequencing provided between 16% - 75% of viral genomes. All viruses derived from human samples (VRDL1, VRDL2 and VRDL-4) belonged to the *picornaviridae* family and ranged from 77% to 99% amino acid identity to known viruses. Insect derived viruses (VRDL-3, VRDL-5, VRDL-6) exhibited amino acid identities between 25% to 98% to the segmented *reoviridae* family. VRDL-4 and VRDL-5 represent viruses which at the time of collection and initial typing were unknown but have since been well characterized. VRDL-3 and VRDL-6 are highly divergent viruses, potentially members of a new viral genus within the *reoviridae* family. VRDL-1 shared a high percentage of sequence identity to several simian picornaviruses sequences within the provisional "Sapelovirus" genus. VRDL-1 likely originated from the primary primate cell lines used during tissue culture as many simian enteroviruses were identified as contaminants between 1950 and 1980. The entire VRDL-1 genome was obtained, representing a new member of the "Sapelovirus" genus. **Conclusions**: Nonspecific shotgun sequencing of virus particles is both simple and effective for rapidly detecting highly divergent viruses, including *reoviridae* and *picornaviridae* family members, where traditional techniques, such as consensus PCR, have failed.

Surveillance for Community-onset *Clostridium difficile*, Connecticut, 2006

T. Rabatsky-Ehr[1], K. Purviance[1], D. Mlynarski[1], P. Mshar[1], A. D. Thompson[2], J. Hadler[1];

[1]Connecticut Department of Public Health, Hartford, CT, [2]Centers for Disease Control and Prevention, Atlanta, GA.

Background. The emergence of a more toxigenic *C. difficile* (CD) strain in hospitals and its appearance in the community has made it important to monitor its community impact. In 2006, community-onset (CO) *Clostridium difficile*-associated disease (CDAD) was made healthcare provider reportable in Connecticut (CT) to determine the magnitude, descriptive epidemiology and trends, and risk factors for infection. **Methods**. A case was defined as a positive (CD) toxin assay in a symptomatic individual with no known hospitalizations or long term care facility stay in the 3 months before specimen collection. Patient information was collected from treating physician, ICP, or patient using a standardized form. During a 3-month period, toxin-positive stool samples were collected and tested for toxinotype at CDC. Analysis of data for descriptive epidemiology, and comparison among cases for risk factors for hospitalization was conducted. **Results**. Overall, 241 (53%) of 456 reported patients met the case definition. Annualized incidence was 7.0 cases /100,000 population. Of the 241, 46% were hospitalized, 5.4% in the intensive care unit; 2 (1%) died. Median length of hospitalization was 4 days. Median age of all cases was 55 years; 67% were female. Among all cases, 29% had a health care interaction (HCI) in the preceding 3-12 months; 67% had at least one underlying medical condition; and 68% used an antibiotic prior to onset. Independent predictors of hospitalization by multivariate analysis included: age ≥65 years, fever, and HCI. There were 59 (27%) cases with no underlying conditions or prior HCIs. Compared to all others, they were much younger (64% vs 33% <45 years old, $p<0.001$). In a multivariate analysis controlling for age, they were also less likely to use PPI than cases with underlying conditions or HCI (2% vs 32%, $p<0.001$). Twelve isolates were characterized; 8 produced binary toxin and 3 (25%) were toxinotype III (new epidemic strain). **Conclusions**. Multiple strains of *C. difficile,* including the "epidemic" strain, are present in CT and causing illness in the community, including among persons with no traditional risk factors. The CO CDAD rate is similar to that found in Philadelphia in 2005. Clinicians need to consider a diagnosis of CO CDAD in outpatients with severe diarrhea, even in the absence of traditional risk factors.

Correlation of Anti-Influenza Prescription Data to U.S. Sentinel Provider Surveillance Network Data

C. M. Hales, R. English, J. Tokars;

Centers for Disease Control and Prevention, Atlanta, GA.

Background: Influenza surveillance provides public health officials and healthcare providers with data on the onset, duration, geographic location, and level of influenza activity in order to guide the local use of interventions. The Influenza Sentinel Provider Surveillance Network tracks influenza-like illness (ILI) across the U.S. population. Electronic anti-influenza prescription data may augment sentinel provider data, providing timelier data in more geographical detail. **Methods:** BioSense has recently acquired real-time anti-infective prescription data from a national electronic pharmacy claims management services provider. Anti-influenza prescription data from a historical dataset from approximately 30,000 pharmacies in all 50 states over the period of October 2003 to May 2007 were used for this analysis. The weekly proportion of anti-influenza drug prescriptions among all anti-infectives was compared to the sentinel provider ILI percent. Correlation coefficients were calculated for each anti-influenza drug for each of the 4 influenza seasons at the national and regional levels. **Results:** On the national level, the overall correlation of all anti-influenza drugs to sentinel provider data for all 4 influenza seasons was 0.95. However, there was substantial variation in the correlation by individual drug, season, and region. Amantadine and rimantidine prescriptions were highly correlated to sentinel provider data in the 2003-4 and 2004-5 influenza seasons, but volume of prescriptions (and associated correlations) decreased precipitously after CDC recommended discontinuation of their use for influenza treatment during the 2005-6 season. Oseltamivir prescriptions were highly correlated to sentinel provider data except during the 2005-6 season (0.78 vs. 0.98, 0.98, and 0.92 in the other 3 seasons), when individuals began stockpiling the drug following extensive media coverage of the threat of avian and pandemic influenza. Similar patterns were also seen at the regional level. **Conclusions:** Oseltamivir prescription claims data may be a timely supplement to traditional data, especially if media coverage of influenza is taken into account. The geographical detail in the prescription data may be particularly useful in areas with sparse coverage by traditional influenza surveillance.

Variation in Seasonality Among *Salmonella* Serotypes Isolated in Georgia

D. J. Cole, M. Tobin D'Angelo, E. L. Murray;

Georgia Division of Public Health, Atlanta, GA.

Background: The Georgia Division of Public Health frequently reports the highest annual case rates of salmonellosis among the Foodnet sites. In addition to well-described foodborne routes of exposure, several commonly isolated *Salmonella* serotypes may have environmental sources since distinctive seasonal distributions are observed. In an effort to better understand the epidemiology of different *Salmonella* serotypes in Georgia and improve cluster detection, reported cases of salmonellosis in the years 2000 through 2006 were fit to sinusoidal seasonal models to establish expected seasonal patterns of salmonellosis in Georgia. **Methods**: A cyclical regression model adapted by Simonsen et al. from work of Lui and Kendal to predict seasonal patterns of human influenza was used to fit historic salmonellosis case data for the following serotypes: *S.* Heidelberg, *S.* Typhimurium, *S.* Javiana, *S.* Newport, *S.* Montevideo, and *S.* Enteriditis. Evaluation of model fit was used to determine the usefulness of the modeled baseline to predict expected seasonal case rates of salmonellosis. Dates of known clusters were used to evaluate model sensitivity to salmonellosis cluster detection. **Results**: Cyclical regression models were most useful to establish baselines for those serotypes with poorly described reservoirs such as *S.* Javiana. Those serotypes with well-documented foodborne sources such as *S.* Typhimurium and *S.* Enteriditis did not demonstrate a cyclic seasonal pattern. Model sensitivity to cluster detection was poor until the time point that traditional means of cluster detection found an increase in cases. **Conclusions**: The results of cyclical regression modeling of salmonellosis in Georgia suggest that seasonality plays a large role in the epidemiology of some but not all serotypes. Serotypes usually associated with foodborne sources do not exhibit strong seasonal trends compared to those with poorly described exposure pathways. Establishing predictive models of expected salmonellosis case rates was of limited usefulness in detecting clusters above baseline in Georgia prospectively. The poor utility of predictive models for detecting clusters of salmonellosis was largely attributed to time-dependent factors of data entry and the inability of predictive models to estimate expected sporadic cases.

Coccidioidomycosis Surveillance: Improving Assessment of Disease Burden

R. H. Sunenshine[1], S. Chen[1], L. Erhart[2], S. Anderson[2], B. Park[3], B. Casimir[2], T. Chiller[3], K. K. Komatsu[2];

[1]Arizona Department of Health Services and CDC, Phoenix, AZ, [2]Arizona Department of Health Services, Phoenix, AZ, [3]Centers for Disease Control and Prevention, Atlanta, GA.

Background: Coccidioidomycosis (Valley Fever) is an emerging fungal disease endemic to the Southwestern US, Central and South America; 60% of known US cases occur in Arizona, where physician and laboratory reporting is mandatory. To improve case definition sensitivity, the Council of State and Territorial Epidemiologists (CSTE) voted in 2007 to include clinical cases diagnosed with a single rather than rising titer of coccidioidal immunoglobulin G. Arizona's simpler case definition is similar, but does not require correlation with clinical symptoms. To evaluate Arizona's coccidioidomycosis surveillance system and identify issues contributing to delayed or under-reporting, we collected additional clinical presentation and diagnostic data. **Methods:** We telephoned every tenth coccidioidomycosis case reported to the Arizona Department of Health Services from January-August 2007 to conduct interviews using a standardized questionnaire. If the case could not be reached after ≥3 attempts, the subsequent reported case was contacted.**Results:** Of 3268 cases reported, 262 were successfully interviewed (80% of targeted sample). Over 98% of cases reported ≥1 and 95% reported ≥2 symptoms consistent with coccidioidomycosis at diagnosis [positive predictive value (PPV) 98%]. Case-patients waited a mean of 49 days from symptom onset before seeking medical care. A mean of 2.8 provider visits occurred before providers ordered coccidioidomycosis diagnostic testing; 18% of case-patients reported initiating the request for testing themselves.**Conclusions:** Elimination of requirement for clinical criteria from the coccidioidomycosis case definition simplifies surveillance, has little effect on PPV, and may facilitate implementation of mandatory coccidioidomycosis reporting in other endemic states. Combined with physician and patient education to improve timeliness and utilization of coccidioidomycosis diagnostic testing, these changes would allow for a more accurate estimate of US and possibly international disease burden.

D4. Zoonotic & Animal Diseases II

Monday, March 17
3:00 PM – 4:30 PM
Centennial III

Risk Factors for Human Anthrax, Jalalabat and Osh Districts, Kyrgyzstan, August-October 2005

M. Favorov[1], S. Ajeilat[1], V. Maityeva[2], D. Nabirova[1], D. Nabirova[1];

[1]CDC Central Asia Regional Office, Almaty, KAZAKHSTAN, [2]Sanitary and Epidemiology Station, Almaty, KYRGYZSTAN.

Background: Anthrax is a public health problem in Kyrgyzstan. During the last 60 years, anthrax in domestic animals was documented in 1200 areas around the country; those areas are currently under surveillance and are regarded as possible sources for disease transmission to animals and subsequently to humans. From August to October, 2005, 35 patients with cutaneous anthrax were hospitalized in Jalalabat (18) and Osh (17) districts. Upon the request of the Ministry of Health in Kyrgyzstan, a case-control study was carried out from October 31 to November 8 to identify the source and risk factors for human anthrax so that appropriate recommendations can be made. **Methods:** A 'case-patient' was a resident of the two districts with an acute illness clinically consistent with cutaneous anthrax during August-October, 2005. Patients were identified through routine surveillance; for each case-patient, two healthy neighborhood controls matched by gender and age (± 4 years), were selected. Exposures to animals or animal products and clinical and laboratory data for case-patients were ascertained by interviews and reviewing medical records. Risk factors for disease were evaluated using conditional logistical regression analysis in the statistical software Epi Info 3.3. **Results:** 32 case-patients and 64 controls were studied. 20 case-patients had positive laboratory test for Anthrax; 72% (23) were males; all were above nine years of age; 62.5 % (20) had domestic animals; 34% (11) prepared food from raw meat, and 53% (17) reported having skin wounds prior to disease onset. History of exposure to raw meat (OR=15.5, 95% CI 4.2-100.0) and having skin wounds (OR=15, 95% CI 2.3-328.0) were significantly associated with disease. There was weak evidence that having domestic animals was a risk factor (OR=7.0, 95% CI 0.8-158.2). **Conclusions:** The significant association between disease and certain exposure in this study indicates that residents may not take necessary precautionary measures to prevent disease when handling animals or animal products. We recommend that veterinary services should be improved in the affected areas and that home-owned animals be vaccinated. Health education should be provided to the local residents on how to protect themselves while working with animals or animal products.

A Veterinary Curriculum in the Appropriate Use of Antibiotics

P. C. Bartlett;

Michigan State University, E. Lansing, MI.

Background: Debate still continues regarding the relative importance of agricultural antibiotic usage in fostering antimicrobial resistance (AR) among human pathogens. This debate may have delayed the development of educational materials aimed at promoting the prudent and judicious use of antibiotics in veterinary medicine. However, a consensus exists that unnecessary or wasteful usage should be curtailed whenever possible. **Methods:** The U.S. Centers for Disease Control and Prevention (CDC) funded the development of an interactive and multi-media educational web site to aid in teaching veterinary students about their responsibilities and obligations to curtail the unnecessary use of antibiotics. The overall purpose is to preserve antibiotic efficacy for both humans and animals. Audio, video, interactive questions and animation are used to make the presentation varied and entertaining. Written for veterinary students, the site also has applicability to others in the food animal industries. **Results:** The web site is designed to supplement existing courses in public health, epidemiology, pharmacology and species-specific veterinary medicine. The introductory module emphasizes the interconnectedness of animal and human health as it follows an outbreak investigation scenario to teach basic microbiologic and epidemiologic principles of AR. Also taught are methods for determining AR and the importance of AR to public health. Species-specific modules regard international issues and multiple clinical situations for dairy cattle, beef cattle, exotic animals and swine. Future modules will address companion animals and poultry. Emphasis is on therapeutic situations when antimicrobial agents are often used unnecessarily when alternative treatment methods are available, when the use of antibiograms (susceptibility profiles) is possible or when antibiotic treatment may be less efficacious and economical than are available preventive medicine procedures. **Conclusions:** This web site is being written for training veterinary students throughout the USA, but it will be freely available to the international public. The web site is due for release in 2008. Search: CDC Get Smart on the Farm or find the link at the CDC web site: http://www.cdc.gov/narms/get_smart.htm or www.cvm.msu.edu

The Emergence of Vaccinia virus in Brazil

G. Trindade[1], F. G. da Fonseca[2], Z. Lobato[2], M. I. Guedes[2], E. G. Kroon[2], I. Damon[1];

[1]CDC, Atlanta, GA, [2]Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, BRAZIL.

Background, Methods, Results: Naturally occurring infections with *Orthopoxvirus* have been recognized in Brazil during the past 10 years. Infections typically occur as a zoonosis transferred from affected dairy cows to their handlers. Outbreaks have caused notable economic losses to the rural community in the region. Often, the entire herd, all dairy workers, and the owners from a single farm have been infected. *Vaccinia virus* (VACV) has been consistently isolated in association with the outbreak,s which have had substantial impact on local economies and public health. Retrospective epidemiological data revealed that 100% of the patients develop classical poxvirus infection symptoms after direct contact with symptomatic cows. The origins of Brazilian vaccinia viruses (BVV) are unclear but previous analyses have shown that at least two distinct clades of BVV exist. The natural host of VACV remains unknown but the virus clearly persists today in Brazil. Serological analysis of wild mammals captured in wildlife preservation areas with little human presence indicated a high prevalence of animals with anti-orthopoxvirus antibodies. Although the World Health Organization (WHO) declared global smallpox eradicated in 1980, concerns over emergent poxvirus infections have increased. **Conclusions:**Considering that poxviruses affecting humans are largely zoonotic, the emergence of VACV in Brazil represents a very important model to study the epidemiology, pathogenesis, and molecular characteristics of these viruses. This understanding could also provide insights to establish ways to prevent and control poxvirus infections.

Methicillin-resistant *Staphylococcus aureus* (MRSA) Infections among Pets in Minnesota

J. B. Bender[1], K. Coughlan[1], K. Waters[1], D. Boxrud[2], K. Peterson[3], J. Buck[4];

[1]University of Minnesota, Veterinary Public Health, St. Paul, MN, [2]Minnesota Department of Health, Public Health Laboratory, St. Paul, MN, [3]University of Minnesota, Veterinary Medical Center, St. Paul, MN, [4]Minnesota Department of Health, St. Paul, MN.

Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) infections are increasingly being reported in dogs, horses, pigs, and cats. The zoonotic potential from these infections is unknown and requires further assessment. To document the occurrence among select animal populations, samples were collected from animals residing in a long-term care facility, pets of patients recently diagnosed with MRSA infection, and clinically ill animals presenting to a veterinary hospital. **Methods:** Nasal and rectal swabs were collected from asymptomatic animals in a long-term care facility and pets of patients recently diagnosed with MRSA. Culture-confirmed MRSA recovered from ill animals were identified through surveillance in a veterinary hospital. Collected isolates were sent to the Minnesota Department of Health for confirmation, antimicrobial susceptibility testing, and molecular subtyping. **Results:** Two of 11 resident cats from the long-term care facility were identified with MRSA. All isolates were genotype USA100. MRSA was isolated from 2 of 28 asymptomatic pets of pet owners diagnosed with community-associated MRSA. Isolates from the 2 animals were genotype USA300. Since October 2003, MRSA has been identified in 18 refractory cases presented to the veterinary medical clinic. Isolates were obtained from 12 dogs, 5 cats, and 1 horse. Thirteen of 16 available isolates were genotype USA100 and the remaining 3 were genotype USA300. Nine of 12 interviewed family members of the infected pet were recently hospitalized or had on-going severe illnesses (i.e. chemotherapy), or were healthcare providers. Spread within the veterinary clinic was suspected from several case clusters supported by isolation of indistinguishable strains among case isolates. **Conclusions:** Pets with MRSA likely acquire their infection from their owners as demonstrated by the presence of common genotypes among the various populations. There is a need to re-enforce precautionary measures and hand hygiene to pet owners diagnosed with MRSA infection. Owner education should describe the potential risk of transmission from and/or to pets. Further research to quantify this household risk, the length of carriage in pets, and the potential treatment options is needed.

Risk Factors for Hantavirus Infection among Patients in Rural Areas and Application of Prevention Measures, Minas Gerais, Brazil, 2006

C. F. Borges[1], P. C. Souza[1], M. M. Souza[2], J. R. Silva[3], I. B. Ferreira[4], A. Suzuki[4], H. H. Duarte[1], R. M. Dusi[1];

[1]EPICAMPO, Secretariat of Health of Minais Gerais, Belo Horizonte, BRAZIL, [2]Secretariat of Health of Minais Gerais, Belo Horizonte, BRAZIL, [3]Santa Casa Araxá Hospital, Araxa, BRAZIL, [4]Adolfo Lutz Institute, Sao Paulo, BRAZIL.

Background: Hantavirus pulmonary syndrome (HPS) is a highly fatal illness first detected in Brazil in 1993. In 2005, at Araxá County Minas Gerais, the HPS fatality rate was 71%. We conducted an investigation of risk factors and implemented control

methods. **Methods**: We conducted a case-control study. Laboratorial confirmation was by EIA. A case-patient was defined as a visitor or inhabitant of the rural area of Araxá county, who between January 1 and September 30, 2006 presented sudden fever and others two symptoms and had positive serum IgM for hantavirus; a control was a person exposed to a same rural areas as a case-patient at the same period and had no detectable serum IgG for hantavirus. A questionnaire was applied to document demographic, exposure and behavior data. Frequencies, odds ratio (OR) and p value (p) were calculated. Fisher exact and Kruskal-Wallis tests were applied as appropriate. Training of healthcare providers and officials, and community education, were conducted. **Results**: From January to September, 2006, eight cases and 128 controls were enrolled in the case-control study. The case-fatality rate was 37%. Case-patients did not differ significantly from controls with respect to median age (32 years) and male predominance (88%). Risk factors associated with HPS were: living in an urban area (7 [88%] cases, Odds Ratio [OR]= 23.9, $p < 0.01$); and recreational activities in rural areas (4 [50%] cases, OR= 9.6, $p<0.01$). Accordingly, the following control measures were instituted: Twenty-seven locations for referral of rural inhabitants to hospitals were established. Training was provided to 123 technicians and rural inhabitants about hantavirus disease. Hantavirus prevention information was disseminated via two television channels, five radio channels, three newspapers and two thousands pamphlets. **Conclusions**: In this region of Minas Gerais, living in an urban area and visiting rural areas for recreation were associated with HPS. Following intensive education efforts and establishing a rural hospital referral system, the HPS fatality rate in 2006 was lower than in 2005.

Human Rabies Prophylaxis Due to Bat Attacks in Brazil, 2006

A. A. Oliveira[1], M. Y. Wada[2], L. M. Pereira[2], R. C. Oliveira[2], T. S. Teixeira[2], A. S. Silva[2], W. N. Araújo[1];

[1]Field Epidemiology Training Program, Secretariat of Health Surveillance, MoH, Brasilia, BRAZIL, [2]Secretariat of Health Surveillance, MoH, Brasilia, BRAZIL.

Background: Rabies transmitted by bats is an emerging public health problem in Brazil, with accidental human cases caused by attacks by non hematophagous bats and outbreaks of human rabies caused by vampire bats. We describe the bat attacks on humans and subsequent prophylaxis provided to prevent rabies. **Methods:** We analyzed data from the human rabies prophylaxis (HRP) system. A case-patient was a person who sought treatment from the national health service due to bat attacks, and was reported to the National Notifiable Disease Information System, in 2006. **Results:** Bat attacks accounted for 1% (4,953/497,126) of total HRP reports and for two of nine (22%) cases of human rabies in Brazil in 2006. The number of attacks peaked in January (13%) and decreased during the year year (R^2=0.88). Of cases, 61% occurred in urban areas; 41% (2,031) in the Northern region, 36% (1,785) in Pará State, in which 64% (1,102/1,711) cases occurred in rural areas. Most (60%) case-patients were male; adults aged 15-34 years (31%) and 35-64 years (33%) were the most frequently attacked. Attacks occurred during leisure activities in 19% (876/4,660) of cases. The principal types of injuries were bites (81%), indirect contact (10%) and scratches (7%). The wounds were located in the hands or feet (52%), lower limbs (20%) and head (14%); 67% of cases had one wound and 53% had superficial wounds. Of 4,625 case-patients who received rabies prophylaxis, 92% were post-exposure, with 72% (2,856/3,977) receiving rabies antiserum. Of prophylaxed case-patients, 18% (645/3,674) had interrupted treatment and 88% (568/643) abandoned treatment. Local, systemic or neurological reactions following vaccination occurred in 0.4% of treated case-patients. **Conclusions:** HRP due to bat attacks highlights the importance of rabies prophylaxis, given the uniform fatality of the disease. The high number of cases in urban areas suggests accidental attacks by non hematophagous bats. However, in Pará State, the predominance of cases in rural areas suggest attacks by vampire bats. We recommended education aimed at reducing accidental attacks and prophylaxis abandonment.

D5. Noscomial Infections

Monday, March 17
3:00 PM – 4:30 PM
Regency VI

Clinical Severity of *Clostridium difficile* 027 versus Non-027 PCR Ribotypes: a Case-Case Study

O. Morgan[1], B. Rodrigues[2], T. Elston[3], N. Q. Verlander[4], D. Brown[5], J. Brazier[6], M. Reacher[1];

[1]Health Protection Agency: East of England Regional Epidemiology Unit, Cambridge, UNITED KINGDOM, [2]2. Norfolk, Suffolk, and Cambridge Health Protection Unit, Cambridge, UNITED KINGDOM, [3]Essex Rivers NHS Trust, Colchester, UNITED KINGDOM, [4]Health Protection Agency: Statistics, Modelling and Bioinformatics Department, London, UNITED KINGDOM, [5]Addenbrookes Hospital Trust: Clinical Microbiology and Public Health Laboratory, Cambridge, UNITED KINGDOM, [6]National Public Health Service, University Hospital of Wales, Cardiff, UNITED KINGDOM.

Background: *Clostridium difficile* is a leading infectious cause of healthcare-associated diarrhoea. Several industrialised countries have reported an increase in *C .difficile* infections and outbreaks, which have been attributed to the emergent PCR ribotype 027 strain (North American pulsed-field type 1). We conducted a case-case study to compare the severity of *C .difficile* disease for patients with 027 versus non-027 ribotypes. **Methods:** We retrospectively identified *C.difficile* case-patients admitted to 16 National Health Service (NHS) hospitals in the East of England region and for whom stool isolates were cultured and ribotyped as part of a 2006 national hospital survey of *C.difficile.* We defined severe *C .difficile* disease as having one or more of shock, paralytic ileus, pseudo membranous colitis or toxic megacolon. We used multivariable logistic regression to assess several putative risk factors: infection with 027 or non-027 ribotypes; age; sex; discharge from hospital within 60 days prior to current admission; having gastroenteritis at admission; being immunocompromised; use of proton pump inhibitors, H2 agonists and antibiotics in the 8-weeks before illness onset; and the hospital to which the patient was admitted. **Results:** Information was available for 123 case-patients. Median age was 83 years old (range 3 to 98), 86% were prescribed antibiotics in the eight weeks before illness onset, 41% had ribotype 027 and 30-day all cause mortality was 21%. Severe disease occurred in 24% (95%CI 13% to 37%) and 17% (95%CI 9% to 27%) of patients with PCR ribotype 027 and non-027 ribotypes, respectively. In a multivariable model, ribotype 027 was not associated with severe disease after adjusting for sex , discharge from hospital prior to 60 days of current admission, gastroenteritis on admission, number of initiator antibiotics for *C .difficile* disease, and hospital where the patient was admitted. **Conclusions:** Our study found no evidence that ribotype 027 is more virulent than other PCR ribotypes. This finding does not support suggestions that greater virulence of ribotype 027 infections contributes to increased in incidence of *C.difficile* disease throughout North America and Europe.

National Outbreaks of Mycobacterial Infections Following Fiberoptic-Guided Surgical Procedures, Brazil, 2003-2007

J. R. Melo[1], M. H. Garcia[1], A. Madeira[1], J. C. Barrado[1], S. M. Gomes[2], G. S. Dimech[1], W. N. de Araujo[1];

[1]Field Epidemiology Training Program (EPISUS), Secretariat of Health Surveillance (SVS), Ministry of Health, Brasilia, BRAZIL, [2]National Agency for Sanitary Surveillance (ANVISA), Ministry of Health, Brasilia, BRAZIL.

Background: Laparoscopic fiberoptic-guided procedures greatly reduce the invasiveness of abdominal surgical procedures. However, a wave of outbreaks of surgically-related infections related to these procedures has occurred in Brazil. We reviewed outbreaks of Rapidly Growing Mycobacteria associated with video laparoscopies in Brazil between 2003-2007. **Methods:** We reviewed reports of investigations conducted by trainees of the Brazilian Field Epidemiology Training Program (FETP/EpiSUS) and subject matter experts of the National Sanitary Inspection Agency. We defined a suspect case as: a video laparoscopy patient who presented the following symptoms up to one year post-procedure: hyperemia, fever, edema, vesicles, granulomas on tissue pathology, fistula, serous secretion with difficulty healing, and failure to respond to conventional antimicrobial therapy. **Results:** Outbreaks of post-video laparoscopy mycobacterial outbreaks were detected in 11 of 27 Brazilian states, involving 1,711 suspect cases and 479 (23%) laboratory-confirmed cases, in private and public hospitals. The greatest numbers of suspected cases were from the states of Rio de Janeiro (969) and Para (311); 72% of case-patients were female. Associated procedures included: cholecystectomy (60%), laparoscopy (11%), vidoarthroscopy (5%) and breast implants (1%). The Brazilian Ministry of Health instituted a triple-therapy daily regimen of clarithromycin, 500 mg, ethambutol, 1,200mg and terizidone 500 mg. The cost of treatment in the public sector so far has been approximately $2,600 per month. The most frequently identified species of mycobacteria have been *Mycobacterium Abscessus* and *Mycobacterium fortuitum*. The most commonly reported hypothesis for infection was contamination of surgical instruments used in these procedures. **Conclusions:** These results indicate a national crisis of post-surgical mycobacterial infections associated with video laparoscopies, attributable to widespread failures in cleaning, disinfection and sterilization of surgical instruments, and possibly to re-use of single-use items. A careful revision of current strategies for surgical infection control, including surveillance, training, and vigorous enforcement areurgently needed to improve this situation.

Limiting the Spread of Respiratory Infections in Kenyan Provincial Hospitals: A Report from the Field

C. J. Ngongo[1], T. Mwangi[2], M. Katz[1], J. Kioli[2], K. Ellingson[3], C. Lucero[3], T. MacCannell[3], M. Jhung[3], P. Patel[3], M. Bell[3], R. Breiman[1];

[1]CDC - Kenya, Nairobi, KENYA, [2]Kenya Ministry of Health, Nairobi, KENYA, [3]CDC - Division of Health Quality Promotion, Atlanta, GA.

Background: The ability to limit the spread of pandemic influenza and other dangerous emerging pathogens in Africa will depend on the application of proper hospital infection control measures. These measures are often lacking in resource-limited countries, where patient crowding, short staffing, inadequate infrastructure, and limited infection control training for healthcare personnel are common. In order to address these gaps, CDC and Kenyan Ministry of Health (MoH) initiated a project to improve infection control in provincial hospitals. **Methods:** A group of MoH-supported doctors and nurses from Kenyan provincial general hospitals received training in Nairobi. Training focused on the low-cost interventions of respiratory cohorting, hand hygiene, and the development of hospital-specific isolation strategies. After training, teams from the MoH and CDC visited each hospital to implement respiratory cohorting in selected wards deemed to be at high risk for transmission of respiratory infections. Respiratory cohorting consisted of identifying and segregating patients with febrile respiratory illness, including use of a systematic patient-numbering strategy. Audit tools were provided to monitor hand hygiene and cohorting compliance.**Results:** After four months, all of the eight participating hospitals had implemented respiratory cohorting in at least two hospital wards; thirty staff were trained. Half of the hospitals adopted a numbering system to improve organization and efficiency of cohorting. All eight hospitals developed written isolation strategies for pandemic influenza; six of eight hospitals resurrected hospital infection control committees. Increased awareness of respiratory illness led five hospitals to revise patient placement decisions for Tuberculosis (Tb) patients. Project implementation is ongoing. **Conclusions:** Following a low-cost centralized training program and on-site supervision, improvements occurred in infection control practices and planning at provincial hospitals in Kenya. In resource-limited settings confronting infection control challenges including pandemic influenza, drug-resistant Tb, and other acute respiratory infections, this approach to improving infection control capacity can be practical and effective.

Investigation of a Multidrug-resistant *Acinetobacter baumannii* Outbreak -- Phoenix, 2007

C. A. Lucero[1], A. Kallen[1], C. Gould[1], R. Sunenshine[2], V. Berisha[3], J. Noble-Wang[1], B. Jensen[1], A. Shams[1], M. J. Arduino[1], A. Srinivasan[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Arizona Department of Health Services, Phoenix, AZ, [3]Maricopa County Department of Public Health, Phoenix, AZ.

Background: *Acinetobacter* is an important nosocomial pathogen that typically causes ventilator-associated pneumonia, bloodstream and wound infections in hospitalized patients. Multidrug-resistant *A. baumannii* (MDR-Ab) has emerged making treatment and control more difficult. Infections with MDR-Ab are associated with increased mortality, hospital stays and costs of care. Previous outbreaks have been linked to cross-transmission between patients and contaminated objects and surfaces. In June 2007, we investigated an MDR-Ab outbreak involving 13 adult patients in a community hospital. **Methods:** We conducted a case-control study; environmental sampling; a cleaning assessment and evaluated infection control practices. Cases were infected or colonized with MDR-Ab diagnosed ≥48 hours after admission while controls had negative respiratory, urine, groin, or wound culture for MDR-Ab. Patient and environmental isolates were typed by pulsed-field gel electrophoresis (PFGE) and multilocus sequence typing (ST). **Results:** MDR-Ab isolates from 13 patients and 2 portable x-ray machines were indistinguishable based on PFGE and belonged to a single outbreak strain, identified as ST10. A genetically-related strain (ST12) was recovered from a mobile ultrasound machine. An unrelated strain (ST69) was also recovered from the ultrasound and a portable x-ray machine. Over 50 additional environmental samples were negative for *Acinetobacter*. Compared to controls (n=30), cases were more likely to transfer in from a long-term care facility (p=0.02), receive mechanical ventilation (p=0.01), have a central venous catheter (p=0.02) or been admitted to another healthcare facility in the last 30 days (p<0.01). Systematic observations, hand hygiene audits and Glo Germ™ cleaning assessment revealed lapses in infection control and inadequate environmental cleaning. Disinfection of all portable radiology machines as well as reinforcement of hand hygiene and environmental cleaning resulted in termination of the outbreak. **Conclusions:** This is the first report to identify contaminated mobile radiology equipment in the setting

of a clonal outbreak. The investigation underscores the importance of thorough and consistent cleaning of shared equipment and staff education in preventing the spread of hospital infections.

Nosocomial Transmission of Newly Identified Adenovirus Serotype 14 in Healthcare Workers Caring For Patients With Severe Pneumonia - Oregon, 2007

P. L. Gould[1], H. Clayton[1], A. Balaji[1], J. Jackson[2], L. Tsaknaridis[3], X. Lu[1], E. Dean[1], A. Thomas[4], L. Grenz[3], M. Cortese[1], A. Srinivasan[1], P. Lewis[4], L. Anderson[1], D. Gilbert[2];

[1]CDC, Atlanta, GA, [2]Providence Hospital, Portland, OR, [3]Oregon State Public Health Laboratory, Portland, OR, [4]Oregon Department of Human Services, Portland, OR.

Background: A previously rare serotype, adenovirus type 14 (Ad14) was identified as the cause of severe pneumonia in patients in the Portland, Oregon area in the first 4 months of 2007. At one hospital, an intensive care unit (ICU) healthcare worker (HCW) also developed severe Ad 14 pneumonia, prompting this study. We investigated the extent of Ad 14 infection among the hospital's HCWs and evaluated their risk factors for infection. **Methods**: Three cohorts of HCWs were recruited among personnel from the ill HCW's hospital: 1) personnel from ICUs and units where Ad14 pneumonia patients had been treated ("High exposure"), 2) personnel in contact with Ad14 patients for brief periods of time, e.g. emergency department staff, ("Low exposure"), and 3) personnel from units not caring for pneumonia patients ("Unexposed"). HCWs were offered serology testing and polymerase chain reaction (PCR) testing of throat and nasopharyngeal swabs for evidence of Ad14 infection. Each tested HCW completed an anonymous questionnaire on respiratory illness during the previous 3 months and risk factors for infection, including infection control practices. A confirmed case of Ad14 infection was defined as an HCW with a titer of Ad14 neutralizing antibody >= 1:40 or positive Ad14 PCR. **Results**: Among the cohorts, 206 (39%) agreed to be tested: 124 of 199 (62%) of the high exposure cohort, 43 of 168 (26%) of the low exposure, and 42 of 166 (25%) unexposed. Of these, 18 (9%) met the case definition: 17 (94%) were positive by Ad14 serology and 1 (6 %) by PCR for Ad 14. Fourteen (78%) were in the high exposure cohort, 4 (22%) were in the low exposure, none were unexposed ($p = 0.04$). Cases were associated with reported febrile respiratory illness (RR 3.2, 95% CI 1.3 - 7.9), contact with ill coworkers with pneumonia (11 cases reported contact, 0 reported no contact; RR undefined, $p<0.001$), but not contact with ill family members (RR 1.0, 95% CI 0.4 - 2.8). Twelve cases (67%) reported working with respiratory illness symptoms. **Conclusions**: The findings support nosocomial acquisition of Ad14, albeit at a low level, likely through contact with ill coworkers, and supports excluding employees from work when they are ill with symptoms of a febrile respiratory illness.

Outbreak of Group A Streptococcal Infections in a Long Term Care Facility - New York, 2006-2007

A. E. Burns[1], L. M. Haskin[2], J. K. Schaffzin[2], D. J. Schoonmaker-Bopp[2], G. S. Johnson[2];

[1]New York State Department of Health, Syracuse, NY, [2]New York State Department of Health, Albany, NY.

Background: Clinically, group A streptococcus (GAS) can range from asymptomatic colonization to invasive disease. Although the elderly are at increased risk of death from GAS infection, no standardized guidelines exist for GAS disease management in long-term care facilities (LTCFs). Between October 2006 and March 2007, we investigated an outbreak of GAS infections in an Upstate New York LTCF. **Methods:** A case was defined as any LTCF staff or resident with GAS isolated from a sterile site or from a nonsterile site with consistent clinical illness during 10/15/06-3/31/07. A carrier was defined as any asymptomatic LTCF staff or resident with GAS isolated from a nonsterile site. Cases were identified by retrospective and prospective surveillance. Carriers were identified by screening of epidemiologically determined target groups. All isolates were sent to New York State Department of Health (NYSDOH) Wadsworth Center Laboratory for pulsed-field gel electrophoresis (PFGE) analysis. NYSDOH conducted site visits to asses transmission mechanisms and infection control (IC) practices. **Results:** We identified 4 invasive and 2 noninvasive resident cases; there was one death. No screening occurred after identification of two epidemiologically-linked cases. Further case identification prompted three separate targeted screenings. Following identification of a sixth case, all residents and staff were screened by throat, rectum, vagina, catheter site, and open wound culture. Nine carriers (one staff, eight residents) were identified, treated, and tested for cure, at a cost of $16,000. Two distinct PFGE patterns were identified. Basic IC, including hand and respiratory hygiene, was reinforced. **Conclusions:** Tailoring control measures to investigation findings lead to repeated staff and resident screening. Once facility-wide screening was conducted and general IC recommendations were implemented, the outbreak subsided. Without standardized guidelines, tailored response resulted in a protracted outbreak with excess morbidity, resource utilization, and cost. This outbreak demonstrates the need for standardized guidelines for surveillance, screening, and IC to reduce GAS transmission risk and maximize resource utilization when GAS infection occurs in LTCFs.

D6. Late Breakers

Monday, March 17
3:00 PM – 4:30 PM
Regency VII

Vaccines & Vaccine-Preventable Diseases

Monday, March 17
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 74. High Vaccination Coverage Prevented Large-Scale Measles Spread in Poland Following Ukrainian Epidemic in 2006-2007

P. Stefanoff, M. P. Czarkowski, W. Gut, B. Litwinska;

National Institute of Public Health - National Institute of Hygiene, Warsaw, POLAND.

Background: Along with WHO EURO elimination strategy, a high, over 95% immunization coverage of 2 doses of measles vaccine was maintained since 1997. In 2006 an unexpected rise of measles cases was notified. The aim of this study was to describe the measles outbreak investigation in Poland in 2006-2007 in order to review recommendations for outbreak management. **Methods**: Individual reports summarizing investigation of each case in 2006-2007 were reviewed. Available information on epidemiological links and laboratory investigations was described. **Results:** A total of 156 measles cases were notified in 2006-2007, of which 116 (74%) were serologically confirmed, and 4 were epidemiologically linked. This was a significant increase, compared to 25 cases (9 serologically confirmed, 36%) reported in 2004-2005. The highest disease activity was observed during three distinct periods: weeks 2-12 (p1, 35 cases), weeks 15-28 (p2, 71 cases) in 2006, and weeks 8-16 in 2007 (p3, 31 cases). During the initial period 2 cases were imported

from Ukraine, chain of infection could be tracked in 14/35 cases, but no material for genotyping was collected. During p2 one case was imported from Ukraine, the chain of infection was tracked in 25/71 cases, and the genotype detected was a local D4 strain. During p3 the chain of infection could be tracked in 9/31 cases, and the genotype was D6, related to Ukrainian strain. When exluding clinically-confirmed cases, 93/120 (77.5%) were aged 20 years or more, of which 43/93 (46.2%) were not vaccinated. **Conclusions**: Poland borders with Ukraine, with increasing tourist traffic, reaching over 5 milion Ukrainians visiting Poland in 2006. A massive epidemic of measles caused by D6 strain started in Ukraine in November 2005, involving over 47,500 cases up to date. Despite detection of some cases imported from Ukraine, no genetic evidence was found that the preliminary phase of the outbreak in Poland was linked to Ukraine. Also, identification of the Ukrainian strain in 2007 cases did not help to track epidemiological links with this country. This stresses the need to closely monitor epidemiological links in each case and attempt virus isolation in each chain of transmission. Checking vaccination of close contacts and immunizing all unvaccinated among them should be considered in each case.

Board 75. An Explosive Outbreak of Modified Measles Posing as a Rash Illness of Unknown Etiology in a High School, Taiyuan, Shanxi Province, China, 2007

P. Zhang[1], R. Fontaine[2], L. Li[3], B. Zhao[4], W. Xia[5], L. Zhang[5];

[1]Chinese Field Epidemiology Training Program, Beijing, CHINA, [2]Centers for Disease Control and Prevention, Atlanta, USA, Atlanta, GA, [3]Chinese Center for Disease Control and Prevention, Beijing, CHINA, [4]Center for Disease Control and Prevention, Taiyuan City, Taiyuan, CHINA, [5]Centers for Disease Prevention and Control of China, Beijing, CHINA.

Background: Extensive use of measles vaccine has led to the appearance of modified measles (MM) and can create confusion in initial diagnosis. In May 2007, an explosive outbreak of rash illness affected a high school. The initial investigation focused on emerging infections with high epidemic potential and included extensive laboratory testing for potential emerging infections. We continued this investigation to identify the causative agent and determine the method of exposure. **Methods**: We identified al students or teachers with fever >37.5C or rash with onset during May and June 2007. We collected serum for anti-measles IgG and IgM determinations and tracked the change in antibody titers on serial serum specimens. We defined typical measles (TM) fever >37.5 C and rash beginning from face and chest and extending to the extremities. We defined modified measles as fever >37.5 with sparse rash beginning on extremities or anti-measles IgM on acute serum of a 4-fold rise in anti-measles IgG. We interviewed case-patients about exposures using a standard questionnaire. **Results**: We found 17 TM and 60 MM among 3543 students. 13 TM and 43 MM had anti-measles IgM or a four-fold rise in anti-measles IgG on appropriately timed specimens and the remaining TM and MM had a high anti-measles IgG on a convalescent specimen. By 10 days after onset anti-measles IgG reached ≥1:12800 in 87% of MM and 53% of TM. All cases had onset within a 26 day period. The first case was in a student in the 12th grade who presented with TM. He attended class while he was sick and vomited three times in the classroom. All other MM and TM followed his onset of illness by 10 to 21 days. The attack rate in his classroom was 48%, compared to 2.5% in the rest of the 12th grade and 0.2% in the other grades. No written records of measles vaccination were available and 51% could not remember if they had or did not have MV. **Conclusions**: This explosive outbreak a rash illness of unknown etiology was from MM that resulted from exposure to a single case of TM. Investigations of rash illnesses of unknown etiology need to consider MM and other variants of common diseases before launching extensive searches for emerging agents.

Board 76. Report of the United States Rotavirus Strain Surveillance System from 2005-2007

J. J. Hull[1], E. N. Teel[1], T. K. Kerin[1], M. M. Cortese[1], U. D. Parashar[1], R. I. Glass[2], J. R. Gentsch[1], National Rotavirus Strain Surveillance System;

[1]CDC, Atlanta, GA, [2]Fogarty International Center, NIH, Bethesda, MD.

Background: Rotavirus is the most common cause of severe diarrhea in young children worldwide. In February 2006, the rotavirus vaccine, RotaTeq® (Merck) was licensed in the United States. RotaTeq is a bovine-human reassortant vaccine designed to provide protection for four globally common strains G1 to G4. To provide data on serotype distribution during the pre and post vaccine era in the United States, we continued strain surveillance studies with the collaborating laboratories of the National Rotavirus Strain Surveillance System. **Methods:** Six laboratories in the United States participated in the 2005-2006 season and twelve in the 2006-2007 season. A total of 1041 fecal specimens positive for group A rotavirus by antigen enzyme immunoassay were received at the CDC from these laboratories. The positive samples were G and P genotyped using RT-PCR based assays. Nontypeable samples were genotyped through nucleotide sequencing. **Results:** The five globally common strains were detected in the 2006-2007 season. Genotype P[8]G1 was the most prevalent (60.9%) followed by P[4]G2 (9.8%), P[8]G9 (1.0%), P[8]G3 (0.2%) and P[8]G4 (0.2%). These are similar to the results of 2005-2006. The globally emerging G12 genotype accounted for 6.2% (1.9% P[8]G12, 4.3% P[6]G12) of all the specimens in the 2005-2006 season, appearing in two of the six laboratories. The uncommon P[6]G2 strain was detected in two laboratories in each season, representing 1.2% of the total specimens in 2005-2006 and 2.2% in 2006-2007. Through nucleotide sequencing it was observed that 3.9% of the P[8] genotype was originally nontypeable by RT-PCR due to mutations in the primer binding region. To date, 25.7% of the strains from 2006-2007 are nontypeable or have unconfirmed genotypes. **Conclusions:** These data demonstrate that the prevalence of common strains detected in the 2006-2007 season was similar to levels seen in 2005-2006 and previous seasons. More than 90% of the typeable strains have a G or P antigen included in licensed vaccine. The identification of variant P[8] strains in 2006-2007 and previous seasons demonstrates the need to revise standard RT-PCR genotyping procedures. The emergence of G12 genotype in United States reinforces the need for ongoing surveillance subsequent to vaccine introduction to monitor potential changes in rotavirus strains.

Board 77. Pneumococcal meningitis among adults and children in the era of the pneumococcal conjugate vaccine: an update from Active Bacterial Core surveillance (ABCs)

H. E. Hsu[1], K. A. Shutt[1], M. R. Moore[2], B. Beall[2], N. M. Bennett[3], A. S. Craig[4], M. M. Farley[5], J. H. Jorgensen[6], C. A. Lexau[7], S. Petit[8], A. Reingold[9], A. Thomas[10], C. G. Whitney[2], L. H. Harrison[1];

[1]University of Pittsburgh, Pittsburgh, PA, [2]Centers for Disease Control and Prevention, Atlanta, GA, [3]Monroe County Health Department, Rochester, NY, [4]Tennessee Department of Health, Nashville, TN, [5]Emory University, Atlanta, GA, [6]University of Texas Health Sciences Center, San Antonio, TX, [7]Minnesota Department of Health, Minneapolis, MN, [8]Connecticut Department of Public Health, Hartford, CT, [9]University of California at Berkeley, Berkeley, CA, [10]Oregon State Public Health Division, Portland, OR.

Background: Invasive pneumococcal disease incidence declined among children and adults following introduction of the pediatric heptavalent pneumococcal conjugate vaccine (PCV7) in

2000, but impact on pneumococcal meningitis is unclear. **Methods**: We examined trends in pneumococcal meningitis from 1998 through 2005. Data were collected using active, population-based surveillance at 8 U.S. Active Bacterial Core Surveillance sites. We defined pneumococcal meningitis cases as isolation of *Streptococcus pneumoniae* from cerebrospinal fluid or meningitis diagnosed clinically with pneumococcus isolated from another sterile site. Changes in incidence between two-year periods were assessed using 1998-1999 as the baseline. **Results**: We identified 1,379 meningitis cases; incidence declined from 1.13 to 0.79 cases/100,000 between 1998-1999 and 2004-2005 (-30%, p<0.001). Among <2 and ≥65 year olds, incidence decreased 64% and 54%, respectively (p<0.001 for both groups). Rates of PCV7-serotype meningitis declined from 0.66 to 0.18 cases (-73%, p<0.001) among all ages. While rates of PCV7-related serotype meningitis decreased 32% (p=0.08), rates of non-PCV7 serotype disease (including serotype 19A) increased from 0.32 to 0.51 (+61%, p<0.001). The proportion of meningitis caused by non-PCV7 serotypes 19A, 22F, and 35B each increased significantly. Twenty-eight percent of isolates were nonsusceptible to penicillin but fewer isolates were nonsusceptible to chloramphenicol (6%), meropenem (17%), and cefotaxime (12%). The proportion of penicillin nonsusceptible isolates decreased from 1998 to 2003 (32% to 19%, p=0.01) but increased from 2003 to 2005 (19% to 30%, p=0.04).**Conclusions**: Pneumococcal meningitis rates have decreased among children and adults since PCV7 introduction. Although the overall impact of the vaccine remains substantial, a recent increase in meningitis caused by non-PCV7 serotypes, including antibiotic nonsusceptible strains, is concerning.

Board 78. Epidemiology of meningococcal disease in California, 2001-2007

K. Winter, K. Harriman;

California Department of Public Health, Richmond, CA.

Background: The meningococcal conjugate vaccine (MCV4) was first licensed in the United States in January 2005. This vaccine confers protection from *Neisseria meningitidis* serogroups A, C, Y and W-135 and was initially licensed for use in individuals aged 11-55 years. In May 2005, the ACIP recommended routine vaccination of adolescents 11-12 years of age, unvaccinated persons entering high school and other high risk persons including college freshmen living in dormitories. In June 2007, ACIP revised these recommendations to include routine vaccination of all persons aged 11-18 years at the earliest opportunity. In October 2007, licensure for MCV4 was expanded to include use in children aged 2-10 years. **Methods:** We analyzed surveillance data in California from July 2001-June 2007, examining rates of meningococcal disease and death by age and serogroup both before and after the licensure of MCV4. We consider the time period of July 2001-June 2005 to be "pre-MCV4" and July 2005-June 2007 to be "post-MCV4". **Results:** 1129 cases of meningococcal disease were reported during the study period for overall incidence and mortality rates of 0.52 cases and 0.049 deaths per 100,000 population. Rates were highest for infants under 1 year and for adults 65 years and older. Of the 900 cases with serogroup information, 460 (51.1%) were a vaccine-preventable serogroup and 423 (47.0%) were serogroup B. Overall incidence declined pre-MCV4 to post-MCV4 from 0.55 to 0.46 cases per 100,000 population and declined across all age groups except adults 65 years and older. Mortality rates also declined overall from 0.058 to 0.032 deaths and from 0.032 to 0.018 deaths per 100,000 population in vaccine-preventable serogroups. Serogroup-specific trends were difficult to interpret because serogroup identification improved over this time period and earlier data were incomplete. **Conclusions:** The overall incidence and mortality rates of meningococcal disease have declined since the initial licensure of MCV4. This analysis provides good baseline data for comparison of future trends of disease as vaccine uptake increases.

Antimicrobial Resistance

Monday, March 17
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 79. Antimicrobial Resistance in *Salmonella* Isolates Recovered from Cattle at Slaughter

P. J. Fedorka-Cray[1], J. G. Frye[1], M. Rose[2], N. Anandaraman[3], J. Haro[1];

[1]USDA-ARS, Athens, GA, [2]Intervet Innovation GmbH, Schwabenheim, GERMANY, [3]USDA-FSIS, Washington, DC.

Background: Since 1997, the animal arm of the National Antimicrobial Resistance Monitoring System (NARMS) has monitored changes in antimicrobial susceptibilities of *Salmonella* isolates from animal origin. Additionally, since 2000, susceptibility of bovine *Salmonella* isolates collected in the US has been monitored against the 4th generation cephalosporins (4-GC) cefquinome, exclusively developed for veterinary medicine, and cefepime. Cephalosporins are used extensively to treat human and cattle diseases. To identify emerging resistance patterns, resistance trends to the cephalosporins (ceftriaxone, ceftiofur, cefoxitin and cefquinome) in *Salmonella* isolates collected from cattle at slaughter were analyzed. **Methods:** *Salmonella enterica* isolates (n=7,199) obtained from cattle at federally inspected slaughter/processing plants during 1997 - 2006 and submitted to NARMS were tested for minimum inhibitory concentrations (MICs) using a custom panel of antimicrobials. Isolates collected during 2000-2006 (n=4,685) were also tested on a second panel with cefquinome and cefepime. **Results:** Resistance to ceftriaxone remained below 1%, except in 2005 when resistance increased to 2.1%. From 1997 to 2005, resistance to ceftiofur increased from 0% to 21.6%, with the exception of 2004 when it decreased to 13.3%. Resistance decreased again in 2006 to 18.9%. A similar pattern was observed for cefoxitin (testing started in 2000). Cefoxitin resistance increased from 2000 to 2005 from 9.1% to 19.8%, except in 2004 when it decreased to 13.2%. As with ceftiofur, a decrease was observed in 2006 when resistance was 17.9%. From 2000 to 2006 the MIC50 of cefquinome remained at 0.06 µg/ml, except in 2002 when the MIC50 increased by one dilution to 0.12 µg/ml. The highest MIC90 for cefquinome was 1.0 µg/ml in 2002 and 2005. MICs of cefepime were generally about one dilution step below those of cefquinome. Changes in resistance for all drugs were in large part driven by serotype, particularly *S.* Newport, Reading, Typhimurium and Agona. **Conclusions:** *Salmonella enterica* isolates remained highly susceptible to the human 3-GC ceftriaxone and the 4-GCs cefquinome and cefepime. Overall, an increase in both veterinary 3-GC ceftiofur and human 2-GC cefoxitin has been observed at similar levels and appears to be serotype dependent.

Board 80. Prevalence of Antibiotic Use, Knowledge and Attitudes Toward Antibiotic-free Meat

S. C. Rankin[1], N. M'ikanatha[2], R. Dewar[2], E. Lautenbach[1];

[1]University of Pennsylvania, Philadelphia, PA, [2]Pennsylvania Department of Health, Harrisburg, PA.

Background: Inappropriate use of antibiotics is a major public health concern as it contributes to antimicrobial resistance. Understanding consumers' knowledge and attitudes can inform multifaceted actions to achieve judicious use of antibiotics. **Methods:** In 2006 questions regarding antibiotic prescriptions and attitudes toward antibiotic-free meat were asked as part of Pennsylvania Behavioral Risk Factor Surveillance System (BRFSS). **Results:** Among Pennsylvania adults, 38.1% (95% CI,

36.4-39.8%) responded they had been prescribed antibiotics in the previous 12 months and 43.9% (95%CI, 41.1-46.7%) of these had received at least two prescriptions. Among adults taking antibiotics in the past year, 11.4% (95%CI, 9.6-13.6%) had not completed the course of treatment. Prescriptions for self-identified diagnoses usually not caused by bacteria (e.g., cough or cold) were reported by 30.3% (95%CI, 27.7-33.1%). Knowledge about use of antibiotics in animal husbandry varied by demographic characteristics (Figure): 53.6% (95% CI, 52.8%-55.4%) of non-Hispanic whites were aware of antibiotics in feed, whereas 42% (95% CI, 34.8-50.1%) of African Americans and 39.8% (95%CI, 29.0-51.7%) of Hispanics were aware. Knowledge also increased with age, education, and income. Overall 26.2% (95% CI, 24.6-31.9%) of the survey participants reported that that they try to purchase antibiotics-free meat. **Conclusion:** Inappropriate prescriptions and noncompliance with treatment regimens call for simultaneous interventions among clinicians and patients. To promote judicious use of antibiotics in food animals, additional measures to engage consumers are needed.

Board 81. Antimicrobial Resistance in *Salmonella* Serotypes Paratyphi A, Paratyphi B, Paratyphi C, and Paratyphi B var. L(+) Tartarte+ (Formerly Java), NARMS, January 1996 - March 2006

F. Medalla[1], J. M. Whichard[1], S. Gupta[1], A. Stuart[2], K. Joyce[2], R. M. Hoekstra[1], P. Fields[1], E. Mintz[1], E. J. Barzilay[1], and the NARMS Working Group;

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Atlanta Research and Education Foundation, Decatur, GA and Centers for Disease Control and Prevention, Atlanta, GA.

Background: Paratyphoid fever, a systemic infection caused by *Salmonella* serotypes Paratyphi A, Paratyphi B, and rarely Paratyphi C, is increasing in incidence in the U.S. Most cases are acquired while traveling to endemic countries. Nalidixic acid resistance, associated with decreased susceptibility to ciprofloxacin and treatment failure, has risen globally in the major serotype, Paratyphi A. Differentiation of serotype Paratyphi B from Paratyphi B var. L(+) tartrate+ (Paratyphi B var. Java), which causes gastroenteritis, is important but not routinely done; it requires tartrate testing. In Paratyphi B var. Java, resistance to ampicillin, chloramphenicol, streptomycin, sulfonamide, and tetracycline (ACSSuT) has been reported in Europe but not described in the U.S. **Methods:** Since 1996, sites submitted non-Typhi *Salmonella* (NTS) isolates to the National Antimicrobial Resistance Monitoring System (NARMS) at CDC for susceptibility testing. Participation increased from 14 sites in 1996 to nationwide in 2003. Sites sent 10% of NTS from 1996-2002 and 5% since 2003. From April 2005-March 2006, sites sent all Paratyphi A, Paratyphi B, and Paratyphi C isolates for enhanced paratyphoid fever surveillance. If tartrate-positive, Paratyphi B isolates were reclassified as Paratyphi B var. Java. Minimum inhibitory concentrations for 15 agents were determined by broth microdilution and interpreted using CLSI criteria when available. **Results**: From January 1996-March 2006, 156 (80%) of 196 Paratyphi A isolates were nalidixic acid-resistant, 1 (0.5%) was ciprofloxacin-resistant, and 3 (2%) were ACSSuT. In Paratyphi B, 1 (4%) of 24 isolates was nalidixic acid-resistant and none were ACSSuT; 21 (88%) were pan-susceptible. In Paratyphi B var. Java, 37 (14%) of 271 isolates were ACSSuT, while nalidixic acid resistance was not noted. Two Paratyphi C isolates were tested, and both were pan-susceptible. **Conclusions:** Nalidixic acid resistance is high in *Salmonella* Paratyphi A and rare in other serotypes causing paratyphoid fever. ACSSuT is not uncommon in Paratyphi B var. Java; it is rare in paratyphoidal *Salmonella* serotypes. Further studies are needed to determine the sources of Paratyphi B var. Java, particularly ACSSuT strains. Monitoring of resistance needs to continue to inform public health and clinical guidelines.

Board 82. First *E. coli* Isolate Resistant to Amikacin and Nine Other Antimicrobial Subclasses, NARMS, 2004-2006

A. L. Krueger;

Oak Ridge Institute for Science and Education, Oak Ridge, TN.

Background: *Escherichia coli* is a common cause of gastrointestinal symptoms, urinary tract infections (UTI) and sepsis. It is part of the normal human intestinal flora and an important reservoir of resistance genes for pathogenic bacteria. Antimicrobial resistance complicates treatment options. A study in a U.K. hospital found that 4.3% of *E. coli* isolated from urine were resistant to amikacin. Amikacin resistance has rarely been reported in the U.S. **Methods:** From 2004-2006, Maryland and Michigan cultured 10 human stool samples monthly for generic *E. coli* from outpatients or healthy adult volunteers. Outpatients had not been hospitalized or nursing home residents in the six months before stool collection. *E. coli* isolates were sent to the National Antimicrobial Resistance Monitoring System (NARMS) at CDC for susceptibility testing to 15 agents, representing 10 Clinical and Laboratory Standards Institute (CLSI) antimicrobial subclasses. Minimum inhibitory concentrations (MICs) were determined by broth microdilution (Sensititre) and interpreted using CLSI criteria when available. For isolates that grew in all amikacin dilutions on the Sensititre panel (MIC >4 µg/mL), E-test was done to determine amikacin MIC. **Results:** Of 511 *E. coli* isolates, one isolate was resistant to amikacin, other aminoglycosides (gentamicin, kanamycin, and streptomycin), and nine other CLSI antimicrobial subclasses: aminopenicillin (ampicillin), β-lactam/β-lactamase inhibitor combination (amoxicillin-clavulanic acid), cephalosporin (ceftiofur), phenicol (chloramphenicol), quinolone (ciprofloxacin, nalidixic acid), folate pathway inhibitor (trimethoprim-sulfamethoxazole), sulfonamide (sulfizoxazole), cephamycin (cefoxitin), and tetracycline. This isolate was collected in 2004 from a 50-year-old woman in Michigan who denied antimicrobial use, history of travel or contact with farm animals in the 6 months before stool collection. **Conclusion:** The Michigan isolate is the first amikacin-resistant *E. coli* isolate reported in NARMS. It is also the first *E. coli* isolate identified by NARMS as resistant to all 10 antimicrobial subclasses. Because *E. coli* is an important reservoir of resistance for pathogenic bacteria, monitoring resistance will be important when developing future treatment guidelines.

Board 83. Critical or Fatal Illness Due to Community-associated *Staphylococcus aureus* (CA-SA) Infection, Minnesota (MN), 2005-2007

L. Lesher[1], J. Buck[1], J. Bartkus[1], S. Jawahir[1], D. Boxrud[1], K. Harriman[2], R. Lynfield[1];

[1]Minnesota Department of Health, Saint Paul, MN, [2]California Department of Public Health, Richmond, CA.

Background: CA-SA infections have been associated with critical illness and death. **Methods**: Reporting for rapidly fatal or critical illness due to CA-SA infection, including isolate collection, was instituted statewide in MN in 2005. Cases were defined as previously healthy people who had fatal illness or ICU admission and no healthcare-associated (HA) MRSA risk factors per CDC definition, excluding hospitalization for birth. Isolates were characterized by pulsed-field gel electrophoresis (PFGE) and PCR for toxic shock syndrome toxin 1 (TSST1), Panton-Valentine leukocidin (PVL), and staphylococcal enterotoxin (SE) genes A, B, C, D. **Results**: 32 cases were reported January 2005 through October 2007; 21 (66%) methicillin-resistant SA (MRSA) and 11 (34%) methicillin-susceptible SA (MSSA) cases. 14 (67%) MRSA cases were male; median age, 17 years (12 days-88 years), and 5 (45%) MSSA cases were male; median age, 18 years (1 day-59 years).

Two cases had multifocal infections; MRSA with pneumonia and septic arthritis; MSSA with meningitis, lumbar wound, pneumonia (fatal). Of MRSA cases, 11 (52%) had pneumonia (3 fatal), 5 (24%) had skin infections (4 bacteremic - 1 fatal; 1 necrotizing fasciitis - fatal), 2 (9%) had sepsis (1 fatal), 1 (5%) had meningitis, 1 (5%) had osteomyelitis. Of MSSA cases, 4 (36%) had pneumonia (2 fatal), 2 (18%) had skin infections with bacteremia, 2 (18%) had TSS, 1 (9%) had meningitis (fatal), 1 (9%) had sepsis. The median age of fatal cases was 58 years for MRSA, 27 years for MSSA. PFGE typing and toxin PCR were performed on 17 MRSA and 7 MSSA isolates. All MRSA isolates belonged to clonal groups associated with CAMRSA; USA300 (15), USA400 (1), USA1000 (1). MSSA isolates were found in groups associated with CA and HAMRSA; USA200 (1), USA400 (1), USA600 (2), USA700 (1), USA1000 (2). Among MRSA, toxin PCR found PVL in 14 USA300 isolates (2 fatal) and 1 USA400 (fatal), which also had SEA and SEC. Among MSSA, SEB was found in 1 USA1000 isolate (fatal) and TSST1 in 1 USA200 (clinical TSS), and 2 MSSA isolates from fatal cases were negative for all toxins tested. **Conclusions**: Most critical/fatal CA-SA reported cases were MRSA. A high fatality rate was observed in cases with meningitis or pneumonia. Fatal MRSA cases were older than MSSA cases. Most isolates contained toxins previously implicated in severe disease.

Emerging Aspects of HIV

Monday, March 17
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 84. An Analysis of Histoplasmosis in an Endemic, Resource Poor Area with a High HIV Prevalence Rate _ Guatemala, 2007

R. Miramontes[1], B. Samayoa[2], A. Herrera[2], C. Scheel[1], B. Gomez[1], E. Arathoon[2], T. Chiller[1];

[1]CDC, Atlanta, GA, [2]CFLAG, Guatemala City, GUATEMALA.

Background: Disseminated histoplasmosis is an important opportunistic infection in AIDS, often representing the first manifestation of the syndrome in endemic regions. Central America is known to be highly endemic for histoplasmosis, however little is known about the true prevalence of infections in persons with AIDS. In Guatemala, lack of appropriate medication, extended travel to health care facilities and the unavailability of rapid diagnostics pose significant barriers to patient treatment. **Methods:** A prospective cohort study of hospital patients was conducted from February 2005 through October 2007 in a large public hospital in Guatemala City. Study criteria required that a patient be HIV-infected and have three out of five of the following: fever, pancytopenia, weight loss, radiological evidence consistent with histoplasmosis, or skin/mucosal lesions suspicious for histoplasmosis. A histoplasmosis case was defined as either a positive *Histoplasma capsulatum* culture from a clinical specimen or a seroconversion of an immunodiffusion assay from negative to positive and/or a four-fold rise in complement fixation titer. **Results:** Of the 250 patients that met surveillance criteria, 181 (72%) were enrolled in the study. A total of 53 (29%) of 181 patients met the case definition for histoplasmosis. There were 19 (36%) deaths among the 53 case patients. The median time to death was 13 days. A total of 10 (19%) case patients were co-infected with tuberculosis and 3 of those were among the reported deaths. The mean CD4 cell count among case patients on the date of diagnoses was 55 (sd = 77.21). **Conclusion:** There is a high incidence of histoplasmosis in this cohort of Guatemalan HIV patients and medical care is complicated by the lack of availability of a rapid diagnostic test. Mortality occurred rapidly after admission in more than one third of these patients, emphasizing the need for rapid diagnostics in this population. This study highlights the importance of histoplasmosis as an opportunistic infection in persons with AIDS in Guatemala. Further study is required to better define the incidence and burden of this disease in patients with HIV, especially those patients co-infected with TB, in order to provide guidance for better diagnosis and more rapid treatment.

Board 85. Handbook of Diagnosis, Treatment and Follow-up Recommendations for *Trypanosoma cruzi*-HIV Co-infection

S. O. Santos[1], E. Tatto[1], A. N. Ramos Jr.[2], M. F. Simao[3], M. A. Shikanai-Yasuda4[4], G. F. Pereira[1];

[1]Secretariat of Health Surveillance (SVS), Ministry of Health, Brasilia, BRAZIL, [2]Federal University of Ceará, Fortaleza, BRAZIL, [3]Federal University of Uberlândia, Uberlandia, BRAZIL, [4]University of Sao Paulo, Sao Paulo, BRAZIL.

Background: Chagas Disease Reactivation (CDR) is considered an AIDS-defining condition in Brazil since January, 2004. The frequency of reactivation is not completely known; about 120 cases of CDR were reported still 2004, manifesting as meningoencephalitis or myocarditis; few publications exist.. In 2005, a work group was created to establish criteria of CDR definition, constitute a national network for studies of *Trypanosoma cruzi*-HIV co-infection, and create a technical handbook, with the objective of providing clinical guidance for diagnosis and treatment of co-infected patients. **Methods:** The Secretariat of Health Surveillance of the Ministry of Health of Brazil (SHS/MoH), by means of the National Programs of Sexually Trasmited Diseases/Aids and Control of Chagas Disease, conducted a subject-matter-expert meeting on *T. cruzi*-HIV co-infection which created subsequently published the handbook of clinical diagnosis and treatment. **Results:** The Handbook of Diagnosis, Treatment and Follow-up Recommendations for *T. cruzi*-Human Immunodeficiency Virus Co-infecction, emphasizes the principal clinical manifestations, laboratory diagnostic testing, and treatment and follow-up of co-infection and reactivation cases. For epidemiologic surveillance, the following case definition was established for CDr: In an immunosuppressed patient, the presence of *T. cruzi* tripomastigotic forms observed by direct microscopic examination of body fluids (blood or pericardic, peritoneal, cephalorrachidian fluids, etc), or occurrence of compatible histopathologic manifestations with acute inflammatory processes and presence of nests of amastigotes. **Conclusions:** Medical professionals are unfamiliar with the diagnosis and treatment of Chagas Disease reactivation (CDr) in HIV-infected persons, an AIDS-defining condition. Dissemination of a standardized manual with clinical guidelines and case-reporting instructions may improve diagnosis and public health surveillance.

Board 86. Comparison of Survival after AIDS in pre-HAART and HAART Eras Confirms High Population Effectiveness of Antiretroviral Treatment in Poland

M. Rosinska, A. Zielinski;

National Institute of Public Health - National Institute of Hygiene, Warsaw, POLAND.

Background: Poland and other Central European countries are relatively little affected by HIV epidemic with estimated prevalence of 0.5%. Antiretroviral treatment (ART) is available for HIV infected free of charge through a governmental program. However, in the HAART era Poland is still experiencing increasing AIDS incidence. The aim of the study was to explore survival after AIDS as a measure of population effectiveness of ART program in Poland. AIDS cases as opposed to newly diagnosed infections were selected to compare groups with similar initial risk of death in the HAART and pre-HAART eras. **Methods**: The study used surveillance data

collected between 1986 and 2006, including reports of new AIDS diagnoses (first AIDS defining condition) and deaths of AIDS cases. The system is name based and allows linkage of reports at central level. The survival was estimated by Kaplan-Maier method allowing for delayed entry and compared with Cox models. Cases diagnosed with AIDS until 31.12.2005 were included. End of observation was defined as the date of death or 31.12.2006. HAART was considered to be available after end of June 1996 and no individual level data on treatment were used. **Results**: In total we analyzed 1,695 cases, of which 326 were females (19.2%). 410 persons (24.2%) were diagnosed with AIDS prior to July 1996. The probable transmission route was most commonly injecting drugs (900, 53.1%) followed by sex between men (356, 21.0%) and sex between man and woman (298, 17.6%). It was unknown for 141 cases (8.3%). 675 cases (39.8%) were diagnosed with HIV within 6 months of first AIDS event. Risk reduction in the HAART era among injecting drug users was 10.3% during the first 6 months, 23.5% during 6-12 months and 67.2% for over 12 months after AIDS diagnosis. The respective numbers for cases infected by sexual contact were: 48.8%, 67.5% and 85.0%. **Conclusions**: Routinely collected data are useful for monitoring ART program and demonstrate overall dramatic death risk reduction in the era of HAART. Patients with severe HIV disease continue to be at high risk of dying shortly after experiencing first AIDS event. All effort should be put to limit delayed treatment entry. Short term prognosis was worse among injecting drug users, which requires further investigation.

Foodborne & Waterborne Infections

Monday, March 17
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 87. Foodborne Disease Outbreak Trends, and Sources and Timeliness of Detection in Connecticut, 2004-2007

D. Mlynarski, Q. Phan, T. Rabatsky-Ehr, K. Purviance, J. Brockmeyer, J. Krasnitski, A. Nepaul, L. LoBianco, K. Frenette, P. Mshar, J. L. Hadler;

Connecticut Department of Public Health, Hartford, CT.

Background: It is critical to public health preparedness (PHP) to understand the epidemiology of outbreaks, and means and timeliness of their detection. In Connecticut (CT), foodborne disease outbreaks (FOs) are considered public health emergencies reportable by telephone to state and local public health authorities. We examined 3.5 years of FO surveillance in CT as part of a broader effort at enhancing PHP-related surveillance. **Methods:** CT data reported to CDC by the electronic Foodborne Outbreak Reporting System was reviewed for January 2004-June 2007. The number, causative agents, settings and food vehicles implicated were examined. Methods of detection were summarized; median time delay from first illness onset to public health notification was calculated. **Results:** From 1/1/04-6/30/07, 58 FOs were reported. The number increased annually from 13 to 19 between 2004 and 2006 with 10 FOs in the first 6 months of 2007. Causative agents included norovirus (62%), bacterial pathogens (28%), toxins (3%) and parasites (2%). The increase from 2004 to 2006 was mainly due to norovirus (7 to 12). Overall, 64% of FOs were associated with contamination or mishandling of food at food service establishments and 19% with widely distributed contaminated food items. Private citizens reported 62% (median 3-day delay) and clinicians reported 12% (median 1-day delay) of FOs. Public health surveillance, including routine Pulsed Field Gel Electrophoresis (PFGE) of selected bacterial pathogens, detected 21% (median 26-day delay). Most (71%) PFGE-identified outbreaks were associated with widely distributed food items. **Conclusions:** Reported FOs have been increasing, in part driven by an increase in those due to norovirus. Astute citizens and clinicians are the most important sources of rapid detection and reporting. Clinicians have a responsibility to report suspected outbreaks and assist in their detection by ordering appropriate diagnostic testing on persons with acute gastrointestinal illness. Active public health surveillance, including routine PFGE typing, is important to detection of outbreaks caused by widely distributed contaminated food items; however, it is not very timely. Efforts are needed to improve timeliness of detection of outbreaks, particularly those using molecular subtyping methods such as PFGE.

Board 88. Indiana Outbreak of *Salmonella* I 4,[5], 12:i:- monophasic at a Supermarket Deli – 2006

L. Granzow[1], S. Gorsuch[1], B. Swearingen[2];

[1]Indiana State Department of Health, Indpls, IN, [2]Johnson County Health Department, Greenwood, IN.

Background: On July 11, 2006, the Indiana State Department of Health (ISDH) initiated an investigation in response to an increase in salmonellosis in two adjacent counties. Geographic information system (GIS) mapping confirmed the clustering of cases at the respective north-south borders of the two counties. The most common exposure (76.2%) among cases was a supermarket (SM) location, with 78.9% of cases having purchased items from the deli. Pulse-field gel electrophoresis (PFGE) confirmed 199 cases in a 2-enzyme matched outbreak of *Salmonella* I 4,[5],12:i:- monophasic, an emerging serotype. The PFGE pattern was unique during the outbreak period on the national PulseNet database with a rare Bln I pattern (0.35%). The multiple-locus variable-number tandem repeat analysis (MLVA) pattern was also unique (N of I 4,[5],12:i:- database = 450). The outbreak ended after a near 4-month period, including 15 counties and 2 out-of state residents. A knife block at the SM was a 2-enzyme match for the outbreak strain. **Methods:** The ISDH conducted a case-control study (1:1, N=32), matched by zip code, using a reverse digit dialing system. The study case definition included those with onset dates in July and met the clinical definition of salmonellosis. The Fisher's exact test (SAS 9.1) was used to evaluate the association between illness and exposure. **Results:** Of the five supermarkets reported, a statistically significant relationship ($\alpha = 0.05$) was found between illness and shopping at the SM deli (OR=21.21, $p<0.0001$). No food categories or items were significant. An environmental sample from a knife block located in the deli/bakery area was a 2-enzyme match for the for *Salmonella* I 4,[5],12:i:- monophasic. All food samples provided by cases tested negative. **Conclusions:** The outbreak ceased shortly after the removal of the knife block from the SM deli. Raw chicken, cooked on the rotisserie, was the only raw food item in the deli. The likely mode of transmission was environmental cross-contamination; the knife block was likely originally contaminated by a knife used to open bagged raw chicken. Knives housed in the contaminated knife block were then used to open packages of ready-to-eat foods, contaminating a small surface area.

Board 89. Enhanced Laboratory Testing of Enteric Disease Outbreaks of Unknown Etiology in Minnesota

C. Fuller, E. Cebelinski, J. Bartkus, B. Juni, K. Smith, J. Besser;

Minnesota Department of Health, St. Paul, MN.

Background In 2004, the Minnesota (MN) Department of Health received funds from CDC to conduct enhanced laboratory testing to better describe causes of enteric illness, and a variety

of novel tests were implemented. The resulting expanded testing panel included tests for known and possible bacterial, viral, and parasitic pathogens. The panel was used in an attempt to establish etiologies of enteric disease outbreaks in MN that initially tested negative for standard bacterial pathogens and norovirus. **Methods** Enteric disease outbreaks in MN during 2002-2006 for which an etiology was not laboratory confirmed, and stool samples were still available (n=16), were tested using enhanced methods. Rotavirus, sapovirus, and astrovirus testing used conventional RT-PCR. Norovirus testing used a real time RT-PCR; primers and probes detected genogroups I, II and IV. *Listeria monocytogenes* testing used *Listeria* Enrichment Broth, Oxford Medium, and PALCAM Agar. If there were no positive results for an outbreak after all tests were completed, pathogen discovery methods were used. This included sequencing of unusual banding patterns on RT-PCR products. **Results** Positive findings were obtained for 8 (50%) outbreaks of unknown etiology. These included an outbreak of febrile gastroenteritis due to *L. monocytogenes* associated with a restaurant; three sapovirus outbreaks in nursing homes; one sapovirus outbreak in an elementary school; one norovirus outbreak associated with a family gathering; one daycare outbreak which included astrovirus, rotavirus, and norovirus positive results; and the first ever detected Saffold virus (*Picornaviridae*, genus *Cardiovirus*) outbreak, which was associated with a family gathering (route of transmission unknown). **Conclusions** Enhanced testing explained the etiology of half of enteric disease outbreaks of unknown etiology for which samples were available. Pathogens that are not tested for in traditional laboratory settings may be significant contributors to enteric disease. Outbreaks represent a critical opportunity to identify new or unusual causes of enteric disease. Public health laboratories should retain stool samples from all outbreaks until an etiology has been established and pursue enhanced testing when standard methods fail to identify a probable causative agent.

Board 90. Trends in incidence of frequently identified non-typhoidal *Salmonella* serotypes, Foodborne Diseases Active Surveillance Network 1996-2006

C. Long[1], P. Cieslak[2], D. Vugia[3], C. Medus[4], C. Lyons[5], D. Aragon[6], S. Solghern[7], K. Larson[8], O. Henao[9];

[1]CDC/VA Medical Center, Atlanta, GA, [2]OR Public Health Division, Portland, OR, [3]CA Dept of Public Health, Richmond, CA, [4]MN Dept of Health, St. Paul, MN, [5]CT EIP, New Haven, CT, [6]CO Dept of Public Health and Environment, Denver, CO, [7]EIP NY State Health Dept, Albany, NY, [8]MD Dept of Health and Mental Hygiene, Baltimore, MD, [9]CDC, Atlanta, GA.

Background: The Foodborne Diseases Active Surveillance Network (FoodNet) continues to report little change in the overall incidence of laboratory-confirmed *Salmonella* infections since 1996. However, trends differ markedly by serotype. **Methods**: We examined population-based active surveillance data from FoodNet to determine the incidence of laboratory-confirmed infections due to the 20 most commonly identified non-typhoidal *Salmonella* serotypes by year, sex, race, age, state, hospitalization, and outcome status. A negative binomial model was used to estimate changes in incidence. **Results**: From 1996 to 2006, FoodNet ascertained 52,659 cases of salmonellosis; 47,524 (90%) were fully serotyped and 20 serotypes accounted for 83% of cases. Comparing 2006 with a 1996-1998 baseline period, a significant decrease in incidence was seen only for *S.* Typhimurium (-41%). Significant increases were seen for serotypes Paratyphi B var. L(+) tartrate+ (203%), I 4,[5],12:i:- (114%; using a baseline period of 2002), Javiana (95%), Stanley (61%), Newport (44%), and Enteritidis (27%). Infection by serotypes Typhimurium, Javiana, and I 4,[5],12:i:-, occurred most frequently in children ≤5 years of age. In contrast, 66% of *S.* Enteriditis infections were among persons ≥20 years of age. The age distributions for *S.* Newport, *S.* Paratyphi B var. L(+) tartrate+, and *S.* Stanley infections were bimodal with peaks in persons ≤5 and 20-49 years of age. There were no differences in sex or race distribution by serotype. The percent of *Salmonella* infections with known hospitalization ranged from 16% for *S.* Agona to 28% for *S.* Poona. Overall, the case fatality rate was 4.7 deaths/1,000 *Salmonella* infections with the highest rate for *S.* Agona (8.2). **Conclusion**: Patterns in the incidence of *Salmonella* infections vary widely by serotype with decreases in *S.* Typhimurium being obscured by increases in other serotypes. Understanding the epidemiology of *Salmonella* infections by serotype is imperative to guide efforts to reduce the incidence of *Salmonella* infections.

Board 91. Estimating Under-reporting of Foodborne Diseases to Australian Surveillance to Estimate Community Incidence

G. V. Hall[1], K. Yohannes[2], J. Raupach[3], N. Becker[1], M. Kirk[2];

[1]Australian National University, ACT, AUSTRALIA, [2]Department of Health and Ageing, ACT, AUSTRALIA, [3]Department of Health, South Australia, AUSTRALIA.

Background: It is recognised that surveillance data do not capture all disease and represent only a fraction of that actually occurring in the community. While this may not be essential in order to detect outbreaks and to monitor changes over time, knowledge of the absolute number of cases in the community is be extremely useful for prioritising public health policy and for estimating the cost of illness. **Methods**: The under-reporting of salmonellosis, campylobacteriosis and Shiga Toxin producing *Escherichia coli* (STEC) to national surveillance in Australia were estimated using data from a gastroenteritis survey and other sources. Multipliers to estimate community incidence from national laboratory data were derived from the component probabilities for a case visiting a doctor, having a stool test, sensitivity of the test and reporting to surveillance. Compared with mild gastroenteritis, under-reporting was lower for cases with bloody diarrhoea and long duration. Under-reporting factors were estimated for different severities of gastroenteritis and appropriate factors were applied according to the pathogen average severity of illness. Precision of estimates was quantified using simulation techniques to construct 95% Credible Intervals (CrI). **Results**: The under-reporting factor for salmonellosis was estimated at 7(95%CrI 4,16), campylobacteriosis at 10(95%CrI 6,22) and STEC at 8(95%CrI 3,75). Australian community incidence rates per 100,000 population were 257 (95%CrI 79,480), 1173(95%CrI 493,1909) and 20(95%CrI 5,174) respectively. **Conclusions**: There is a high burden of these diseases in the community. Estimation of under-reporting improves public health practice through assessment of the true burden of diseases and better understanding of public health surveillance. Assessment of precision of estimates is also important in order for policy makers to make informed decisions.

Board 92. The Prevalence of Reactive Arthritis Symptoms in the General Population, FoodNet Population Survey, 2006-2007

J. Ou[1], L. B. Moyer[2], K. Smith[3], J. Townes[4], K. L. Ong[2], O. Henao[5];

[1]Foege Fellowship Emory University, Atlanta, GA, [2]CDC and VA Medical Center, Atlanta, GA, [3]MN Dept of Health, St Paul, MN, [4]Oregon Health and Science University, Portland, OR, [5]CDC, Atlanta, GA.

Background: A prospective cohort study conducted in 2002-2005 by the Foodborne Diseases Active Surveillance Network (FoodNet) found that, in the 4-8 weeks following their illness, 13% of persons with culture-confirmed *Campylobacter*, *E. coli* O157, *Salmonella*, *Shigella*, and *Yersinia* infections developed one or more symptoms that are also reported by persons with reactive arthritis. The prevalence of reactive arthritis symptoms in the general population is unknown. We used the FoodNet population survey to

ascertain the prevalence of reactive arthritis symptoms among the general population of FoodNet sites. **Methods:** FoodNet conducted a 12-month population-based telephone survey in 10 states during 2006-2007 to collect demographic, behavior, and health information including symptoms compatible with reactive arthritis (joint pain, heel pain, joint swelling/redness, morning joint stiffness, or low back pain). A respondent was classified as having suspect arthritis if he/she reported developing new onset of ≥1 of the above symptoms in the previous 6 weeks which lasted ≥3 days. Respondents with symptoms associated with injury or trauma were excluded. **Results:** Of 17,088 interviews, 13,449 had complete information and were eligible for inclusion in the analysis. The weighted prevalence of persons reporting ≥1 newly acquired arthritis symptom was 16.8% (95% CI 15.6-18.1), and 5.7% reported ≥2 symptoms. The proportion reporting arthritis symptoms was highest among persons ≥65 years old at 23.6%. Among all respondents, the most common symptom reported was low back pain (12.1%), followed by joint pain or discomfort (5.7%), morning joint stiffness lasting >1 hour (3.7%), heel pain (2.1%), and joint swelling or redness (1.9%). **Conclusion:** The FoodNet population survey indicates that the proportion of persons who reported developing reactive arthritis symptoms following bacterial enteric infections is not greater than the background prevalence of arthritis symptoms in the general population. More studies are needed to distinguish those persons who develop reactive arthritis, and the proportion of persons with arthritis whose symptoms can be attributed to bacterial enteric infection.

Board 93. Foodborne Disease Outbreaks in the State of São Paulo, Brazil, 1999-2007

M. B. Eduardo[1], S. Fernandes[2], E. M. Katsuya[1], N. P. Bassit[1], A. T. Tavechio[2], A. C. Guilardi[2], T. M. Vaz[2];

[1]SP Center for Epidemiologic Surveillance, São Paulo, BRAZIL, [2]Adolfo Lutz Institute, São Paulo, BRAZIL.

Background: Foodborne disease outbreaks are identified through three surveillance subsystems coordinated by the Center for Epidemiologic Surveillance (CVE) in the State of São Paulo: diarrhea surveillance, outbreaks surveillance based on passive reported, and laboratory-based active surveillance, including the purposes of WHO Global Salmonella Surveillance project, implanted since 2006. We summarize the characteristics of foodborne outbreaks occurred in the State of São Paulo, from 1999 to 2007. **Methods:** We reviewed foodborne outbreaks reported to CVE from 1999 to August 2007 to determine trends in the burden of disease attributable to pathogens groups and contributions of the surveillance subsystems to identify outbreaks and intervention measures. **Results:** A total of 2,192 of foodborne outbreaks were identified in this period with 69,224 cases (median number of cases per outbreak = 7; range = 1-2,775), including botulism events (0.3%), hepatitis A (12.2%) and diarrhea outbreaks (87.5%). Among the diarrhea outbreaks with identified etiology, 24% were caused by bacterial pathogens, 10% by virus and 3.6% by parasites. Most bacterial diarrhea outbreaks were caused by *Salmonella* (42.5%). *Salmonella* Enteritidis were the principal serotype (>70%), associated with consumption of dishes with raw or undercooked eggs, prepared in restaurants and other commercial establishments (34%). The median number of *Salmonella* cases per outbreak was 11 (range = 2-1,020 cases). Comparisons of *Salmonella* outbreaks data obtained from passive surveillance with data from laboratory-based active surveillance, in 2006, showed that 60% of *Salmonella* outbreaks were identified or elucidated through laboratory-based active surveillance. **Conclusions:** Among diarrhea outbreaks *Salmonella* remains as an important public health problem, due to the consumption of raw or undercooked eggs. Despite of the sanitary control on farm, the *Salmonella* trend indicates the need to introduce specific sanitary regulation with orientation to the consumers, in the label/packaging of eggs and poultry. The laboratory-based active surveillance has showed an important tool for enhancing foodborne disease surveillance and outbreak response.

Board 94. Rural Exposure to Shiga Toxin-Producing *E. coli* _ South Dakota, 1998-2007

N. S. Chappelle[1], N. Tarkhashvili[2], N. Hill[1], L. Schaefer[1], L. Kightlinger[1];

[1]South Dakota Department of Health, Pierre, SD, [2]Center for Disease Control and Prevention, Pierre, SD.

Background: *Escherichia coli* O157:H7 causes an estimated 70,000 infections annually in the United States and can result in bloody diarrhea, hemolytic uremic syndrome (HUS), and death. South Dakota has the highest reported rate of Shiga toxin-producing *E. coli* in the US averaging 5.2/100,000 population per year (annual national average 1.2/100,000 population 1998-2005). We describe characteristics of South Dakota's Shiga toxin-producing *E. coli* cases reported during 1998-2007. **Methods:** We abstracted demographic, clinical, and exposure data from investigation records gathered at the time of disease during 1998-2007 and archived at the South Dakota Department of Health (SD DOH). **Results:** A total of 432 cases was reported to SD DOH. *E. coli* serotype O157:H7 was identified in 91% of cases, O111 was the primary other serotype identified. Of all cases, 55% were female and 48% were children ≤10 years old, median age was 11 (range 0-97 years). Outbreak-associated cases were 26% of cases, and 50% were hospitalized. Bloody diarrhea was reported in 81% of cases and 10% developed HUS. The case-fatality rate of patients infected with laboratory-confirmed Shiga toxin-producing *E. coli* was 0.7%. Exposure to animals was reported in 53% of cases and 35% reported visiting locations with animals. Direct exposure to cattle was reported in 34% of cases, with direct exposure to animal dung reported in 29% of cases, and 61% of cases lived in rural counties where beef cattle or dairy production is common. Yet, 63% of urban cases reported recent exposure to cattle. Overall, 85% of cases either lived in rural counties or reported recent exposure to cattle. **Conclusions:** Our data are consistent with previously reported rates of non-O157 serotypes, case-fatality, and HUS. Exposure to animals, particularly cattle, emerged as the most often reported risk. This differs from predominantly urban states, where exposure to contaminated food is more common. Agricultural data showing that South Dakota has the highest cattle per person ratio in the nation: 4.8 (national average 0.33) support our results. Understanding these variables is important for devising prevention strategies related to cattle-to-human transmission in rural agricultural states.

Board 95. Tomato Handling Policies and Practices in Restaurants

E. G. Kirkland, V. J. Radke, C. A. Selman; CDC, EHS-Net, Atlanta, GA.

Background: Recently, several foodborne illness outbreaks have been associated with tomatoes served in restaurants. Prevention of foodborne illness outbreaks requires proper food storage and preparation practices; these tomato outbreaks suggest that tomatoes are being stored and prepared improperly in restaurants. Yet relatively little data exists on tomato storage and preparation policies and practices in restaurants. Thus, the purpose of this study is to gain a better understanding of how tomatoes are stored and prepared in restaurants. **Methods:** Data were collected in 450 restaurants through interviews with restaurant managers and observations of tomato storage, washing and cutting in restaurant kitchen environments. This study was conducted by the Environmental Health Specialists Network (EHS-Net). EHS-Net is a collaboration involving the Centers for Disease Control and Prevention (CDC), the U.S. Food and Drug Administration (FDA), and nine Emerging Infections Program sites (California, Connecticut, Georgia, Iowa, Minnesota, New York, Rhode Island and Tennessee); these partners have come

together in an effort to better understand the environmental causes of foodborne illness. **Results:** The median temperature of prepared tomatoes in storage and holding was 44°F degrees; the median temperature of cut tomatoes in storage and holding was 43°F degrees. In 94% of restaurants, managers reported that tomatoes were washed; in 83% of washing observations, tomatoes were rinsed or held under running water and in 18% of washing observations, tomatoes were soaked or immersed in water. Produce-only cutting boards were used in 51% of tomato-cutting observations, and gloves were used in 64% of observations. **Conclusions:** Some good tomato handling practices were observed. For example, most restaurants reported washing their tomatoes, and gloves were used in the majority of tomato-cutting observations. However, some practices did not meet FDA recommendations for preventing pathogen contamination and proliferation on tomatoes- cut tomatoes were stored above 41 degrees, tomatoes were washed by soaking in water rather than by placing under running water, and produce only cutting boards were not always used. These data indicate that education concerning safe tomato handling practices is needed in restaurants.

Board 96. A Study on The Statue of Diarrhea and Contaminant Seafood Caused by Norovirus in China

R. Li[1], S. Song[2], M. Cheng[1], W. Tan[2], X. Zhang[3], Y. Song[1], Y. Sun[3];

[1]cdc, Beijing, China, [2]yuhang District Cdc, Hangzhou, China, [3]yuhang District Cdc, Beijing, China.

Background A sensitive method and a perfect diarrhea and food surveillance system for the NoV have not been developed in China, so the morbidity of diarrhea, the contaminated food statue and economic burden caused by NoV have not cleared in China. **Methods** Developing detection method of real time PCR, its sensitivity and specificity were compared with the method provided by Japan NIH. 12 monitoring sites have been establish respectively in both bank of the upstream, midstream and downstream of the Yellow River, the Yangtze River and the Zhujiang River. All the sites collect diarrhea specimens but the downstream 6 sites also for oyster in vary seasons **Results** The detection limit of the method we developed was 100 copies per reaction mixture, which was 100 times more sensitive than general PCR. Compare with the method Japan NIH offered, the accordance rate is 100%. About 24.4% (GGII23.8%,GGI0.6%) of fetal specimens from the 12 monitoring sites in 2006 were associated with NoV, and vary in seasons and areas, no combined infection has been detected. The contaminated rate of GGII, GGI and GGII/GGI combined in oyster respectively is 27.9%, 21.8% and 12.7%. Contaminated rate are involved with oyster types and detection rate of fecal specimens, but independent of seasons and areas at the identical monitoring sites significantly. Sequencing analysis results are consistence with the real-time RT-PCR results. **Conclusions** The real-time RT-PCR successfully detected NoV RNA in fetal samples and food samples containing low concentrations. 12 human diarrhea and 6 oyster surveillance sites along the both bank of 3 rivers for studying NoV will provide a reference for the Molecular epidemiological characters and the trends /rules of NoV-caused diarrhea.

Health Communication

Monday, March 17
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 97. Community-Based Surveillance Models for Avian Influenza

B. Moore, **W. Pyles**;

CARE USA, Atlanta, GA.

Background:CARE and the Food and Agriculture Organization (FAO) currently implement models of community based surveillance (CBS) for avian influenza (AI) in Northern and Southern Vietnam. Though different, both aim to strengthen AI surveillance and community rapid response capabilities. CARE's model trains community leaders and mobilizes volunteer networks to detect and respond to suspected cases, while FAO uses informant interviews and rumor surveillance to improve current passive surveillance. **Methods:** A joint evaluation is planned to assess strengths and weaknesses of each model and propose a more sustainable and scalable joint design. The evaluation will include two CARE intervention villages paired with two FAO sites and two non-intervention villages. Working with national counterparts, the evaluation will employ evidence-based research targeting those involved in CBS - village and animal health workers, pharmacists, private providers, village leaders, and government staff. The evaluation will examine the impact of active surveillance, drills, community outreach and strengthened infrastructure on preventing, reporting, and detecting AI. Assessments of knowledge, attitudes and practices of households, market sellers, poultry farmers, restaurateurs and pharmacists will be evaluated. Methods will include FAO designed performance indicators, observation, semi-structured interviews, focus groups, and SWOT analyses. **Results:** In a CARE intervention area, community members successfully identified and reported three outbreaks of confirmed H5N1in poultry, immediately banning poultry movement, and mobilizing surveillance and communications systems. CBS may improve timeliness of reports and local response. Other preliminary findings indicate that intensive volunteer surveillance networks may be difficult to sustain. Intensive surveillance only at high-risk times may be more effective. Communities often expand the scope of these networks in low-risk seasons. **Conclusion:** Technical input from FAO's model paired with CARE's community mobilization experience may yield a more sustainable approach, such as launching a trained community surveillance network during a potential outbreak identified through rumor surveillance.

Partners

Food and Agriculture Organization
CIRAD

Board 98. Asymptomatic Carriers of Typhoid Fever and Patient Care

V. Berisha, S. Wright;

MCD Public Health, Phoenix, AZ.

Background: In March, 2006, the Maricopa County Department of Public Health (MCDPH) received a report on a 2 year-old girl diagnosed with typhoid fever. She was hospitalized with symptoms of fever, abdominal pain, and a known diagnosis of sickle cell anemia. **Methods:** An investigation was initiated immediately by the MCDPH staff. The little girl was born in the

US, had no recent travel, no recent overseas visitors, however her parents had emigrated from a foreign country several years ago. Interviews with family members were conducted (grandmother, father, mother, 3 siblings) and stool specimens were collected from family members. **Results:** Through laboratory testing, it was determined that the mother and 8 year sibling were asymptomatic carriers of the disease. The pulsed field gel electrophoresis (PFGE) results for the mother matched those of the two year-old. A national database search showed no Salmonella typhi isolates that matched these two cases in US. **Conclusions:** The mother was involved in direct patient care at a long term care facility and attended nursing school. Coordination and communication between MCDPH, the patient's physician, employer and school was needed to avoid patient contact in the workplace and assure proper treatment. The patient's employer and school were made aware of disease reporting requirements or procedures related to disease. As result of this collaboration, the individual was assigned other types of work, the nursing program allowed later enrollment without penalty, and the reporting system in these institutions was improved. All 3 patients cleared of the bacteria and returned to their work and school. Other family members were immunized.

Board 99. Public Health Situational Awareness and the Global Disease Surveillance Platform (or GDSP)

H. Greenspun;

Northrop Grumman, McLean, VA.

Background: Global public health threats (e.g., pandemic flu, bioterrorism, and emerging diseases) continue to grow. In order to mitigate the potential impacts of these threats, early health-related event characterization and identification, situational awareness, and the ability to translate these into timely, appropriate responses must be achieved. This is done through planning and improved cooperation between localities, regions, states and countries. **Methods:** The Northrop Grumman Global Disease Surveillance Platform (or GDSP) prototype was developed to provide health and public health organizations with access to critical decision-making information in a timely fashion. GDSP's processes can create a situational awareness that makes analysis, intervention, and response possible. Built to the specifications of the DHHS Biosurveillance use case, a national-level target pilot project demonstrated how a consolidated, common operating picture with a shared mental model of disparate information can improve preparedness and timely, coordinated response. **Results from Using GDSP:**

- Earlier identifying, detecting, notifying, monitoring, and evaluating responses to health-related events by integrating distributed electronic resources
- Predicting the rate, tracking the spread of a health-related event, and analyzing the potential risks
- Making unified, standardized information accessible to coordinators and responders to facilitate responsiveness
- Enabling all levels of the healthcare and public health infrastructure to make recommendations and quickly initiate a response to emergencies of national and global concern
- Improving bi-directional communication across all these levels

Conclusions: This presentation will focus on the complex requirements for situational awareness, the advanced processes and technologies developed to achieve it, and the use of information to respond to serious health threats. The presentation will allow the audience to understand the components of situational awareness, become aware of the tools being used in this field and ppreciate the complex relationships required for effective response

Board 100. Individual and Community Influences on Adherence to Directives in the Event of Plague Attack

R. J. Wray[1], N. Henderson[2], R. Tardif[3], E. Mitchell[4], E. Zielinski-Gutierrez[4], W. Pollard[4];

[1]Saint Louis University School of Public Health, St. Louis, MO, [2]University of Oklahoma, Oklahoma City, OK, [3]Oak Ridge Institute for Science and Education, Oak Ridge, TN, [4]Centers for Disease Control and Prevention, Atlanta, GA.

Background. During a public health emergency, public health officials will issue directives with actions people need to take to protect themselves. Past research has shown that adherence to these directives depends on individual beliefs and circumstances. This paper presents new research about the effects of community factors on adherence. Using a multi-level perspective in assessing factors related to adherence, this study expands the focus from individual to household and community factors. **Methods**. Qualitative household and key informant interviews were conducted and stratified by neighborhood characteristics to assess the effects of community factors. This study examined response to public health directives during a hypothetical intentional release of pneumonic plague in St. Louis, Missouri. **Results**. The paper presents findings for individual and community factors bearing on likelihood of adherence, barriers to adherence, communication needs, and preferred information sources. Our research suggests that most people will adhere to these directives, if they have adequate resources, know their family is safe, and are confident they understand the particulars of a directive, including an explanation for why it has been invoked, and how it will keep them safe. People living in disadvantaged neighborhoods may be less likely to have adequate resources and less able to ascertain family safety, and have less reason to be confident about a directive. Our research suggests that such differences may be explained by limited household income, but lackluster community resources and social distrust are also plausible explanations. **Conclusions**. We conclude with implications of the research for message and dissemination strategies and institutional response.

Influenza

Monday, March 17
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 101. Unique Results from Febrile Respiratory Illness Surveillance aboard U.S. Navy Ships

P. E. Kammerer, D. J. Faix, A. W. Hawksworth, M. Osuna, M. A. Irvine, C. A. Myers, D. Metzgar, K. L. Russell;

Naval Health Research Center, San Diego, CA.

Background: Deployed U.S. Navy personnel make port-stops throughout the world, including locations where emerging pathogens may arise. In 2002, the Naval Health Research Center (NHRC) initiated a laboratory-based shipboard febrile respiratory illness (FRI) surveillance program in the 3rd Fleet (San Diego, CA). This program was expanded to include 2nd Fleet (Norfolk, VA) and 7th Fleet (Yokosuka, Japan) ships in 2006. Influenza A was the primary etiologic agent identified from 2002 through 2006 in numerous clusters of FRI following port stops in diverse regions of the world, despite consistent vaccination of the crews. **Methods:** Specimens were collected from patients with FRI (fever ≥ 100.5° F, and sore throat or cough) and stored at -70°C. Specimens were tested with molecular techniques, viral and bacterial culture. **Results:** In 2007, *Mycoplasma pneumoniae* was identified in 25 of

45 FRI specimens collected aboard a single ship in an outbreak of lower respiratory illness during a Persian Gulf deployment. Also in 2007, another Naval ship collected specimens in several different ports during a deployment in the Pacific Ocean. Many of these samples subsequently tested positive for influenza A. Both H1 and H3 subtypes were found; H3 after a stop in Japan, and an H1 and two H1/H3 co-infections after a port-stop in Indonesia. **Conclusions:** The shipboard FRI surveillance program enables collection of viable respiratory pathogens, including influenza, from around the world. The first reported shipboard *Mycoplasma pneumoniae* outbreak was identified. The wide geographic exposure of shipboard personnel over a short time period raises the possibility of influenza co-infections and potential viral reassortments. Shipboard FRI surveillance identified currently circulating influenza strains in areas where new strains may emerge, and it identified H1/H3 human co-infection from these geographically distinct areas; such co-infections are rarely reported. This surveillance contributes to the identification of emerging pathogens, as well as to global influenza surveillance.

Board 102. Persistent Impairment of T Lymphocyte Subset Function in Severe Acute Respiratory Syndrome Patients 2 Years After Discharge

H. Luo, Z. Guo, X. Deng, J. He, S. Wang;

Fourth People's hospital of Taiyuan, Taiyuan, CHINA.

Background: Long-term affects on T lymphocyte subsets in patients who recovered from severe acute respiratory syndrome (SARS) have been unclear. **Methods**: In this study, we evaluated 100 survivors of SARS in our hospital at 2 years after discharge and 29 healthy blood donors (Control). The ratio of peripheral blood CD_3^+, CD_4^+ and CD_8^+ T lymphocytes, and leukocyte count and classification were detected using flow cytometer and whole-automatic cytoanalyze, respectively. **Results**: In 70 SARS (70%), CD_4^+/CD_8^+ was less than 1.5. $CD_3^+CD_4^+$ was significantly lower in SRAS (30.3±7.7%) than that in Control (43.2±3.0%, P<0.01). $CD_3^+CD_8^+$ was significantly higher in SARS (69.5±6.5%) versus Control (49.5±4.2%, P<0.01). CD_3^+/CD_8^+ was significantly lower in SRAS (56.4±6.7%) than that in Control (94.6±4.8%, P<0.01). The absolute value of the lymphocytes was significantly lower in SRAS (0.83±0.44%) than that in Control (1.87±0.68%, P<0.01). Importantly, There was remarkable difference in CD_4^+/CD_8^+ in SARS cases between with and without administering immunomodulators at symptom onset. The administration of the immunomodulators significantly decreased CD_4^+/CD_8^+ (P<0.05). However, there was no difference of CD_4^+/CD_8^+ between glucocorticoid-treated and -untreated SRAS cases (P<0.0 5). **Conclusion**: Our study provides the evidence that SRAS-CoV infection in human can induce a persistent T cell subset impairment for a long time. These data may imply that applying immunomodulators during SRAS treatment might aggravate the damage of T cell subset function.

Board 103. Detecting Reduced Susceptibility Of Influenza A And B Viruses To Neuraminidase Inhibitors

T. Sheu, M. Okomo-Adhiambo, V. Deyde, A. Foust, X. Xu, A. Klimov, L. Gubareva;

Centers for Disease Control and Prevention, Atlanta, GA.

Background: Two classes of drugs are available for control of influenza infections. In recent years, a dramatic increase in resistance to the first class of drugs, adamantanes, has been reported by CDC and other laboratories. This highlights the importance of monitoring resistance to the second class: neuraminidase inhibitors (NAIs). NAIs are also the only drugs available for control of influenza B virus infections. Two NAIs, oral oseltamivir and inhaled zanamivir, are FDA-approved therapeutics; a third drug, peramivir (intramuscular), is undergoing clinical trials. The goal of this study is to monitor resistance among seasonal influenza A and B viruses. **Methods:** Viruses collected over the last 3 seasons (2005-2007) during routine surveillance were screened for resistance by NA inhibition assay with chemiluminescent substrate (NAStar® kit). Sequencing was done to identify changes in NA of drug resistant variants. Data (IC_{50} values) were statistically analyzed by (sub)type and drug to detect viruses with reduced susceptibility. Reference strains (resistant and sensitive pairs) from CDC and the Global Neuraminidase Inhibitor Surveillance Network (NISN) were used as controls. **Results:** To assess susceptibility to NAIs, IC_{50} values for ~3000 influenza A and B isolates were determined. Viruses with IC_{50} values greater than mean IC_{50} value + 3 standard deviations were considered outliers. Based on this criterion, outliers containing known (e.g. H274Y) as well as novel NA mutations (e.g. G145R, D151A, H274N) were identified. Mutation at residue 274 was detected across NA (sub)types. Viruses of A(H3N2) subtype tested with zanamivir exhibited the broadest range of IC_{50} values (0.6nM - 30.5nM, mean 3.7nM). A single virus isolate (influenza B) with mutation R371K was resistant to both NAIs. **Conclusions:** Based on the NA inhibition assay, overall resistance to NAIs remains low (<1%); however, more oseltamivir-resistant viruses were detected compared to zanamivir-resistant viruses. Here, we report elevated IC_{50} values indicating a presence of natural variants of A(H3N2) viruses with potentially decreased susceptibility to zanamivir. In view of increased reliance on NAIs, enhancing the systematic monitoring of emergence of resistant viruses in treated and untreated individuals is critical.

Board 104. Pandemic Influenza, do Miami Residents Care?

F. C. Leguen, G. Zhang, M. Bustamante;

Miami-Dade County Health Department, Miami, FL.

Background: Federal and local authorities in the United States have engaged in extensive planning and preparedness activities to respond to a pandemic influenza threat, the deployment of educational interventions to the community is an important component of this federal and local response. On this study we explored the knowledge, attitudes, and perceptions of Miami-Dade residents regarding pandemic and avian influenza and the extent to which recommended precautionary measures could be adopted by this population. **Methods:** From September 13 to October 24, 2006 the Miami-Dade County Health Department conducted a survey of county residents. This survey was conducted by computer-assisted telephone interviewing. Households were selected at random from all telephone-equipped dwelling units in Miami-Dade. Within each household, residents ages 18 and older were selected at random to be interviewed. A survey instrument with versions in both Spanish and English was used to collect data for this project. All percentage data is presented as weighted percentage. **Results:** A total of 563 individuals completed the interview, 62% of them were of Hispanic origin, 17% were Non-Hispanic White, and 14% Non-Hispanic Black. Seventy-four percent of the respondents mentioned the television news as one of their sources of avian flu information; Eighty-two percent of the respondents had some degree of awareness about avian flu. College graduates were 7 times more likely to express some knowledge about avian flu than individuals with no high school education. Senior citizens (age group 65 and over) were four times less likely to be aware about avian flu than individuals in the age group 45 to 64 years old. Eighty-three percent of the respondents said that they will comply with the isolation measures recommended by health authorities if they were diagnosed with avian flu. **Conclusions:** There is a need for the development of specific messages and the identification of channels of communication to reach certain segments of the Miami-Dade community that might not be receiving adequate avian/pandemic flu preparedness information.

Board 105. Estimates of Influenza-Associated Deaths by Region in the United States For The 1976/1977 Through 2002/2003 Respiratory Seasons

W. W. Thompson, E. Weintraub, P. Cheng, L. Brammer, J. Bresee, D. K. Shay;

Centers for Disease Control and Prevention, Atlanta, GA.

Background: Using a Poisson regression model, the Centers for Disease Control and Prevention has estimated that an annual average of 36,000 underlying respiratory and circulatory (R&C) deaths is associated with influenza in the United States from the 1990/91 through 1998/99 respiratory seasons. In this study, we assess whether regional estimates are similar to national estimates using Poisson regression models and robust regression models. **Methods**: Weekly data for the 1976/77 through 2002/03 respiratory seasons were obtained from the National Center for Health Statistics for underlying R&C deaths (ICD-8 codes 390-519, ICD-9 codes 390-519, and ICD-10 codes I00-I99, J00-J99). Population data for the US and the 9 census regions were obtained from the US Census. Weekly numbers of positive influenza tests and total specimens tested were obtained from the U.S.World Health Organization collaborating virology laboratories. We estimate the number of influenza-associated deaths nationally and regionally using Poisson regression models and robust regression models. Only national level viral surveillance data was used in the region-level Poisson regression models. **Results**: For the 1976/77 through 2002/03 seasons, the annual average of the sum of the region-level Poisson regression model estimates was 22,700 (range 4,400 - 51,000) deaths. The annual average of the sum of the region-level robust regression estimates was 21,400 (range 1,500 - 45,000) deaths. For the Poisson regression models, the national estimate was correlated 0.98 with the sum of the region-level estimates. For the robust regression models, the national estimate was correlated 0.99 with the sum of the region-level estimates. The sum of the Poisson regression region-level estimates was correlated 0.72 with the sum of the robust regression region-level estimates. Within region, the correlation of the annual estimates for the two models ranged from 0.48 to 0.79. **Conclusions**: When summed, estimates from region-level Poisson regression and robust regression region-level models yield similar national estimates of influenza-associated deaths. However, region-level estimates vary more by method. Additional work on producing region-level estimates of influenza mortality is needed.

Board 106. A Cross-Sectional Study On Risk Behaviors For Avian Influenza Human Infection-China, 2007

Y. Shi[1], H. Yu[2], L. Zhou[2], Q. Liao[2], L. Li[2], Z. Peng[2], H. Zhou[2], M. Ye[2];

[1]Chinese field epidemiology training program, Beijing, CHINA, [2]Chinese Center for Disease Control and Prevention, Beijing, CHINA.

Background: The current H5N1 avian influenza (AI) virus could trigger a pandemic if the virus should acquire the capability for human-to-human transmission. Most of the Chinese cases had no known history of direct contact with sick poultry. The objective of this study was to evaluate exposures and factors known to increase the risk for AI human infection in urban and rural areas, to help the government develop strategies for AI control and prevention. **Methods:** A cross-sectional study using a standardized questionnaire collected information on demographic characteristics, poultry exposure, and risky behaviors in an urban and a rural area where AI human infections had previously occurred. A two stage, probability-proportional-to-size (PPS) sampling scheme was used in this study. The sample was weighted by age and sex to reflect the 2000 census data for China **Results:** In total, 4950 residences (2058 urban and 2892 rural) were interviewed (response rate: 98%). In the urban area, 34% of the population had visited a wet market during the past year. For those who had visited a wet market, 80% of women had bought freshly slaughtered poultry, compared with 65% of men ($p<0.001$). Of those who had purchased freshly slaughtered poultry, 15% reportedly had frequent, direct contact with a live poultry. After touching a live poultry, 15% reported that they would touch their eyes or mouth "frequently" or "sometimes". In the rural area, 50% of the families raised poultry in their backyards, mostly small (median=7 birds) and free ranging (77%); 48% of the birds had been vaccinated with a poultry vaccine. On average, 24% the families had had 5 poultry deaths during the past year; however, only 1% of the families who had had a poultry death reported those deaths to local authorities. When asked how the dead poultry were disposed of, 5% of those interviewed said they would eat them, 44% would sell them or give them to others; 39% would burn or bury them. **Conclusions:** Visiting wet markets in urban areas and raising backyard poultry in rural areas are common. Many rural and urban residents are engaged in risky behaviors that could expose potentially them to the avian influenza virus.

Board 107. An Historical Perspective of the 1918 Spanish Influenza Pandemic in Michigan

J. Averill[1], J. Crawford[2], E. Wells[1];

[1]Michigan Department of Community Health, Lansing, MI, [2]Michigan State University, College of Veterinary Medicine, East Lansing, MI.

Background: Beginning in the spring of 1918 three successive waves of pandemic influenza swept through the world leading to an estimated 50 million deaths. The possibility of another novel influenza virus emerging in the human population currently drives an enormous surveillance and preparedness effort. A great deal of insight can be gained from how our communities survived the 1918 influenza pandemic and enable us to incorporate any beneficial practices into current public health preparedness plans. **Methods:** A number of collections were searched for information detailing Michigan's public health response to the 1918 influenza pandemic: Michigan Department of Health records, other governmental records, the State Journal, Detroit Free Press, and private collections. **Results:** 13 cases of influenza were reported to the State Health Department on October 1st. A total of 116,000 cases and 6700 deaths were reported between October and December of 1918. Community mitigation measures were implemented in small communities on October 12th but larger cities did not do so until the 17th. Governor Sleeper declared state-wide bans of public gatherings on October 19th that were in effect until November 7th. During the height of the pandemic wave, measures to accommodate the surge in healthcare needs were instituted: teachers helped nurses or law enforcement officers, the Red Cross altered their response from World War I towards the domestic needs of Michigan communities, vacant buildings were used for triage and medical care, and many citizens assisted in the making of masks. **Conclusions:** During a time when the phrase "public health preparedness" was not even coined, public health officials in Michigan were able to implement non-pharmaceutical interventions that could be used today. In 1918 there was much debate, as there is today, as to when community mitigation measures should be implemented and for how long. Further, while measures were put in place to mitigate social gatherings, compliance to maintain such prolonged measures was short-lived. The examination of those effective measures that mitigated the spread of influenza in 1918, allows practitioners today to develop and incorporate public health practices that will maximize efficacy and compliance for future communicable disease outbreaks such as pandemic influenza.

Board 108. Geographical Patterns in Pneumonia and Influenza (P&I) Mortality in Brazil, 1996-2006: Transmissibility and Mortality Impact

G. Chowell[1], C. Viboud[2], A. Rodrigues-Neto[3], L. Simonsen[4], M. Miller[2], W. Alonso[2];

[1]Arizona State University, School of Human Evolution and Social Change, Tempe, AZ, [2]Fogarty International Center, National Institutes of Health, Bethesda, MD, [3]Origem Scientific Consultancy, Florianópolis, BRAZIL, [4]George Washington University, School of Public Health and Health Services, Washington, DC.

Background: Influenza transmission dynamics in the Tropics are poorly understood. An important quantity for disease control is the reproduction number (R), which defines the transmissibility of a pathogen. In temperate regions, R estimates for influenza range between 1.0-2.0 for epidemics, and 1.7-5.4 for pandemics, but no estimates exist for tropical regions. In previous work focused on Brazil, we identified an annual wave of influenza mortality, traveling from the Equator to the subtropics. Here we explore geographical variations in influenza transmissibility and P&I mortality rates across the Southern states and micro-regions of Brazil. **Methods**: Brazil's Ministry of Health provided weekly P&I mortality rates for years 1996-2006 stratified by age group (<59 years, 59-69, >70), state (28 states between latitude 12°S and 35°S), and micro-region (n=584). To estimate R, we fitted a SEIR compartmental transmission model to weekly P&I mortality epidemic curves in each state. An *urbanization index* was based on the proportion of the population living in rural areas in each micro-region. **Results**: The average R across all Southern Brazilian states and seasons was 1.03 (95% CI: 1.01-1.06), and did not change after 1999 when influenza vaccination was introduced (P>0.05). The reproduction number increased moderately with population size (Spearman correlation ρ=0.42, P=0.001) and with distance from the Equator (ρ=0.47, P<0.001). P&I mortality rates in Southern Brazil's micro-regions increased with *urbanization*, even after adjusting for population size and stratifying by age (Partial rank correlation, ρ=0.3-0.4, P<0.0001). **Conclusion**: Estimates of transmissibility for seasonal influenza were slightly lower in Southern Brazilian states (average R~1.1) than in temperate countries (average R~1.3), consistent with a latitudinal trend in transmissibility observed throughout Brazil. Sensitivity of these results to measurement error will be explored in further work. P&I mortality rates in rural areas appeared to be lower than in urban areas, suggesting that lower population density and greater social distancing may protect rural residents from P&I-related death. Similar disparities related to urbanization were evidenced during the 1918 influenza pandemic in several regions of the world including the UK and US.

Molecular Epidemiology

Monday, March 17
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 109. Staphylococcal Cassette Chromosome *mec* (SCC*mec*) Characterization and Panton-Valentine Leukocidin Gene Occurrence for Methicillin-Resistant *Staphylococcus aureus* in Turkey, from 2003 to 2006

A. Kilic, A. Uskudar Guclu, Z. Senses, H. Aydogan, A. C. Basustaoglu;

Gulhane Military Medical Academy, Ankara, TURKEY.

Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) cause serious community-acquired and nosocomial diseases all over the world. **Methods**: We determined the SCC*mec* types and occurrence of the PVL gene by using TaqMan real-time PCR method, and correlated these with phenotypic antibiotic susceptibility patterns for MRSA strains collected from Gulhane Military Medical Academy Hospital (GMMAH) during four years study period. To our knowledge, this is the first report from Turkey of molecular SCC*mec* typing analysis of MRSA stains. From 2003 through 2006, a total of 385 clinical MRSA strains were collected in the Clinical Microbiology Laboratory at GMMAH were included in the study. **Results**: Overall, SCC*mec* types-I, II, II, IV, V, nontypeable and PVL occurrence were detected in 11 (2.8%), 3 (0.8%), 316 (82.1%), 20 (5.1%), 20 (5.1%), 15 (3.9%) and 5 (1.3%) isolates, respectively. A total of 330 (85.5%) were SCC*mec*-I/II/III, and of 40 (10.3%) were SCC*mec*-IV/V. SCC*mec*-I/II/III isolates were recovered more from serious infections in surgical departments especially having intensive care units than the SCC*mec*-IV/V isolates (χ^2=13.560, p<0.001). SCC*mec*-I/II/III MRSA strains were predominantly recovered from the blood stream as 53.0% (χ^2=6.016, p=0.014), while SCC*mec*-IV/V strains were predominantly isolated from skin, soft tissue and abscess as 55.0% (χ^2= 11.025, p<0.001). The PVL gene was detected in 10.0% of SCC*mec*-IV/V isolates in contrast to 0.3% in SCC*mec*-I/II/III (χ^2= 25.164, p<0.001). SCC*mec*-I/II/III MRSA strains were more resistant to clindamycin (χ^2=5.078, p=0.024), amoxicillin-clavulanate (χ^2=84.912, p<0.001), erythromycin (χ^2=4.651, p=0.031), gentamicin (χ^2=24.869, p<0.001), and rifampin (χ^2=18.878, p<0.001) than SCC*mec*-IV/V MRSA strains. **Conclusions**: These data indicate that SCC*mec*-III MRSA strains not to carrying PVL gene are the predominant MRSA strains in our hospital settings in Ankara, capital of Turkey. SCC*mec*-I/II/III MRSA strains may cause serious infections in surgical department especially having intensive care units.

Board 110. Phylogenetic Analysis of Novel G12 Rotaviruses in the United States: A Molecular Search for the Origin of a New Strain

M. M. Freeman[1], T. K. Kerin[1], J. Hull[1], E. N. Teel[1], M. Cortese[2], U. Parashar[2], J. Gentsch[1], R. I. Glass[3], National Rotavirus Strain Surveillance System;

[1]Gastroenteritis and Respiratory Viruses Laboratory Branch, Centers for Disease Control and Prevention, Atlanta, GA, [2]Gastroenteritis and Respiratory Viruses Epidemiology Branch, Centers for Disease Control and Prevention, Atlanta, GA, [3]Fogarty International Center, National Institutes of Health, Bethesda, MD.

Background: Rotavirus serotype G12 was initially identified in the Philippines in 1990 and was not described again until it emerged in Thailand in 2001 and in India in 2002. The first strains were detected in the United States in 2002 and since then, G12 strains have assumed a worldwide distribution. The high similarity between the sequence of the major outer capsid VP7 gene of human G12 strains and the single reference porcine G12 isolate raised the prospect that the human strains may have arisen through reassortment with porcine strains or, alternatively, that the porcine strain originally came from humans. **Methods**: We sequenced portions of the remaining 10 segments of two human G12 strains (G12P[8] and G12[P6]) and a currently-circulating common strain (G1P[8]) and compared the sequences with those of numerous strains available through Genbank. The phylogenetic relationships of the aligned nucleotide sequences were determined using a neighbor joining method with the PUZZLE program. **Results**: All segments, except for VP4 and VP7, of the 3 strains analyzed grouped with Wa-related strains in phylogenetic trees, suggesting a human origin for these G12 strains. Interestingly, comparison of the porcine NSP5 sequence with the human G12 sequences yielded high nucleotide similarity (96-97%) making the true origin of the human strains more difficult

to determine. These results suggest that the novel G12 and P[6] strains could have been formed by introduction of a solitary VP4 or VP7 gene into a globally common rotavirus, G1P[8]. **Conclusions**: Classifying rotavirus strains based only on VP4 (P) and VP7 (G) genotype potentially underestimates diversity and some sequence analysis of the other segments is required to assess the complete genetic relationships between strains. Full sequence data on other porcine strains will help clarify the true origin of the novel human G12 strains. More detailed understanding of rotavirus genotypes is needed to identify novel human viruses that arise naturally by reassorting with animal strains.

Board 111. Characterization of a Highly Divergent Picornavirus Prevalent In Stool Samples of Children with Acute Flaccid Paralysis

A. Kapoor[1], J. G. Victoria[1], A. Naeem[2], S. Sharif[2], S. Shaukat[2], M. Masroor[2], M. Angez[2], C. Wang[3], R. W. Shafer[3], S. Z. Zaidi[2], E. L. Delwart[1];

[1]Molecular Virology, Blood Systems Research Institute, San Francisco, CA, [2]Department of Virology, National Institute of Health, Islamabad, PAKISTAN, [3]Division of Infectious diseases, Stanford University, Stanford, CA.

Background: RNA viruses implicated in acute flaccid paralysis (AFP) include enteroviruses, echoviruses, coxsackieviruses and flaviviruses. Existing molecular reagents frequently fail to identify highly divergent variants or novel viruses. **Methods**: Stool samples from children presenting with AFP were used for virus isolation in cell culture. Some virus isolates could not be identified using serological and PCR assays. We used a metagenomic shotgun sequencing approach and found several sequences in one sample showing distant protein similarities to Picornaviruses. Large scale sequencing (454 pyrosequencing) and RACE were used to acquire the complete genome of a new virus, tentatively named Dekavirus type-1. PCR primers targeting conserved nonstructural genes were used to determine the prevalence of Dekavirus in stool samples from children with AFP. **Results**: The Dekavirus genome codes for a single polyprotein flanked by 5'- and 3'- non-translated regions, similar to all Picornaviruses. Phylogenetic analysis of Dekavirus establishes it as an outlier showing mean protein identity of only 16-32% to other genera of Picornaviridae. Six genetic variants of Dekavirus were found in 14 stool samples from AFP children suggesting a high prevalence among this disease group. The complete genome sequence also was acquired from another divergent Dekavirus virus variant showing 82% amino acid identity to Dekavirus type-1. **Conclusions**: We characterized two new Picornaviruses from AFP cases and provisionally named them Dekavirus type 1 and type 2. Dekavirus type-1 is divergent enough to be assigned as the prototype member of a new genus in Picornaviridae. A large study based on PCR detection and serology is underway to determine if Dekaviruses are linked to AFP.

Board 112. Detection and Characterization of stx Variants Found in Non-0157:H7 Shiga toxin producing *E. coli*

P. A. Michel[1], J. Kase[2];

[1]APHL-CCID/CDC Emerging Infectious Diseases Fellowship - North Carolina State Lab of Public Health, Raleigh, NC, [2]Public Health Scientist - North Carolina State Lab of Public Health, Raleigh, NC.

Background: Non-0157:H7 Shiga toxin producing *E. coli* (STEC) isolates have been associated with outbreaks of diarrhea, hemorrhagic colitis, and hemolytic-uremic syndrome in humans. The production of Shiga toxin (stx), stx1, stx2, or a combination of the two (stx1/stx2), is a major factor in non-0157:H7 STEC virulence. Often, molecular biological methods are used to document the prevalence of STEC in humans and animals based on positive identification of stx1, stx2, or both. **Methods:** Using a real-time PCR method, all EIA positive stool broth samples submitted to the North Carolina State Laboratory of Public Health (NCSLPH) from 2006 to the present were DNA extracted and tested for the presence of stx1 and stx2. To discriminate between gene variants of stx1 (stx1, stx1c, and stx1d) and stx2 (stx2c, stx2d, stx2e, and stx2f), melting temperature (T_m) analysis of the stx1 and stx2 specific probes was employed. Stx2 gene variants were further investigated using a multiplex PCR strategy that utilized primers, from published data, specific to each stx2 variant. **Results:** Of the 134 EIA positive samples tested at the NCSLPH, 87(64%) were non-O157:H7 STEC, of which 64(48%) contained stx1, 14(10.4%) stx2, and 9(6.7%) stx1/stx2. T_m analysis showed that of the 64 stx1 positive isolates, 49(76.6%) were stx1c, 6(9.4%) stx2d, 5(7.8%) stx1, and 4(6.3%) non-determined based on T_m analysis alone. T_m analysis was also used to identify the stx1 variants of the 9 stx1/stx2 positive isolates. From this 7(78%) contained stx1c and 2(22%) stx1. T_m and multiplex PCR results for stx2 gene variant identification were ambiguous; the observed T_m's and PCR fragment sizes were inconsistent with published results. **Conclusions:** The preliminary results of this study indicate that the majority of non-O157:H7 STEC isolated from human samples harbors the stx1c gene variant. Furthermore, stx1c is also the most common gene variant seen in those isolates which contain stx1/stx2. Based on inconclusive results from the multiplex PCR designed to identify stx2 gene variants; it can be inferred that there are potential variants of stx2 that have a significant sequence diversity from those published in the current literature. This assumption is currently being tested using direct nucleotide sequencing of the stx2 PCR fragments.

Board 113. Human Herpesvirus Type 7 in Cerebrospinal Fluid of a Patient with Acute Demyelinating Encepholapathy (ADEM) after Smallpox Vaccination

S. Ruone[1], Y. Li[2], C. N. Van Dam[3], J. J. Eron[3], R. J. Engler[4], J. J. Sejvar[2], Z. Braden[2], R. Regnery[2], I. Damon[2], L. J. Anderson[1], S. Tong[1];

[1]Division of Viral Diseases, Centers for Disease Control and Prevention, Atlanta, GA, [2]Division of Viral and Rickettsial Diseases, Centers for Disease Control and Prevention, Atlanta, GA, [3]Division of Infectious Disease, Department of Medicine, University of North Carolina, Chapel Hill, NC, [4]Vaccine Healthcare Centers Network and Allergy-Immunology Department, Walter Reed Army Medical Center, Washington, DC.

Background: In September 2007, a 19-year-old airman became critically ill with Acute Demyelinating Encephalomyelopathy (ADEM) 10 days after primary smallpox vaccination. While Post-Vaccinal Encephalitis (PVE) with ADEM was felt to be the most likely diagnosis, other bacterial and viral causes for encephalitis were sought. Serum and CSF samples from the patient were sent to the Centers for Disease Control and Prevention (CDC) for analysis. We applied a panel of broadly reacting PCR assays to the patient's CSF. **Methods**: The total nucleic acids (TNA) were extracted from the serum and CSF using the QIAamp MinElute Virus Spin kit (QIAGEN). A panel of broadly reacting viral family PCR was performed on the TNA. The virus families screened included orthopoxviruses, flaviviruses, alphaviruses, bunyaviruses, adenoviruses, coronaviruses, polyomaviruses, bornaviruses, paramyxoviruses, rhabdoviruses and herpesviruses and all were known to have encephalitis-causing members. PCR positives of the correct band size were sequenced with the ABI Prism 3130 sequencer. **Results**: TNA from the CSF, but not from serum, was found positive for herpes virus using the pan herpesvirus PCR assay and negative for the other tested viral families. The positive result was confirmed by independent PCR assays on a separate aliquot of

the same CSF. The PCR amplicon product was purified and both strands sequenced. The partial sequence from RNA polymerase (L) amplicon (200 bp) matched the human herpesvirus type 7 (HHV7). A subsequent semi-quantitative real-time PCR experiment suggested a low herpes viral load in the CSF of the patient. No evidence was found for vaccinia (smallpox vaccine) DNA in the CSF. However, small amounts of orthopoxvirus-specific IgM were detected in CSF in the absence of measurable IgG. **Conclusions**: We identified HHV7 DNA in the cerebrospinal fluid of a patient with ADEM-related PVE which developed 10 days after smallpox vaccination. The significance of HHV7 to the observed pathologic features of the patient's encephalitis is unclear. It is known that herpes viruses establish latency after primary infection and are common in humans. It is more likely that our patient was previously infected with HHV7 and that in the setting of massive CNS inflammation caused by PVE and ADEM from smallpox vaccination HHV7 virus was reactivated.

Outbreak Investigation: Lab & Epi Response

Monday, March 17
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 114. Use of a Web-based Survey Application to Investigate a Large Outbreak of Norovirus Among Venture Capitalists

D. Hill, B. Davis, S. Cody;

Santa Clara County Public Health Department, San Jose, CA.

Background: A large outbreak of gastrointestinal illness was reported to the Santa Clara County Public Health Department's Disease Prevention and Control Program (SCCPHD DPC) among persons who attended a national venture capitalists meeting at Hotel X in April 2006. Hotel X hosts many large conferences catered from the hotel kitchen; 750 people had reportedly attended this meeting. Ten catered events were scheduled at the hotel over the following 3 days. The SCCPHD DPC sought to rapidly investigate the outbreak to determine etiology and ongoing risk of exposure in order to facilitate prompt public health action and prevent additional cases. **Methods**: We used a commercially available web-based application (SurveyMonkey.com, Portland OR) to survey ~750 meeting attendees. A link to a survey instrument designed with tools available on the site was forwarded to the liason from the conference, who in turn forwarded it to attendees. Data collected included symptoms, food exposures, and demographics. Survey data were exported into SPSS and analyzed using the Chi-Squared test and logistic regression models. In addition, we inspected the kitchen, conducted structured interviews with all foodhandlers, and collected stool specimens from ill staff. Stool specimens were tested for norovirus by RT-PCR. **Results**: Within 12 hours of emailing the survey to participants, 250 attendees had completed (and returned) the survey and preliminary results were available for analysis. These initial responses represented 84% of the completed surveys (n=296) received. The investigation demonstrated that Foodhandler K worked while ill with probable norovirus infection, and passed infection to other foodhandlers, staff, and over 100 guests in attendance. Analyses showed a dose-response relationship between number of food items eaten prepared by Foodhandler K and illness. **Conclusions**: The web-based application facilitated rapid dissemination of a survey instrument, retrieval of data, and analysis. Quick turnaround and analysis enabled us to focus interviews and specimen collection. Hotel management and kitchen staff were educated about norovirus and instructed to 1) report gastrointestinal illness, 2) not work while symptomatic with diarrhea or vomiting for 48 hours following, and 3) maintain strict handwashing practices.

Board 115. Spread of Adenovirus B14 from a Major Military Training Facility to Secondary Training Sites, May to September 2007

J. Trei[1], M. Johns[2], J. Garner[2], L. Noel[3], N. Johns[4];

[1]Core6 Solutions, San Antonio, TX, [2]Henry M. Jackson Foundation, Rockville, MD, [3]Air Education and Training Command, Randolph Air Force Base, TX, [4]Air Force Institute for Operational Health, Brooks City-Base, TX.

Background: In mid-May 2007, a respiratory disease outbreak associated with a novel strain of adenovirus, serotype B14 (Ad14), was recognized at a large military basic training facility in Texas. Response and control efforts had to consider the high mobility of the trainee population; following the 6-week basic training course, students immediately disperse to secondary sites for advanced training. Accordingly, the Air Force Institute for Operational Health (AFIOH) instituted enhanced surveillance at military installations that receive graduates from this basic training facility. This report describes response activities and surveillance findings as of September 30, 2007. **Methods:** To initiate enhanced surveillance, AFIOH sent support materials to secondary training sites, created a website to disseminate information, and released an email message encouraging participation. Sites were instructed to submit specimens to the AFIOH laboratory from all patients meeting the case definition, which included a fever of ≥100.5º and a cough or sore throat. Collected specimens were tested for respiratory pathogens via culture, serum neutralization, and PCR. **Results:** From May 25 to September 30, 2007, AFIOH received 796 respiratory specimens from 16 secondary training sites. A total of 276 (34.7%) were Ad14 positive. Most Ad14 cases [255 (92.4%)] were technical training students, while the remaining 21 occurred in permanent party active duty members. Ad14 was identified at 5 secondary sites located in California, Mississippi, and Texas. Two of the hardest hit sites began quartering patients meeting the case definition, resulting in short-term removal of more than 600 students from training activities. Enhanced handwashing and fomite disinfection practices were also adopted. As of September 30, attack rates had subsided somewhat but not sufficiently to cease surveillance and control efforts. **Conclusions:** Ad14 was able to spread readily among these military trainees, likely due to their rapid mobility following basic training. While halting training operations may have helped, this is not a ready option, particularly during wartime. Future discussions should focus on how to best control the spread of infectious diseases between military sites in the context of high mobility and need for continued operations.

Board 116. An Outbreak Of Acute Respiratory Tract Infection Caused By Adenovirus Type 11

W. Xu, Z. Zhu, Y. Zhang, S. Xu, Z. Liu, L. Tang, N. Mao, Y. Ji, C. Li, S. Wang, D. Li, Emerging Disease Office, China CDC, Emerging DiseaseLaboratory,Shaanxi CDC;

National Institute for Viral Disease Control and Prevention, China Center for Disease Control and Pr, Beijing, CHINA.

Background: An outbreak of 254 patients with acute respiratory tract infection occurred at a county of Shannxi Province in China from March to April of 2006, 247 of 254 patients come from a senior high school and 1 died of the pneumonia. **Methods:** To identify the etiologic agent, 18 throat swabs and 18 pairs of sera were collected from 18 patients; hydrothorax, sputum and serum were also collected from the patient who died of pneumonia. 50 single sera collected from 50 contacts in the same senior high school and another 50 single sera collected from 50 health students in another senior high school in the same county. The throat swabs

were cultured using the Hep-2 cell line and extracted RNA; the RNA identification by a polymerase chain reaction (PCR) using 1 pair of adenovirus specific primers. All of the sera were detect adenovirus IgA antibodies by the Enzyme link immunosorbent assay (EIA); and the 18 pairs sera were detected by adenovirus 11 neutralization antibodies by neutralization test. **Results:** 12 of 18 throat swabs had positive by PCR with 972 bp of partial hexon gene of Adenovirus, the sequence showed that all of the 12 PCR products belong to species B2 of Adenovirus 11. Adenovirus 11 was also isolates from the 5 throat swabs and the hydrothorax, sputum and serum samples of the patient who died. 16 patient's sera of 18 pair sera had IgA positive of adenovirus in either acute or convalescent sera or both. 6 sera of 50 contacts had IgA positive of adenovirus; only 1 of 50 health students had IgA positive of adenovirus. The 16 of 18 pair's convalescent sera have 4 or more than 4 fold rise compared to acute sera by adenovirus 11 neutralization test. **Conclusions:** The outbreak of acute respiratory tract mainly cause by B2 of Adenovirus 11.

Board 117. Adenovirus 21 Outbreak at the Coast Guard Training Center in Cape May, New Jersey

T. R. Brown[1], L. J. Martinez[2], J. K. Llanos[1], E. G. Schwartz[3], J. A. Lynch[1], R. L. Coldren[4];

[1]Walter Reed Army Institute of Research, Silver Spring, MD, [2]Walter Reed Army Medical Center, Washington, DC, [3]US Coast Guard Headquarters, CG-1121, Washington, DC, [4]US Army Center for Health Promotion and Preventive Medicine, Aberdeen Proving Ground, MD.

Background: Adenovirus is a ubiquitous, non-enveloped, double-stranded DNA virus that causes disease in man. Adenovirus is divided into 51 serotypes with most serotypes having specific organ tropism. In the military, febrile respiratory disease caused by adenovirus is endemic at all basic training sites. While serotypes 4 and 7 account for the majority of all acute respiratory diseases in military basic training recruits, other serotypes have caused epidemic disease at these training sites. A recent report found that adenovirus 21 (Ad21) has been increasing in prevalence in both military and civilian populations. **Methods:** An investigation of the Ad21 outbreak at the Coast Guard Training Center in Cape May, NJ was conducted on 27 September 2007. A proctored survey was administered to the recruit company of interest. A clinic chart review was conducted on all recruits from this company using a standardized data abstraction form. Additionally, a walk-through environmental assessment of the training center was performed. **Results:** An increase in febrile respiratory illness at this site was reported by NHRC starting in July 2007 and has persisted through the fall. Illness was most prevalent among the specific recruit company of interest. During this period of febrile respiratory illness there were no cases of lower respiratory disease or severe cases reported. The endemic adenovirus 4p of Cape May has been completely replaced by Ad21 as all culture-positive throat swabs that were processed during this period were Ad21. **Conclusions:** While this Ad21 outbreak has been prolonged, there has been no severe disease. Although Ad21 respiratory epidemics in the training environment have historically been uncommon, the increasing baseline prevalence of this serotype may lead to more frequent epidemics. Additionally, the adenovirus vaccine being developed by the Walter Reed Army Institute of Research for this recruit population may affect future adenovirus epidemics.

Board 118. A Geospatial Analysis of the Spread of Mumps in Iowa during the 2006 Outbreak

P. M. Polgreen[1], L. C. Bohnett[1], M. A. Pentella[2], J. E. Cavanaugh[1];

[1]University of Iowa, Iowa City, IA, [2]The University Hygenic Laboratory, University of Iowa, Iowa City, IA.

Background: In the winter and spring of 2006, Iowa was the epicenter of the largest mumps outbreak in recent US history. Consistent with recent outbreaks, reported cases were older (median: 22) than most cases in the prevacciation era. Several cases were linked to college students and campuses, but colleges were not equally affected. The purpose of this study was to describe county-level risk factors for the geographic spread of mumps and to determine the effect of college spring breaks on the spread of the disease in Iowa. **Methods:** For the geographic analysis we used generalized linear mixed models with an isotropic exponential spatial covariance structure. The number of mumps cases per county (adjusted for population) was the dependent variable. The independent variables considered at the county level included the proportion of 15 to 24 year olds, the number of colleges, the proportion of Iowa's college students, and economic pull factor. To account for propagation, the centroid distance from each county to the epicenter of the outbreak was used to define a categorical risk zone variable. To assess the impact of spring break travel of college students, a chi-square test was used to test the proportion of mumps cases among older and younger persons (below 17 yrs and above 23 yrs) before and after April 1, 2006 (18 days after the mean date for the distribution of college students on spring break to adjust for the average incubation period). **Results:** In the final model, the number of colleges was negatively associated with mumps cases ($p < 0.0001$), and the proportion of Iowa's college students was positively associated with mumps cases ($p = 0.0104$). The proportion of mumps cases among both older and younger persons (below 17 yrs and above 23 yrs) increased after April 1, 2006 ($p=0.0029$). **Conclusions:** The spread of mumps was related to the proportion of college students in a particular county and inversely related to the number of colleges, suggesting that smaller colleges had a protective effect compared to counties with larger schools. Furthermore, the timing of the spring breaks among Iowa colleges was associated with a statistically significant increase in the proportion of cases among people both older and younger than college age persons. Thus, it appears that travel among college students helped amplify the outbreak in Iowa.

Board 119. New Strategies and Collaborations to Investigate Non-event Related *Cyclospora cayetanensis* Outbreaks, British Columbia, Canada, 2007

L. Shah[1], L. MacDougall[2], A. Ellis[3], C. Ong[4], S. Shyng[5], L. LeBlanc[6], Cyclospora Investigation Team;

[1]Canadian Field Epidemiology Program, Public Health Agency of Canada and Epidemiology Services, BC Centre for Disease Control, Vancouver, BC, CANADA, [2]Epidemiology Services, BC Centre for Disease Control, Vancouver, BC, CANADA, [3]Foodborne, Waterborne, Zoonotics Infections Division, Public Health Agency of Canada, Guelph, ON, CANADA, [4]Laboratory Services, BC Centre for Disease Control, Vancouver, BC, CANADA, [5]BC Food Protection, BC Centre for Disease Control, Vancouver, BC, CANADA, [6]Canadian Food Inspection Agency, Ottawa, ON, CANADA.

Background British Columbia Centre for Disease Control (BCCDC) has investigated outbreaks of locally-acquired *Cyclospora cayetanensis* annually since 1999. Traditional epidemiologic investigations were generally insufficient to identify a single source, often identifying two or three suspect food vehicles. Poor case recall due to delays in clinical diagnosis, lengthy incubation period and difficult to recall food vehicles (e.g. garnishes) represent challenges. Detection of *Cyclospora* in food and vehicles by laboratory methods is often hampered by the perishable nature of the specimens. In 2007, we combined multiple investigative techniques to successfully overcome challenges inherent in *Cyclospora* investigations. **Methods** Cases were interviewed with a standardized hypothesis generating questionnaire. A detailed questionnaire collected

information on purchases of high frequency items. Population-based food consumption surveys were used as surrogate controls. Food regulator and environmental health staff assessed importation and distribution patterns of all suspect food items. Several suspect food items were traced back to identify common sources or distributors. Where available, grocery store purchase histories obtained from cases' consumer cards confirmed purchase dates and locations. A visit to the distributor confirmed product distribution of the identified common source item. **Results** We identified multiple high frequency items consumed by cases. No common event linked cases. Surrogate controls and consultation with food regulatory agencies narrowed the list to four suspect food items. Only one item could be traced back to a single distributor. Case purchase histories collected from grocery cards were compared with product shipment dates to identify potentially affected shipments. The distributor confirmed distribution to market under trade names consumed by cases. Product was no longer available for testing. **Conclusion** Identifying a vehicle is difficult in non-event related *Cyclospora* outbreaks. We recommend a multi-faceted approach including detailed food histories, consulting with food regulatory bodies early, traceback of multiple suspect food items and using consumer card purchase histories in order to optimize chances of implicating a single source.

Poverty & Infectious Diseases

Monday, March 17
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 120. Socio-economic Determinants of Prevalence of HIV and HCV Infections in Injecting Drug Users in Poland

M. Rosinska, P. Stefanoff;

National Institute of Public Health - National Institute of Hygiene, Warsaw, POLAND.

Background: Blood borne infections among injecting drug users (IDU) tend to concentrate in socially marginalized users. The extent of the problem among IDU in Poland is not known and is important to advocate harm reduction strategies targeting the most vulnerable populations. The aim of this study was to determine the prevalence of blood borne pathogens in IDU in Poland in relation to socio-economical status. **Methods:** A cross sectional survey was carried out in 2004 - 2005 in 15 locations in 6 regions in Poland. Subjects who had injected illicit drugs at least once in their life were recruited. The recruitment was carried out by snow-ball method from streets and low threshold facilities. Exhaustive method was used in in-patient treatment centers. All subjects were administered a closed ended questionnaire and provided a sample of venous blood. Laboratory investigations included EIA tests for HIV and HCV antibodies. Prevalence was estimated using methods for stratified cluster sampling. Logistic regression was used for multivariate comparisons.**Results:** Out of 776 drug users included in the study, 512 (66.0%) were recruited from streets/low threshold facilities. There were 219 (28.6%) women and 547 (71.4%) men. At the time of study (in case of inpatients prior to entering treatment), 262 (38.5%) participants were working or studying, 363 (53.5%) had stable income, and 90 (11.8%) were homeless. Imprisonment in the past was reported by 348 (45.7%) participants. Overall HIV prevalence was 18.0% (95% CI 9.2% - 26.8%) and HCV prevalence - 58.9% (48.6% - 69.1%). Higher HIV and HCV prevalence was observed among the homeless subjects - 46.4% (vs 14.8%) and 76.5% (vs 57.1%), subjects not working or studying - 22.0% (vs 5.0%) and 67.8 (38.3%) and subjects having been imprisoned - 25.1% (vs 12.4%) and 72.3% (vs 48.3%). Social marginalization was associated with higher frequency of risk behaviors such as needle sharing. **Conclusions:** HIV is more prevalent among Polish IDU than in most of European countries, but the prevalence of HCV is comparable. High prevalence of HIV and HCV among socio-economically disadvantaged groups could be caused by marginalization of the infected users. Nonetheless, outreach harm reduction programs may be necessary to limit further spread of blood-borne infections in this population.

Board 121. Prevalence and Antimicrobial Resistance of *Campylobacter* and *Salmonella* in Chickens Sampled at Slaughterhouses in Antananarivo Madagascar

N. Ravaonindrina[1], A. Ramanoelina[2], L. Raharinivo[1], C. Caillet[3], M. Gouali[1], M. Gay[1], A. Talarmin[1];

[1]Institut Pasteur Madagascar, Antananarivo, MADAGASCAR, [2]Université Antananarivo, Antananarivo, MADAGASCAR, [3]Faculté de Pharmacie, Lyon, FRANCE.

Background: *Salmonella* and *Campylobacter* continue to be major foodborne pathogens and raw poultry is considered to be an important source of these bacteria; we conducted this study to estimate the prevalence and antimicrobial resistance of *Salmonella* and *Campylobacter* in chickens sampled in some slaughterhouse in Antananarivo MadagascarT **Methods:** From December 2005 to August 2006, 150 samples of chicken were analysed for the presence of *Salmonella* and *Campylobacter*; confirmed isolates were further tested antimicrobial resistance **Results:** In total, *Salmonella* and *Campylobacter* were respectively present in 16% and 73% of the chickens.The most prevalent serotype of Salmonalla was *Enteritidis* (75%), followed by *Bardo* (17%), *Lerum* and *Newport* were isolated each from one chicken (4%). 74% of isolated *Campylobacter* were *jejuni*; 17% *coli*, 6% *upsaliensis* and 4% *lari*. 50% of *Salmonella* tested were resistant to at least on antibiotic; 89% of the serovar *Enteritidis* were resistant to the association of amoxicillin and ticarcillin, furthermore there was not resistance to acid nalidixic and fluoroquinolone. In total 109 *Campylobacter* strains 82 (75%) were resistant to a single antibiotic, 12 strains (11%) showed resistance to two antibiotics, multiresistance (to three or more of antibiotics) was found in 14% of the strains; resistance to amoxicillin (19%) was the most finding, followed by resistance to erythromycin (17%), azithromycin (9%), furthermore ciprofloxacin and gentamicin were the best sensible. **Conclusions:** There is no published report about prevalence and antibiotic resistance of *Salmonella* and *Campylobacter* isolated from chicken in Madagascar. The results of this fisrt study would be conducted to evaluate the risk factors to prevent public health.

Board 122. World Rabies Day: A Collaborative Initiative to Make Rabies History

C. A. Hanlon[1], D. J. Briggs[1], P. Costa[2], A. Tumpey[3], S. Cleaveland[4], and the World Rabies Day team;

[1]Kansas State University, Manhattan, KS, [2]Global Alliance for Rabies Control, Manhattan, KS, [3]Centers for Disease Control and Prevention, Atlanta, GA, [4]University of Edinburgh, Midlothian, UNITED KINGDOM.

Background: Although the word alone evokes a highly charged response, rabies remains a severely neglected disease. The continuing loss of lives to rabies infection is directly related to population-level risk factors. **Methods**: The World Rabies Day initiative arose from a group of rabies prevention professionals who built partnerships with the World Health Organization, the World Organization for Animal Health (OIE), the Pasteur Institute, Canadian Food and Inspection Agency, World Society for the Protection of Animals, World Veterinary Association, and many

veterinary medical organizations and student veterinary medical associations. The World Rabies Day initiative advocates for improving the health of the whole population, human and animal, - a "One Medicine Approach" - by raising awareness about the need to control rabies in the main global animal reservoir, the domestic dog, and prevent human rabies through education and appropriate medical prophylaxis - a need that arises primarily from economic and educational disparity. **Results**: During the inaugural year, at least 74 countries participated through a wide variety of events including: vaccination clinics, lectures and educational seminars, media outreach, museum and zoo exhibits, parades, festivals, dances, puppet shows, marches, runs, and dog walks. Numerous countries, including Mexico and Brazil, had events in every state. Although based on preliminary data from 15% of participants, more than 1.2 million people were educated through World Rabies Day events and outreach and over 270,000 animal vaccinations were administered. In some countries, rabies experts convened to discuss goals and plans for rabies prevention and control, with several countries initiating a national Rabies Control Program in honor of this event. Veterinary colleges around the world joined forces towards this effort, with activities at 24 in the US, 15 in India, 5 in Indonesia, and several in Mexico and the Philippines. **Conclusions**: The first World Rabies Day was a major achievement for the rabies prevention community. These efforts are envisioned to be part of comprehensive human and animal health delivery that would develop and augment public health and veterinary infrastructure in regions of greatest need. Now is the time for "Working Together to Make Rabies History!"

Board 123. Evaluation of the Role of School Children in the Promotion of PuR® and the Safe Water System in Schools and Households

E. M. Blanton[1], S. Ombeki[2], G. O. Oluoch[2], A. Mwaki[2], R. Quick[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]CARE, Kisumu, KENYA.

Background: Recent research suggests that promotion of water treatment and handwashing in schools effectively transmits knowledge and helps change behaviors of pupils and their parents. For schools relying on turbid water sources, use of a combined flocculant-disinfectant product to clarify and treat water may enhance acceptability of water treatment interventions. We evaluated the impact of the use of a flocculant-disinfectant product, called PuR®, in a school-based drinking water and hygiene improvement project on the knowledge and practices of Kenyan pupils and parents. **Methods:** We selected a convenience sample of 17 rural primary schools in villages that relied on turbid pond water. We interviewed a random sample of pupils and their parents about water, sanitation, and hygiene practices at baseline and tested stored water in pupils' homes for residual chlorine. We trained schoolteachers about water treatment and handwashing, installed drinking water and handwashing stations in schools, and gave pupils instructional comic books with 3 PuR® sachets. School children treated water in handwashing stations with bleach (marketed as WaterGuard) and drinking water with PuR®. After two school terms, we interviewed pupils and parents about water treatment and handwashing knowledge and practices, and tested household stored water for residual chlorine. **Results:** We interviewed 603 pupils in grades 4-8, and their parents, at baseline and final evaluation. From baseline to final evaluation, awareness of PuR® increased among pupils (31-98%, $p<0{\cdot}01$) and parents (49-92%, p<0.01), and awareness of WaterGuard increased among pupils (91-99%, p<0.01) and parents (94-96%, p=0.10). Knowledge of correct treatment procedure increased for PUR® among pupils (4-64%, $p<0.01$) and parents (17-55%, p<0.01), and also for WaterGuard among pupils (17-53%, p<0.01) and parents (35-59%, p<0.01). Chlorine testing in pupils' homes confirmed an increase in use of PUR® (0.5-8%, p<0.001) and WaterGuard (6-16%, p<0.001). The ability to demonstrate correct handwashing techniques increased in pupils (22-53%, p<0.01) and parents (24-41%, p<0.01). **Conclusions:** This school-based program improved water treatment and handwashing knowledge and practices among pupils and their parents. This promising approach merits wider application.

Board 124. High rates of *Streptococcus pneumoniae* Serotype 1 Bacteremia Among Adults In Western Kenya

G. O. Jagero[1], J. Oundo[2], G. M. Bigogo[2], M. K. Njenga[3], C. Whitney[4], R. F. Breiman[3], D. R. Feikin[2];

[1]IEIP CDC, CGHR KEMRI, Kisumu, Kenya, [2]IEIP CDC, Kisumu, Kenya, [3]IEIP CDC, Nairobi, Kenya, [4]RDB CDC, Atlanta, GA.

Background: Information on invasive *Streptococcus pneumoniae* serotypes among adults is useful in predicting the potential indirect impact of the expected introduction of the 7-valent pneumococcal conjugate vaccine (PCV7) among infants in Kenya in 2008 **Methods:** From September 2006 to August 2007, we performed blood cultures as part of population-based morbidity surveillance in rural Western Kenya, where HIV rates are over 15%. Blood cultures were done on adults presenting at a referral clinic with severe acute respiratory illness, defined as cough or difficulty breathing with temperature >38.0ºC or oxygen saturation <90%, with fever alone (first 2 patients per day), and on those who were hospitalized for any reason. **Results:** Pneumococci were isolated from 31 (5%) of 608 blood cultures and were the most common pathogen isolated. Penicillin (oxacillin) resistance by disk diffusion was observed in 54% of isolates. Sixteen (52%) were serotype 1, whereas the rest were serotypes 5(6%), 6B (3%), 7C (3%), 7F (3%), 9A (3%), 12B (3%), 15A (9.5%), 19F (6%), 20 (3%), 22F (3%), 35B (3%) and 43 (3%). Only 10% were PCV7 serotypes. Among patients with pneumococcal bacteremia, 74% had severe acute respiratory illness, 6% had fever alone, and 19% were cultured because they were hospitalized for another reason. These categories of pneumococcal bacteremia did not differ between serotype 1 and other serotypes. Persons infected with serotype 1 pneumococcus were younger than those infected with other serotypes (mean of 24 years versus 36 years (p=.04). Females accounted for 37% of serotype 1 infections and 60% of other serotypes (p=.22). Among serotype 1 cases, 56% were admitted compared with 80% for other serotypes (p=.16). No deaths occurred. There was no clustering of serotype 1 cases in particular villages or during certain months. **Conclusions:** Serotype 1 pneumococcus accounted for over half of all bloodstream pneumococci isolated in adults, occurring more in younger adults. A serotype 1 epidemic seemed unlikely because of lack of temporal-spatial clustering. Few pneumococcal serotypes isolated are covered by PCV7, suggesting that indirect benefits for adults after PCV7 introduction in children would be small. However, future pneumococcal conjugate vaccines that contain serotypes 1, 5 and 7 could have greater impact.

Surveillance: International and New Strategies

Monday, March 17
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 125. Active Surveillance of Infectious Diseases in Northern Canadian Communities: the Northern Antibiotic Resistance Partnership

P. N. Levett[1], R. R. McDonald[1], E. Nagle[1], G. R. Golding[2], G. B. Horsman[1], J. Irvine[3], M. R. Mulvey[2], Northern Antibiotic Resistance Partnership (NARP);

[1]Saskatchewan Health, Regina, SK, CANADA, [2]Public Health Agency of Canada, Winnipeg, MB, CANADA, [3]Mamawetan Churchill River and Keewatin Yatthe Health Regions, La Ronge, SK, CANADA.

Background: Many remote northern Canadian communities face high infectious disease rates. In northern Saskatchewan communities, approximately 90% of patients who visit primary care practitioners with symptoms suggestive of acute infection are prescribed antibiotics without laboratory investigation of their illness. Among the goals of NARP are to increase appropriateness of antimicrobial prescribing and to determine the effect of this intervention on antimicrobial resistance in isolates from northern communities. One of the components of NARP is an active surveillance study in three northern Saskatchewan communities. **Methods:** From late October 2005, specimens were collected from urinary tract infections (UTI), pharyngitis (URT), pneumonia (LRTI) and skin and soft tissue infections (SSTI). **Results:** In the first two years of this study, 3941 isolates were considered significant (48% from UTI, 34%, SSTI, 13% URTI, 3% LRTI). From UTI, *Escherichia coli* was most frequently isolated (53% of 1802 UTI isolates), but at one site, *Enterococcus faecalis* and *E.coli* were equally common (both 40%). With the exception of resistance to ampicillin (54%) and trimethoprim-sulfamethoxazole (69%) in *E. coli*, there was little antimicrobial resistance associated with UTI. SSTI most often yielded *Staphylococcus aureus*, of which 56% were MRSA, and *Streptococcus pyogenes*. Among MRSA isolates, USA400 was the predominant clone. Mixed infections with *S. aureus* and *S. pyogenes* were common. Isolates of *S. pyogenes* from SSTI and URTI represented a wide range of *emm* types. **Conclusions:** Antimicrobial susceptibilities from this study are being used for the development of empirical treatment guidelines for these common syndromes and provide a baseline for assessing the effectiveness of interventions during the NARP study.

Board 126. Algorithm for Detecting High Priority Animal Health Events from Global Open Source Surveillance

C. Kristensen, J. Akkina, B. Bischoff, V. Bridges, C. Johnson, K. Johnson, S. Sweeney, W. Weber, E. Williams;

Center for Emerging Issues (CEI), Centers for Epidemiology and Animal Health, Animal and Plant Health Inspection Service (APHIS), U.S. Department of Agriculture, Fort Collins, CO.

Background Protecting U.S. animal populations requires constant monitoring of global disease events and conditions that may lead to disease emergence. CEI actively monitors global information to provide early detection, assessments and increased awareness of emerging disease conditions to USDA decision makers. Electronic information sources have, in recent years, changed the way animal health information is gathered and processed. In response to these changes, CEI developed an algorithm designed to identify high-priority emerging animal health events using text-based data obtained primarily from global open source surveillance. **Methods** CEI analysts evaluated animal health events using a text-based algorithm to identify and prioritize items of potential interest, focusing on animal health issues that were significant, or in some way unusual, regarding morbidity, mortality, clinical signs, location, or other epidemiological characteristics. Using the algorithm, analysts determined the level of potential threat by assigning a priority of high, medium, or low to each event. The appropriate response was determined based on this assigned priority. Alerts were generated immediately to decision makers for high and medium priority events. These events were monitored and verified through a network of domestic and international collaborators and were summarized in periodic reports. Additionally, in-depth assessments were developed on select high and medium priority events. **Results** From August 1 to October 31, 2007, nearly 7,000 animal health related records were evaluated and prioritized using the algorithm. Of these, 204 were events of interest, 78 were classified as high or medium priority and were actively monitored, alerts were released for 33 events, and 4 short reports, impact assessments or emerging disease notices were developed. **Conclusions** When assessing text-based surveillance data where quantitative data is unavailable, the use of this detection and prioritization algorithm has been an effective tool that quickly identified high priority events on which analysts and decision makers should focus. It also provided consistency in the evaluation and assessment of these events and minimized bias introduced by the subjective perspectives of individual analysts.

Board 127. Influenza Surveillance: It Takes a Village

E. H. Graf, S. Jirsa;

University of Iowa Hygienic Laboratory, Iowa City, IA.

Background: Point of care testing for Influenza has reduced the number of samples received by public health laboratories, causing loss of surveillance data. Additionally, concern with the accuracy of rapid tests when prevalence of Influenza is low has led epidemiologists to create novel tools for surveillance data collection that also promote communication and awareness among physicians and laboratorians. Previously, the Iowa Department of Public Health has recruited volunteer physicians and hospitals as surveillance sites but participation remains poor. In order to increase the number of sites, level of participation, timeliness of reporting, and awareness of Influenza activity, the University Hygienic Laboratory (UHL) has developed an online Influenza rapid test results survey. **Methods:** More than 160 physicians and hospital laboratories were recruited to participate in a weekly online survey, some as part of the Iowa Laboratory Response Network (ILRN) and others as additional surveillance points, based on their location and populations served. Participants report rapid test results each Monday, for the previous week. Totals are calculated by county, region and state and, if the test differentiates, by Influenza A or B. Laboratories are asked to submit positive rapid test specimens for confirmation by UHL, when prevalence is low. Training was provided to sentinel sites through teleconferences and seminars. **Results:** The weekly survey has been successful in collecting rapid test data and tracking the incidence of Influenza in Iowa. Each week, over 95% of the 164 facilities reported test results. When prevalence of Influenza was low, health care providers were able to assess the accuracy of their positive rapid tests and as a result increased their submission of isolates to UHL for confirmation by PCR and culture. **Conclusions:** Since Influenza is not a reportable disease, Iowa epidemiologists need a better way to gather information on seasonal outbreaks. This survey is an excellent way to monitor the incidence of Influenza across the state in a rapid fashion and is critically important as an early detection measure for pandemic preparedness. It is also a means of

bringing the laboratory system together to focus on influenza and promote communication between physicians, laboratorians and epidemiologists.

Board 128. New strategies in National-level Outbreak Reporting and Response: The Brazilian Center for Strategic Information in Health Surveillance (CIEVS)

V. S. Magalhães[1], N. F. Moura[1], W. Kleber de Oliveira[1], A. B. Gomes[1], E. Nunes[1], J. Sobel[2], E. C. Hage[3], G. S. Dimech[1];

[1]CIEVES, Secretariate of Health Surveillance, Ministry of Health, Brasilia, BRAZIL, [2]Office of Global Health, CDC, Atlanta, GA, [3]DEVEP, Secretariat of Health Surveillance, Ministry of Health, Brasilia, BRAZIL.

Background:Epidemics or endemics of emerging or reemerging diseases like H5N1, SARS or anthrax impelled the international community to improve health surveillance. CIEVS is a Brazilian strategy, based on the WHO - Global Alert Outbreak and Response Network, to improve national capacity for detection of events that could become epidemiologic emergencies and strengthen the alert and response process. **Methods**:All data reported to CIEVS between March 30th 2006 and September 30th 2007 were analyzed by: source of report; number of ill, affected or deceased persons; event type; etiologic confirmation; number of events by week; timeliness of report; and place of occurrence. **Results**:During this period, 336 health-related events were reported (1.8/1,000,000 inhabitants). Sources were: healthcare services (54%), e-mail (32%), telephone notification (7%) and mass media data mining (6%). About 87% of emergencies were human infectious diseases, 1% epizootic diseases and 1% natural disasters. Reported events encompassed 108,364 ill humans (incidene, 588/1,000,000), 344 ill animals, and 182,989 disaster-affected persons. Most reported illnesses were foodborne/waterborne (reported case incidence 114/1,000,000), and respiratory diseases (case incidence, 175/1,000,000 inhabitants). Selected reported outbreaks included: orally transmitted Chagas Disease, measles, rubella, beriberi, and nosocomial mycobacteriosis. Case fatality was 0.5%. Etiological confirmation was obtained in 53% of events; etiology remains unknown in 25%; 22% were discarded. Health Ministry teams investigated 16% of emergencies: 6% were investigated by the Brazilian FETP and 10% by subject matter experts. A median of 4 events (Range: 1-12) were reported per week. Median time, occurrence to report was 11 days (Range 1-795), and to close-out, 18 days (0-253). Highest reporting cities were Brasília and Rio de Janeiro (3.6% each) and highest reporting states were São Paulo and Minas Gerais (33% and 32%, respectively). **Conclusions**:CIEVS is an effective outbreak alert and response system. Foodborne/waterborne and respiratory diseases were the leading causes of reported emergencies. Etiology was confirmed in half of reported events. Challenges are to increase reporting from small cities and improve timeliness of reporting and response.

Board 129. The Impact of WHO-GSS Training Programs in Brazil

R. M. Alves[1], G. Carmo[1], E. Perez[2], O. Henao[3], S. M. Pires[4], A. R. Vieira[4];

[1]Brazilian Health Ministry, Brasília, BRAZIL, [2]Area of Health Surveillance and Disease Management, Food Safety, PAHO, Rio de Janeiro, BRAZIL, [3]Division of Foodborne, Bacterial and Mycotic Diseases, CDC, Atlanta, GA, [4]National Food Institute, Mørkhøj, DENMARK.

Background: WHO Global Salm-Surv was established in 2000 with the objective of developing capacity for the surveillance and study of foodborne illnesses. The most important activity of GSS is training of epidemiologists, microbiologists and other public health officials in how to conduct surveillance and respond to issues related to foodborne illnesses. GSS training in Brazil started in 2005 and is conducted at the national level involving public health officials from the laboratory, sanitary and epidemiology groups. **Methods:** National level training in Brazil was chosen due to the dimension of the country, high number of states and heterogeneity of surveillance in the different regions. Two training cycles have been completed in Brazil. The initial cycle was conducted with a total of 150 participants from 26 states and Federal District. At this time, the course included both laboratorial and epidemiological surveillance components, focusing on *Salmonella* and outbreak surveillance. In late 2007, level II training included participants from the 16 states that, according to the activities, were more likely to benefit from the training. During level II training course, the impact of the GSS training programs, improvements in the surveillance system and limitations of the current situation were assessed. **Results:** Among the most relevant impacts of the implementation of this program in Brazil are the increase in the number of reported cases in the states due to applied incentives to notification, the improvement of the integration between the departments of epidemiological surveillance and the central laboratories of public health and the development of the network between the states. Limitations include the uneven development of the surveillance programs within the states and the identification of other partners playing a major role in the surveillance programs (state health managers and coordinators). **Conclusions:** The aims proposed by GSS are being achieved in Brazil and the national surveillance program has clearly benefited from this program. The output of the assessment was an action plan with activities and tasks for the different partners that take into account the impact of each measure, as well and the feasibility of each planned intervention in the short-term future.

Board 130. Respiratory Disease Surveillance in Royal Thai Army Hospitals

J. Gaywee[1], L. Bodhidatta[1], R. G. Jarman[1], C. Eamsila[1], K. S. Myint[1], T. Briese[2], W. I. Lipkin[2], P. Watcharapichat[1], T. Chuenchitra[1], R. V. Gibbons[1], J. A. Pavlin[1], N. Sirisopana[1];

[1]Armed Forces Research Institute of Medical Sciences, Bangkok, THAILAND, [2]Mailman School of Public Health, Columbia University, New York, NY.

Background The Royal Thai Army (RTA) has 34 hospitals that serve the military and surrounding civilian population with 10 located in rural areas with high border traffic near Myanmar, Malaysia, Laos, and Cambodia. In order to determine the seasonal and regional etiology of respiratory disease, enhance outbreak response capability and detection of avian influenza, and to enable the safe collection of clinical samples, the RTA established a network of respiratory disease surveillance sites at 6 border area hospitals. **Methods** Adults who present with a history of fever and cough, sore throat or rhinorrhea can enroll. Respiratory samples are tested with a rapid test for influenza A and B on-site. Aliquots are sent to AFRIMS in Bangkok for real-time PCR testing for influenza A H1, H3, H5, influenza B and MassTag PCR to identify other respiratory pathogens. MassTag PCR amplifies genetic material by using domain-specific primers tagged with a unique mass to allow spectrometric analysis and detection of up to 30 respiratory pathogens. Our panel identifies influenza A viruses, influenza B, both genotypes of respiratory syncytial virus (RSV) and human metapnuemovirus (hMPV), enterovirus, adenovirus, 3 human coronaviruses including the causative agent of SARS, 3 subtypes of human parainfluenza virus (PIV), *Chlamydia pneumoniae*, *Mycoplasma pneumoniae*, *Streptococcus pneumoniae*, *Legionella pneumophila*, *Haemophilus influenzae* and *Neisseria meningitidis*. **Results** We collected 350 samples from March to October 2007. Using rapid testing, 15 were positive for influenza A and 7 for influenza B. To date, 100 samples have been tested by real-time PCR, 9 were positive for influenza A (H3 subtype) found in 5 of the 6 sites. MassTag PCR of the first 39 samples independently

confirmed 3/3 samples positive for FLU A and revealed 6 *H. influenzae,* 1 PIV-1, 1 PIV-2, and 1 hMPV positive samples. In addition MassTag PCR identified 3 of the *H. influenzae* cases as co-infected with *S. pneumoniae*, FLU A, or PIV-1 (one each). Sixteen of 39 (41%) patient samples remain unknown. **Conclusion** Testing for many respiratory pathogens provides a comprehensive picture of disease burden in this population and greatly improves our ability to detect and respond to emerging diseases including avian influenza. We are continuing to expand this surveillance program in 2008.

Board 131. Bacteremia among Patients with Community-acquired Pneumonia in Rural Thailand|

S. Henchaichon[1], S. Thiamthitiwat[1], S. Dejsirilert[2], S. Maloney[1], P. Jornrakate[1], A. Kaewpan[1], L. F. Peruski[1], P. Areerat[3], D. Sornkij[4], G. Watt[1], H. Baggett[1];

[1]International Emerging Infections Program, Thailand MOPH-US CDC Collaboration, Nonthaburi, THAILAND, [2]National Institute of Health, Ministry of Public Health, Thailand, Nonthaburi, THAILAND, [3]Sa Kaeo Provincial Health Office, Ministry of Public Health, Sa Kaeo, THAILAND, [4]Nakhon Phanom Provincial Health Office, Ministry of Public Health, Thailand, Nakhon Phanom, THAILAND.

Background: Pneumonia is a leading cause of morbidity and mortality globally. Bacteria cause a substantial portion of disease, but little information is available on the frequency and causes of bacteremic community-acquired pneumonia (CAP) in Asia. **Methods**: We conducted active, population-based surveillance for CAP in all 20 hospitals in 2 rural Thai provinces. We defined clinical pneumonia as illness in a patient presenting to hospital with evidence of acute infection and signs or symptoms of respiratory illness. Blood cultures and chest x-rays (CXR) were performed when considered clinically indicated by hospital physicians. **Results:** In Sa Kaeo Province (May 2005 - Feb 2007), blood was cultured from 3,024 (32%) of 9,297 clinical pneumonia patients and a pathogen identified in 209 cases. The most common pathogens were *Escherichia coli* (65 [31%]), nontyphoidal *Salmonella* (26 [12%]), *Staphylococcus aureus* (20 [9.6%]), *Cryptococcus neoformans* (20 [9.6%]), *Burkholderia pseudomallei*, the agent of melioidosis (18 [8.6%]), and *Streptococcus pneumoniae* (18 [8.6%]). In Nakhon Phanom (Nov 2005 - Feb 2007), blood cultures were obtained from 7,240 (81%) of 8,918 clinical pneumonia patients and yielded 311 isolates: *E . coli* (81 [26%]), *B. pseudomallei* (72 [23%]), *K. pneumoniae* (7.4%), and *S. pneumoniae* (7.1%). Bacteremic patients were more likely than non-bacteremic patients to require intubation (20% vs. 6.5%, p<0.001) and have a fatal outcome (17% vs. 4%, p<0.001). Compared with other bacteremic patients, those with *E. coli* were older (median age 67.7 vs. 46.6 yr; p<0.001) and more likely to be female (64% vs. 42%; p<0.001); 10% of patients with *E. coli* required intubation and 5% died. CXRs were done in 4480 (47%) of clinical pneumonia patients and 2558 (53%) were abnormal. Limiting to patients with CXR-confirmed pneumonia and bacteremia (n=132), *S. pneumoniae* was more common (15%), but Gram negative organisms still predominated: *B. pseudomallei* (20%), *E. coli* (14%), nontyphoidal *Salmonella* (10%). **Conclusions:** Our findings suggest that the agents causing bacteremia in CAP in rural Thailand differ from those in the West. *E. coli* and other Gram negative infections are common and severe. Increased awareness and additional studies are needed to guide clinical management, improve outcomes, and inform health programs.

Board 132. A Novel Risk Assessment Tool for Emerging Human Infectious Disease and Bio Warfare Agents and its Use in Assessing Preparedness of 20 Pacific Island Countries and Territories

B. Adlam[1], R. Lake[2], P. Carter[1];

[1]Institute of Environmental Science and Research, Porirua, NEW ZEALAND, [2]Institute of Environmental Science and Research, Christchurch, NEW ZEALAND.

Background Risks from emerging infectious diseases and biological hazards often change rapidly. Most current risk assessment tools and lists of hazardous substances are based on static elements that are inherent to the agent. In an emerging situation, current events and regional or local vulnerabilities may be in a rapid state of change, and the level of risk is often unclear. What is required is a tool that takes into account changing elements of risk, and incorporates new knowledge of inherent threats with changing risk attributes during emergence. Our goal was to develop a dynamic risk assessment tool; DAISY (Disease Attribute Intelligence System), that would monitor and stratify risk of emerging biological agents and provide a guide to risk management. **Methodology** We identified 25 risk attributes with 5 risk levels within each attribute, and using online information, profiled the daily risk of avian influenza spread into Europe during 2005 and 2006. In addition, 45 biological agents were benchmarked against 4 standard lists of hazardous substances. In addition information form a checklist of preparedness for 20 Pacific Island Countries and Territories was used to populate the vulnerability attributes of the tool. **Results** The risk assessment tool was sensitive to the spread of avian influenza into Europe and the risk level for major agency interventions was noted. Threat scores of 45 biological agents aligned well with the four gold-standard lists and country-specific benchmarking enabled risk stratification of agents into preparedness categories. Cross-country comparison was able to provide a risk ranking of preparedness across the Pacific Region **Conclusion** As a tool, DAISY is able to routinely and consistently assess levels of risk from day to day, according to attributes that apply across a wide range of biological agents, from both infectious disease and bio warfare perspectives. An early application of the risk assessment tool has been to compare the risk due to varying pandemic preparedness across 20 Pacific Islands Countries and Territories for the purposes of guiding resource assistance and aid.

Board 133. Risk Factors and Age Differentials for Death among Children Hospitalized with Diarrhea in Rural Western Kenya, 2005 – 2007

C. E. O'Reilly[1], J. Tate[1], E. Yee[1], E. Blanton[1], B. Ochieng[2], P. Jaron[2], A. Nyaguara[2], M. Parsons[1], C. Bopp[1], J. Vulule[3], R. Breiman[4], D. Feikin[2], K. Laserson[2], M. Widdowson[1], E. Mintz[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]KEMRI/CDC, Kisumu, KENYA, [3]KEMRI, Kisumu, KENYA, [4]KEMRI/CDC, Nairobi, KENYA.

Background: Diarrhea is a major cause of childhood morbidity and mortality in Kenya. We conducted hospital-based surveillance to characterize the etiology of diarrheal illness, identify risk factors for death, and examine the age-specific enteric pathogens associated with death, among children hospitalized with diarrhea in rural western Kenya. **Methods**: We enrolled all children <5 years old hospitalized with diarrhea (≥3 loose stools in 24 hours) at two hospitals in rural western Kenya. Clinical and demographic information and stool samples were collected. Specimens were tested for enteric bacterial pathogens (culture) and rotavirus (EIA). **Results**: From May 23, 2005 to May 22, 2007, 1,154 children <5 years old hospitalized with diarrhea were enrolled. Non-Typhi *Salmonella* were identified in 10% (119), *Campylobacter* in 5% (58) and *Shigella* in 4% (47) of 1,144 stool samples; rotavirus was

detected in 19% (198 of 1,051 stool samples). Ninety (8%) children died during hospitalization. Among stool samples from children who died, non-Typhi *Salmonella* were identified in 16 (18%), *Shigella* in 7 (8%), *Campylobacter* in 3 (3%), and bacterial co-infections in 3 (3%); rotavirus was detected in 7% (6 of 83 stool samples). Children who died were more likely to have non-Typhi *Salmonella*, *Shigella*, a bacterial co-infection or any bacterial pathogen identified in stool than children who survived ($P<0.05$), but were not more likely to have rotavirus detected in stool. Infants 0-11 months old who died were more likely than those who survived to have non-Typhi *Salmonella* identified in stool, and children 24-59 months old who died were more likely than those who survived to have *Shigella* identified in stool. Further risk factors for death included a longer duration of diarrhea on admission, seeking care before coming to the hospital, previous treatment with cotrimoxazole, dehydration, and oral thrush on physical exam ($P<0.05$). A clinical diagnosis of malaria, or malaria parasites on blood smear, were not associated with dying. **Conclusions**: Bacterial diarrheal diseases are major causes of mortality among Kenyan children. The study results may help inform community education for caretakers and clinicians about recognizing and appropriately treating potentially fatal diarrheal illness.

Tropical Infections & Parasitic Diseases

Monday, March 17
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 134. Atypical Presentation of Varicella-zoster Virus Infection in a Family Cluster, Republic of Congo, 2007

A. MacNeil[1], M. Reynolds[1], Z. Braden[1], D. Carroll[1], K. Karem[1], S. Smith[1], W. Davidson[1], O. Moundeli[2], J. Mombouli[3], S. Schmid[1], R. Regnery[1], I. Damon[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]District Health Office, Impfondo, Republic of Congo, GA, [3]National Laboratory, Brazzaville, Republic of Congo, GA.

Background: The monkeypox virus (MPXV) and varicella-zoster virus (VZV) both cause illnesses accompanied by fever and pustular rash lesions, in humans. However, MPXV infection is typically associated with greater pathogenicity, with associated case fatality rates up to 10%. While both viruses cause disease characterized by generalized rashes, lesions are characteristically absent from the palms and soles of the hands and feet in VZV infection, providing a marked difference from what is seen in MPXV infection, where lesions on the palms and soles have been observed to occur in up to 76% of non-previously-vaccinated cases. **Methods:** During an investigation of a suspected monkeypox outbreak in the Likouala district, the Republic of Congo, we observed an infant with disseminated pustular lesions, including numerous lesions located on the hands and feet. Based on family member interviews, and case histories, a rash illness had recently occurred in the mother, and 3 siblings, with onset dates indicating 3-4 serial transmissions in the family. Lesion scars were observed on the hands and feet of the mother, and 2 siblings. **Results:** Laboratory testing of multiple lesions from the infant confirmed VZV infection, and serum from the infant, mother, and 2 siblings were negative for orthopox-specific IgM, demonstrating the absence of recent MPXV infection within this familial cluster. **Conclusions:** The results of this investigation indicate transmission of VZV with palm and sole manifestations in a monkeypox endemic area. This finding suggests the need for additional clinical guidelines to differentiate these infections, and for improved surveillance and infection control, in regions of the world that MPXV and VZV co-circulate *The findings and conclusions in this presentation have not been formally disseminated by CDC and should not be construed to represent any agency or policy.*

Board 135. The Concurrence of Malaria and Typhoid Among Adult Patients Admitted in Medical Wards at Iringa Regional Hospital, Tanzania

A. C. Kangolle;

Ocean Road Cancer Institute, Dar es salaam, TANZANIA, UNITED REPUBLIC OF.

Background: Malaria and typhoid are two diseases caused by different infectious organisms. The two diseases have symptoms and signs that are very similar to the extent that one may diagnose one instead of the other. In some parts of the world, both diseases are very common and, may co-exist in one patient making it difficult for health personnel to think of the other diagnosis once they have confirmed presence of one disease. Patients' laboratory blood tests can be done to confirm the presence/absence of these diseases. The objectives of this study were: To determine the proportion of malaria and typhoid among patients admitted in the medical wards at Iringa Regional Hospital (IRH), Tanzania; To determine the association between typhoid and malaria among patients admitted in medical wards at IRH - Tanzania. **Methods**: A cross-sectional analytic study was conducted where 214 patients admitted in medical wards at IRH, Tanzania were studied. For every subject admitted with admission diagnosis of malaria another subject with other admission diagnoses was selected. The diagnoses were determined using blood tests and symptoms and signs of typhoid and malaria. Each study participant gave informed consent. Pearson correlation and proportion ratios were used to assess the concurrence of typhoid and malaria. **Results**: The proportion of 31.8% of admitted study participants had typhoid. This proportion was 46.1% among those with malaria admission diagnosis and 15.2% for other admission diagnoses. Correlation between typhoid and malaria admission diagnosis was significant; Pearson $\chi^2 = 23.485$ ($p < 0.001$); proportion ratio of typhoid among malaria admission diagnosis to typhoid among other diagnoses was 3.04; 95% CI = 1.83 - 5.05, ($p<0.0001$). **Conclusion**: There was high proportion of typhoid among studied patients. The concurrence between typhoid and malaria is significant necessitating medical personnel in areas where malaria and typhoid are common to make these diseases the common differential diagnosis.

Board 136. Intestinal Parasitism Among Hispanic Migrant and Seasonal Farm Workers in Eastern North Carolina

M. D. Russell[1], M. T. Correa[2], C. E. Stauber[3], J. A. Kase[4];

[1]APHL-CCID/CDC Emerging Infectious Diseases Fellowship - North Carolina State Laboratory of Public Health, Raleigh, NC, [2]North Carolina State University, Raleigh, NC, [3]University of North Carolina - Chapel Hill, Chapel Hill, NC, [4]North Carolina State Laboratory of Public Health, Raleigh, NC.

Background: In the US, there are an estimated 4.2 million migrant and seasonal farm workers with over 100,000 farm workers in North Carolina. The majority (75%) of US farm workers are born in Mexico. Many diseases that are uncommon in the US are endemic in areas of Latin America including Mexico. This study investigated the prevalence of intestinal parasitism among Hispanic migrant and seasonal farm workers in Eastern North Carolina during the 2007 planting/harvesting season. **Methods:** Questionnaires, verbally administered in Spanish, documented the demographics, medical history, and lifestyle (e.g. living conditions and hygiene practices) of adult farm workers. Workers were also asked to

submit stool specimens for ova and parasite examination. **Results:** Of the 71 farm workers surveyed, all were born in Mexico, 86% were male, and the median age was 27 (81% aged 20 to 40). Most workers had occupations in agriculture including tobacco (73%) and fruits/vegetables (51%). Parasitism as a child was reported by 38% of workers and 3% reported testing positive for intestinal parasites while in the US. Self-medication for parasitism was common among workers; 69% reported previous medication use and 7% were currently taking medication for prevention or treatment. Most workers shared living quarters with 4 to 6 people. Comparison of facility availability at home (versus work) found that 78% (29%) used private toilets, 7% (12%) used latrines and 7% (44%) used portable bathrooms. Workers reported washing their hands after using the bathroom at home (96%) and work (78%), as well as before cooking (92%). A total of sixteen stool specimens were submitted and examined. Two samples were positive for a foodborne parasite, *Giardia spp.* or *Entamoeba coli*. **Conclusions:** This study documents the prevalence of intestinal parasitism among Hispanic migrant and seasonal farm worker populations, as well as addresses a significant public health concern, food safety. Increased consumption of raw fruits and vegetables harvested by farm workers has introduced an emerging threat to the farm-to-fork continuum. Therefore, gaining a better understanding of the health and hygiene of farm workers will be essential in addressing the safety and reducing the risk of transmission of foodborne parasites from agricultural commodities to consumers.

Board 137. Independent Evolution of Mutant *Dhfr* and *Dhps* Alleles in an Area of High Transmission in Western Kenya

A. M. McCollum[1], S. M. Griffing[1], Z. Zhou[1], D. J. Terlouw[2], S. Kariuki[3], Y. Shi[1], A. Lal[1], F. O. ter Kuile[2], V. Udhayakumar[1], A. A. Escalante[4];

[1]CDC / CCID / NCZVED / DPD / MB, Atlanta, GA, [2]Liverpool School of Tropical Medicine, Liverpool, UNITED KINGDOM, [3]Kenya Medical Research Institute, Kisumu, KENYA, [4]Arizona State University, Tempe, AZ.

Background: The origin and spread of sulfadoxine-pyrimethamine (SP) resistant *Plasmodium falciparum* is a major public health concern. Mutations in the genes *dhfr* and *dhps* have been shown to yield parasite resistance to SP. Previous studies have demonstrated multiple origins of resistance in South America, Melanesia, Southeast Asia, and Kenya, with the predominant mutant *dhfr* lineage arising in Southeast Asia and subsequently spreading to Africa. Our goals in the present research were to assess the extent of lowered variation surrounding both *dhfr* and *dhps* as a result of selection and the relationships between the mutant alleles. **Methods**: We used 236 blood samples collected between 1992 and 1999 from children in the Asembo Bay area of western Kenya. The *dhfr* and *dhps* genotypes for each sample were determined by pyrosequencing. We characterized microsatellite markers spanning 138 kb around *dhfr* on chromosome 4 and *dhps* on chromosome 8 as well as neutral markers spanning approximately 100 kb on chromosomes 2 and 3. **Results**: We found that *dhfr* has a surrounding region of about 11kb with reduced variation and *dhps* has a larger region of 35kb with reduced variation. We find multiple lineages for the mutant *dhfr* and *dhps* alleles, with one predominant lineage for the *dhfr* 51I/108N, 51I/59R/108N, and *dhps* 437G/540E alleles. Using the eBURST algorithm, we show that the mutant *dhfr* alleles (51I/108N, 59R/108N, and 51I/59R/108N) are all distinct lineages from one another. In addition, minor frequency triple mutant alleles are not related to the predominant triple mutant allele lineage that was originally described in Southeast Asia. **Conclusions**: We provide evidence for soft selective sweeps of multiple mutant *dhfr* alleles and selection acting on mutant *dhps* alleles. There is strong genetic differentiation between the alleles of *dhfr* and the alleles of *dhps*. We also find multiple lineages for the highly resistant triple mutant *dhfr* alleles, and our results yield support for gene flow being a major factor in the distribution of mutant alleles in Africa. These results yield support to the use of microsatellite markers as molecular surveillance tools in a parasite population with high amounts of variation.

Vector-Borne Diseases

Monday, March 17
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 138. Potential Predictors of Tick Species Attached to Persons in Georgia

M. Vello[1], L. E. Garrison[1], D. Cole[1], M. J. Yabsley[2], G. Lopez[3];

[1]Georgia Division of Public Health, Atlanta, GA, [2]Southern Cooperative Wildlife Disease Study, College of Veterinary Medicine, The University of Georgia, Athens, GA, [3]Georgia Poison Center, Atlanta, GA.

Background: Rocky Mountain spotted fever is the most commonly reported tickborne disease in Georgia, with an annual incidence typically higher than the national average. To better understand the epidemiology of Rocky Mountain spotted fever and other tickborne diseases, the Georgia Division of Public Health, the University of Georgia, and the Georgia Poison Center conducted the Georgia Tick Attach Study between April 2005 and December 2006. Data from this study were used to examine factors that might affect infestation patterns of *Dermacentor variabilis*, the primary vector for *Rickettsia rickettsii*, and *Amblyomma americanum*, the tick most commonly found attached to humans in Georgia. **Methods:** Persons who were bitten by a tick in Georgia were urged to submit the tick for identification and testing through the Tick Attach Study. Demographic and exposure data were collected by the Georgia Poison Center and the Georgia Division of Public Health during initial enrollment and in a telephone survey administered three weeks after the tick bite, respectively. Tick identification and PCR analysis were performed at the University of Georgia. SAS version 8.2 was used to characterize predictors of attached tick species for 2005. **Results:** Of the 245 study participants who met the inclusion criteria for this analysis, 90 were infested with *D. variabilis* and 155 were infested with *A. americanum*. People infested with *D. variabilis* were more likely to be bitten on the head, live in the Mountain physiographic region of Georgia, and be less than 18 years of age than those infested with *A. americanum*. There was also a significant difference in the odds of being infested with *D. variabilis* versus *A. americanum* among age and dog ownership categories. **Conclusions:** These findings are similar to other studies with regard to site of *D. variabilis* attachment and physiographic region. However, there are many other factors that are potentially involved in the association of tick species and human attachment. These findings could be useful in developing targeted educational materials for the prevention of Rocky Mountain spotted fever and other tickborne diseases.

Board 139. Isolation Of Arboviruses In Kenya (2006 - 2007) By Entomological Surveillance

J. L. Lutomiah[1], R. Sang[2], C. Ochieng[2], M. Warigia[1], P. Cheruiyiot[1], E. Kioko[2], H. Koka[2], M. O'Guinn[3], J. Lee[3], J. Richardson[4];

[1]Kenya Medical Research Institute, Nairobi, KENYA, [2]KEMRI/US Army Medical Research Unit - Kenya, Nairobi, KENYA, [3]US Army Medical Research Institute for Infectious Diseases, FREDRICK, MD, [4]Armed Forces Research Institute of Medical Science, Bangkok, THAILAND.

Background: Arboviruses cause clinical syndromes in humans, ranging from self-limiting febrile illnesses to life-threatening encephalitis or hemorrhagic fever. They replicate in hematophagous arthropods that become infected following a blood meal on viremic vertebrate hosts. Virus isolation from clinical specimens is usually difficult since the virus is transiently present. Arthropods are a viable alternative surveillance target because infection is sustained for life. **Methods:** We conducted entomologic surveillance to determine the distribution of arboviruses circulating in Kenya, their genetic diversity and evolutionary trends. Mosquitoes and ticks were collected from 5 selected sites over two years and samples were subjected to virus isolation procedures. Isolates were characterized by genome amplification and sequencing. **Results:** The most abundant mosquito species in Kisumu were *Mansonia Africana*, *Ma. uniformis*, *Culex univittatus*, and *Cx. Vansomereni*; in Busia, *Cx. Univittatus*; in Isiolo, *Cx. Univittatus* and *Aedes arabiensis*; in Malindi, *Ae. aegypti*, *Cx. vansomereni* and *Cx. quinquefasciatus;* and in Naivasha, *Cx. univittatus* and *Cx. vansomereni*. The most common sampled tick species were *Rhippicephalus pulchellus* and *Amblyomma gemma*. Twelve virus strains were isolated from over 35,000 mosquitoes. Usutu virus, a bird-borne flavivirus, was isolated from *Cx. univittatus* from Kisumu. Three flaviviruses similar to Kamiti River virus were isolated from *Ae. aegypti* from the coast. Two Babanki viruses were isolated from *Culex* species from Kisumu area and one Sindbis virus from *Cx. vansomereni* from Naivasha. Ten viruses were isolated from 993 tick pools. One Dugbe virus was isolated from *Am. variegatum* and five Dugbe-like viruses from *Am. Variegatum*, *Hyalomma dromedary* and *Rh. pulchellus*. **Conclusions:** A range of arboviruses are circulating among mosquitoes and ticks across Kenya and can be detected through active vector surveillance. This method may provide the earliest warning of arbovirus transmission in an area and can help identify the potential risk to the local population.

Board 140. Prospective Study of Symptoms Associated with the Convalescent Period of Dengue Infection in Puerto Rico, 2006-2007

A. Ayala-López, J. Rigau-Pérez;

Centers for Disease Control and Prevention, San Juan, PR.

Background: Dengue, an emerging mosquito-transmitted disease, is characterized by an acute illness consisting of fever, headache, rash, retro-orbital pain, myalgias, arthralgias, vomiting, abdominal pain, and hemorrhagic manifestations. Case and epidemic reports suggest a variable list of symptoms during convalescence, including depression, amnesia, loss of sensation, paralysis of extremities, epilepsy, loss of visual acuity, hair loss, and peeling of skin. The objective of this prospective cohort study was to examine the incidence and characteristics of delayed complications associated with dengue. **Methods:** An exposed group of persons with a positive laboratory diagnosis of dengue was compared with two different unexposed groups: dengue negatives (persons suspected of having dengue but for whom laboratory tests ruled out dengue), and healthy controls (matched to dengue positives by town and selected by random-digit dialing). Island-wide telephone interviews were conducted and information was collected prospectively. Initial interviews took place within four to eight weeks after onset of dengue-like symptoms. Follow-up interviews were conducted 3 months after the first interview. All participants were age 18 years or older. **Results:** From August 2006 to August 2007, 167 individuals (64 persons with dengue, 39 without dengue and 64 same-town controls) were prospectively enrolled. Of these, 100 (60%) were female and the median age was 50 (range 18 to 79). Self-reported symptoms included: hair loss (25% of persons with dengue versus 21% of persons without dengue and 17% in the healthy control group; greater tiredness than usual (59% vs. 31% [$p<0.05$] and 19% [$p<0.05$]), sadness (44% vs. 28% and 28%), feeling depressed (34% vs. 15% and 22%), lack of energy (56% vs. 36% and 31%[$p<0.05$]), poor appetite (34% vs. 38% and 9% [$p<0.05$]), weight loss (66% vs. 62% and 25%[$p<0.05$]), and visual problems (21% vs. 29% and 8%[$p<0.05$]). **Conclusions:** Symptoms significantly associated with the convalescent phase of dengue included greater tiredness than usual, lack of energy, poor appetite, weight loss and visual problems. This is the first prospective study to identify these symptoms as specifically related to dengue infection. Physicians should be aware that patients may develop these problems in the convalescent period.

Board 141. La Crosse Encephalitis in a Pregnant Woman and Possible Congenital Infection

A. J. Hall[1], A. F. Hinckley[2], R. S. Lanciotti[2];

[1]Epidemic Intelligence Service, Centers for Disease Control and Prevention, Atlanta, GA, [2]Division of Vector Borne Infectious Diseases, Centers for Disease Control and Prevention, Fort Collins, CO.

Background: La Crosse encephalitis virus (LACV) is a mosquitoborne Bunyavirus usually located in the Midwest and mid-Atlantic regions of the United States. Severe neurologic disease with possible long-term sequelae resulting from LACV presents most commonly among children aged <16 years. Effects of LACV infection during pregnancy and potential for intrauterine transmission to the fetus are unknown. In August 2006, a woman aged 42 years in her 21st week of pregnancy was treated at a West Virginia hospital for encephalitis resulting from LACV. **Methods:** With her consent, the patient's medical and prenatal histories were reviewed and prospective follow-up was initiated. Maternal sera and umbilical cord serum were tested for LACV-specific antibodies using enzyme-linked immunosorbent assay and plaque-reduction neutralization. Umbilical cord tissue was tested for LACV RNA by polymerase chain reaction (PCR). Data were collected regarding infant health at delivery and through the first 6 months of life. **Results:** The patient delivered a healthy infant of normal birthweight at approximately 40 weeks' gestation. LACV-specific IgM antibodies were detected in umbilical cord serum, although no evidence of LACV was detected in umbilical cord tissue by PCR. Maternal serum collected at 11 weeks postpartum was positive for LACV IgG antibodies, but negative for IgM. The infant remained healthy with normal neurologic and cognitive functions through the first 6 months of life. **Conclusions:** To date, this report summarizes the only case of symptomatic LACV infection identified during pregnancy. Although congenital infection was indicated through identification of IgM antibodies in cord serum, the infant remained asymptomatic and development has been normal. Congenital infection could not be confirmed because the mother declined collection of infant serum. Further investigations are needed to confirm potential for intrauterine LACV transmission and to identify immediate and long-term health risks posed to the infant.

Board 142. Seroepidemiology of *Anaplasma phagocytophilum, Bartonella henselae, Coxiella burnetii* and *Rickettsia typhi* among farm worker populations in the Tianjin area, China.

L. Zhang;

National Institute of Communicable Disease Control and Prevention, China CDC, Beijing, CHINA.

Background: Human granulocytic anaplasmosis and monocytic ehrlichiosis are emerging tick-borne rickettsial diseases caused by the obligate intracellular bacteria *Anaplasma phagocytophilum* and *Ehrlichia chaffeensis* respectively. Despite clear evidence demonstrating the existence of both *A. phagocytophilum* and *E. chaffeensis* infections in ticks and rodents in China , little seroepidemiologic investigation of human infections has been performed. A pilot **r**etrospective laboratory survey of

suspected HGA cases in several Provinces over 2004 to 2005 identified several cases by serology and blood PCR. Subsequently, an unusual cluster of HGA cases occurred in Anhui province during 2006 where nosocomial human to human transmission was demonstrated. As a result of these events, an investigation to assess the seroepidemiologic status of the zoonotic "rickettsial" infection caused by *A. phagocytophilum*, *E. chaffeensis*, *Bartonella henselae*, *Coxiella burnetii* and *Rickettsia typhi* infections among occupationally-exposed persons from Tianjin city, one of the largest municipalities and the biggest trade port in northern China was undertaken in 2007. **Methods**: A total of 365 healthy people were included in the survey analysis. A questionnaire was used to record demographic data, gender, age, occupation, length of service, and contact with poultry. Sera were screened by indirect immunofluorescence assays (IFA). Statistical analysis was performed with SPSS/PC and Microsoft Excel. **Results** :The average seroprevalences against 4 bacteria classically considered rickettsial infections were: *A. phagocytophilum* 8.8%, *C. burnetii* 9.6%, *B. henselae* 6.4%, and *R. typhi* 4.1%. The seroprevalence of *A. phagocytophilum* was similar to that of healthy at risk populations in the USA and Europe. Among the 8 subdivision areas, the Tanggu area had significantly higher seroprevalences for *R. typhi*, which was only detected in this area, and for *B. henselae* (22.92%), that was also found at high rates in the Xiqing (16.7%) and Jinnan (12.5%) regions. **Conclusions**: The results suggest that the emerging *A. phagocytophilum* and *B. henselae*-related diseases are already prevalent in these areas, and that the differential demographics of seropositive individuals suggest distinctive epidemiology, ecologies, and risks.

Zoonotic & Animal Diseases

Monday, March 17
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 143. Quantification of Hepatitis E Virus Transmission in Pigs Due to Contact-exposure

M. Bouwknegt[1], K. Frankena[2], S. A. Rutjes[1], G. J. Wellenberg[3], A. de Roda Husman[1], W. H. van der Poel[3], M. C. de Jong[2];

[1]National Institute for Public Health and the Environment, Bilthoven, THE NETHERLANDS, [2]Wageningen Institute of Animal Sciences, Wageningen, THE NETHERLANDS, [3]Animal Sciences Group of Wageningen UR, Lelystad, THE NETHERLANDS.

Background: Locally acquired hepatitis E in humans from developed countries has been repeatedly suggested to originate from pigs. Pigs may serve as a reservoir of hepatitis E virus (HEV) for humans when a typical infected pig would cause on average more than one newly infected pig; a property that is expressed by the basic reproduction ratio R_0. For instance, an R_0 of 10 for a particular pathogen indicates that one infectious individual causes on average 10 new infections among susceptibles. **Methods:** In this study, R_0 for HEV transmission among pigs was estimated from chains of one-to-one transmission experiments. The experiment was divided in two blocks of five chains each. Per chain, susceptible first-generation contact pigs were contact-exposed to intravenously inoculated pigs. Subsequently, susceptible second-generation contact pigs were contact-exposed to infected first-generation contact pigs, and susceptible third-generation contact pigs were contact-exposed to infected second-generation contact pigs. Thus, in the second and third link of the chain, HEV-transmission due to contact with a contact-infected pig was observed. Transmission of HEV was monitored by RT-PCR on individual faecal samples taken every two or three days. **Results:** For susceptible pigs, the average period between exposure to an infectious pig and HEV excretion was 6 (SD: 4) days. The length of HEV-excretion (*i.e.* the infectious period) was estimated at 49 days (95% confidence interval (CI): 17-141) for block 1 and 13 days (95% CI: 11-17) for block 2. The R_0 for contact-exposure was estimated to be 8.8 (95% CI: 4 - 19). **Conclusions:** The R_0 was significantly greater than 1, showing the potential of HEV to cause epidemics in populations of pigs. Thereby, this study is the first to report evidence that confirms the general assumption that HEV spreads among pigs.

Board 144. Enhanced Neurodegenerative Biomarkers Expressions Accompanied by Impairment of Ubiquitin-Proteasome System in Experimental Cerebral Toxocariasis

C. K. Fan[1], C. W. Liao[2], T. C. Kao[3], K. E. Su[4], Y. H. Lin[5], W. L. Cho[6];

[1]Department of Parasitology & Graduate Institute of Medical Sciences, Taipei Medical University College of Medicine, Taipei, TAIWAN, [2]Institute of Tropical Medicine, National Yang-Ming University College of Medicine, Taipei, TAIWAN, [3]Departmet of Parasitology, Taipei Medical University College of Medicine, Taipei, TAIWAN, [4]Department of Parasitology, National Taiwan University College of Medicine, Taipei, TAIWAN, [5]Department of Pathology, Taipei Medical University College of Medicine, Taipei, TAIWAN, [6]Institute of Tropical Medicine, National Yang-Ming University College of Medicine,, Taipei, TAIWAN.

Background: Human cerebral toxocariasis (CT) is predominantly caused by *Toxocara canis* larval invasion of the brains. Although it is not uncommon for reported clinical CT cases to present eosinophilic meningitis, encephalitis, myelitis, arachnoiditis, and dementia, the actual number of reported cases of cerebral infection with *T. canis* is still limited. In addition, brain involvement is likely too cryptic or not easily detected in humans with CT; thus, the underlying mechanism behind the neuropathogenesis of CT has remained largely unclear. **Methods**: Neurodegenerative biomarkers (NDB) expression, including TGF-β1, S100B, GFAP, NF-L, tTG, AβPP, Tau, and BACE1 as well as ubiquitin-proteosome system (UPS) function in the brains of mice inoculated with a single dose of 250 *T. canis* embryonated eggs was investigated from 3 days to 8 weeks post-infections (dpi or wpi) by Western blot and RT-PCR. **Results**: At 4 and 8 wpi, *T. canis* larvae were found to invade areas around choroid plexus but without eliciting leukocytes infiltration in the brains of infected mice; nevertheless, astrogliosis, an indicator of BI, with 78.9-fold to 142.0-fold increases in GFAP expression was present. Meanwhile, markedly increased levels of other NDB protein, with increases ranging from 2.0-fold to 12.0-fold were found, though their corresponding mRNA expressions were not found to be present at 8 wpi. Concomitantly, UPS impaired as evidenced by over-expression of conjugated ubiquitin and ubiquitin in the brain. **Conclusions**: To the best of our knowledge, this study is the first to provide clear evidence of the concomitant presence of enhanced NDB expression and UPS impairment during *T. canis* larval invasion of the brain. Although there is not strong evidence linking increased expression of NDB and behavioral disorders in experimental CT, the results of present study and those of the others cited in this paper suggest the possibility that cerebral infection by *T. canis* can have deleterious consequences and may increase the risk that CT will develop into neurodegenerative-like disease such as AD cannot be completely excluded due to neurodegeneration associated AβPP, phosphorylated Tau, and BACE1 emerged in the brain.

Board 145. Hantavirus in the Eurasian common shrew (*Sorex araneus*) in Siberia, Russia

L. Yashina[1], S. Abramov[2], V. Gutorov[1], J. Hay[3], R. Yanagihara[4];

[1]State Research Center of Virology and Biotechnology, Koltsovo, RUSSIAN FEDERATION, [2]Institute of Systematics and Ecology of Animals, Novosibirsk, RUSSIAN FEDERATION, [3]State University of New York, Buffalo, NY, [4]University of Hawaii at Manoa, Honolulu, HI.

Background: Hantaviral antigens were reported more than 20 years ago in tissues of the Eurasian common shrew (*Sorex araneus*), captured in European Russia. With the advent of powerful gene-amplification technology, this decades-old finding has been corroborated by the demonstration of a phylogenetically distinct hantavirus, named Seewis virus (SWSV), in *Sorex araneus* captured in Switzerland. As further evidence that rodents are not the sole reservoir hosts of hantaviruses, several other shrew-borne hantaviruses have recently been detected, including Tanganya virus in the Therese shrew (*Crocidura theresae*), Imjin virus in the Ussuri white-toothed shrew (*Crocidura lasiura*), Cao Bang virus in the Chinese mole shrew (*Anourosorex squamipes*), Camp Ripley virus in the northern short-tailed shrew (*Blarina brevicauda*), Ash River virus in the masked shrew (*Sorex cinereus*) and Jemez Springs virus in the dusky shrew (*Sorex monticolus*). **Methods:** To further clarify the geographic distribution and genetic diversity of hantaviruses harbored by soricid reservoir hosts, lung tissues from six *Sorex araneus* and two *Crocidura sibirica*, captured near Teletzkoye Lake in the Republic Altai in Siberia during August and September 2007, were analyzed by RT-PCR using oligonucleotide primers based on conserved regions of the L-genomic segments of Thottapalayam virus and other shrew-borne hantaviruses. **Results:** Hantavirus sequences were detected in three *Sorex araneus*. Alignment and comparison of L-genomic nucleotide and amino acid sequences showed an intra-strain difference of 2-8% and 0-2%, respectively. These sequences appeared to be genetic variants of SWSV, differing from the prototype mp70 strain by 19-21% at the nucleotide level and 0-2% at the amino acid level. Phylogenetic analysis showed geographic-specific clustering of SWSV strains from Switzerland and Russia. **Conclusions:** The detection of SWSV in *Sorex araneus* captured in Siberia represents the first evidence of hantaviruses in this geographic region and forecasts that many more hantaviruses will be found in diverse shrew species throughout Russia. Moreover, the geographic-specific genetic variation of SWSV in *Sorex araneus* is akin to that of rodent-borne hantaviruses, suggesting parallel co-evolution of hantaviruses in their soricid and rodent hosts.

Board 146. Space-time clustering of non-human antimicrobial resistance in Denmark. The case of Escherichia coli (1997-2005)

E. N. Abatih[1], A. K. Ersbøll[1], D. M. Lo Fo Wong[2], H. Emborg[2];

[1]University of Copenhagen, Frederiksberg, DENMARK, [2]Danish Technical University, Copenhagen, DENMARK.

Background: Despite increasing awareness on the public health consequences of antimicrobial resistance in bacteria in animals, spatial and temporal patterns have been rarely investigated in detail. In Denmark, occurrence of resistance in bacteria in animals, animal products and humans, is routinely monitored. This study aimed at determining whether the observed variations in the prevalence of antimicrobial resistance against ampicillin in Escherichia coli isolates from healthy pigs at slaughter were random or clustered in space and time. **Methods:** A total of 2621 bacteria isolates obtained between 1997 and 2005 from the DANMAP (The Danish Integrated Antimicrobial Resistance Monitoring and Research Programme) were used. Data on the quantity of ampicillin consumed was obtained from the VetStat (Danish Register of Veterinary Medicines) database. The effects of ampicillin consumption and seasonality on the distribution of resistance in E. coli were investigated. Space-time interaction was assessed using the space-time K-function and detection and location of significant space-time clusters was done using the space-time scan statistic. **Results:**Significant space-time clusters of farms with resistant E. coli isolates were found in the North Eastern part of Jutland and Funen and in the Southern part of Zealand. A highly significant space-time cluster was also found in autumn in Jutland and Funen. Ampicillin consumption at farm level did not appear to have any significant effects on space-time clustering. **Conclusions:** The results highlighted key areas needing particular attention and should serve as a platform for the implementation of strategies for the reduction of ampicillin resistance in bacteria in pigs in Denmark. The results can also be a valuable tool to risk assessors in their effort to assess the impact of antimicrobial usage on emergence of resistance as well as to epidemiologists in their effort to understand the association between antimicrobial usage and health outcome of animals and humans.

Vaccines & Vaccine-Preventable Diseases

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 147. Was Colorado's 2004-05 Large Increase in Reported Pertussis Cases for Real?

D. Aragon[1], K. Gershman[1], J. K. Todd[2], D. Lezotte[3];

[1]Colorado Department of Public Health and Environment, Denver, CO, [2]The Children's Hospital, Denver, CO, [3]University of Colorado Denver, Denver, CO.

Background: Reported cases of pertussis in Colorado more than tripled during 2004-2005 compared to the previous 5-year average. Our objective was to assess to what extent this represented a true increase in pertussis incidence versus an artifactual increase due to greater awareness and testing for pertussis. **Methods:** We analyzed several data sources including: 1) reported cases of confirmed and probable pertussis between January 1, 1996 and December 31, 2005; 2) statewide hospital discharge data for pertussis hospitalizations among infants <1 year; and (3) polymerase-chain reaction (PCR) testing data from a large provider of pertussis PCR testing. We performed descriptive analyses for 3 time periods: 1996-1999 (Time 1); 2000-2003 (Time 2); 2004-2005 (Time 3), and Poisson regression on infant hospitalization rates and age group-specific incidence rates. **Results:** The <1 year and 1-4 year age groups comprised substantially lower proportions of reported cases from Time 2 to Time 3, whereas, the 15-19 and ≥ 40 year age groups comprised substantially increased proportions of cases. Age group-specific incidence rate ratios for Time 3:Time 2 were greatest for the 10-14 year and older age groups. The overall trends in reported case rates and hospitalizations rates for infants <1 year were unchanged from 1996 to 2005. In contrast, overall trends in incidence rates increased for all other age groups driven by striking rate increases in 2004-05. PCR testing volume increased more than six-fold from Time 1 to Time 3. PCR testing volume in the <1 year age group decreased from Time 2 to Time 3 while positivity remained unchanged. In contrast, testing volume for all other age groups increased from Time 2 to Time 3 and positivity decreased except for the 15-19 year age group. **Conclusions:** Our analysis of multiple data sources did not support the large increase in reported pertussis in Colorado during 2004-2005 as necessarily representing a real increase in disease incidence. The data were consistent with an increase in pertussis awareness and testing. Of note was absence of convincing increases in reported incidence and hospitalizations in the <1 year age group. Our results have implications for interpreting recent reported pertussis increases in other states and nationally.

Board 148. Estimating Vaccination Coverage: Validity of Household-Retained Vaccination Cards and Parental Recall

E. T. Luman[1], T. Ryman[1], M. Salban[2];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]CNMI Department of Public Health, Saipan, CNMI, NORTHERN MARIANA ISLANDS.

Background: Public health programs rely on household-survey estimates of vaccination coverage as a basis of programmatic and policy decisions; however, the validity of estimates derived from household-retained vaccination cards and parental recall has not been thoroughly evaluated. **Methods**: Using data from a vaccination coverage survey conducted in the Western Pacific's Northern Mariana Islands in July 2005, we compared results from household data sources (cards and parental recall) to medical record sources for the same children. We calculated the percentage of children aged 1, 2, and 6 years who received all vaccines recommended by age 12 months, 24 months, and for school entry, respectively. **Results**: Coverage estimated based on vaccination cards (assuming that children without cards were not completely vaccinated) was 14%-30% in the three age groups compared to 78%-91% for the same children based on medical records. When cards were supplemented by parental recall, estimates were 51%-53%. Among children with a vaccination card (71% of children aged 1 and 2 years, 58% of those aged 6 years), card-estimated coverage was 25%-43%. Concordance, sensitivity, specificity, positive and negative predictive values, and kappa statistics generally indicated poor agreement between household and medical record sources. **Conclusions**: These results show that household-retained vaccination cards and parental recall were insufficient sources of information for estimating vaccination coverage in this population. This study emphasizes the importance of identifying reliable sources of vaccination history information and reinforces the need for awareness of the potential limitations of vaccination coverage estimated from surveys that rely on household-retained cards and/or parental recall.

Board 149. Annual Extra-seasonal Spike in Incidence of Invasive Pneumococcal Disease

N. D. Walter, T. H. Taylor, Jr., M. R. Moore, for the ABCs Team;

CDC, Atlanta, GA.

Background: Incidence of invasive pneumococcal disease (IPD) in the U.S. is seasonal, with rates 5-fold higher in winter than in summer. Additionally, sharp but unexplained annual "spikes" in IPD incidence during the weeks around January 1 have been reported. We analyzed 11 years of IPD surveillance data to characterize these spikes. **Methods:** Cases of IPD were defined as isolation of pneumococcus from normally sterile sites among residents of 10 sites participating in CDC's Active Bacterial Core surveillance (ABCs) program. To describe seasonal variation in IPD incidence, we fitted standard sinusoidal curves by least-squares separately for each of 6 age strata during each of 3 periods. Age strata were <5, 5-17, 18-34, 35-49, 50-64, ≥65 years. Periods were: pre-pneumococcal conjugate vaccine (PCV) (July 1995-June 2000), transition (July 2000-June 2001), and post-PCV (July 2001-June 2006). We defined spike weeks (SW) as weeks in which IPD incidence exceeded two standard deviations above fitted seasonal curves and winter spike weeks (WSW) as SW during December-January. We defined shoulder weeks as December-January weeks which were not WSW. For cases occurring among persons ≥50 years old, we compared geographic, demographic, clinical characteristics, and serotypes during WSW and shoulder weeks. **Results:** During 574 weeks, 17 SW were identified, 13 (76%) of which were WSW. All WSW occurred during the last week of December and the first 2 weeks of January. Among persons aged 50-64 and ≥65 years, at least one WSW was detected during 8 of 11 and 9 of 11 winters, respectively. WSW were less common among younger adults and children (0, 2, 4, and 5 of 11 winters among persons <5, 5-17, 18-34, and 35-49 years old, respectively). WSW occurred during all 3 periods. Geographical distribution and serotypes of IPD did not differ significantly during WSW and shoulder weeks. **Conclusions:** A sharp spike in IPD incidence consistently occurs among adults aged ≥50 years around January 1 of most years. The lack of a predominant geographic site or serotype during WSW suggests the phenomenon is not outbreak-related. Timing of the spikes and the predominance of older adults suggest the spikes may be related to older adults' increased exposure to young children around the winter holidays.

Board 150. Safety Review of Quadrivalent Human Papillomavirus (Types 6, 11, 16, 18) Recombinant Vaccine

W. Huang[1], L. Markowitz[2], J. Iskander[3];

[1]Epidemic Intelligence Service, Career Development Division, Office of Workforce and Career Development; Immunization Safety Office, Office of the Chief Science Officer, Centers for Disease Control and Prevention, Atlanta, GA, [2]Division of STD Prevention, National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention, Centers for Disease Control and Prevention, Atlanta, GA, [3]Immunization Safety Office, Office of the Chief Science Officer, Centers for Disease Control and Prevention, Atlanta, GA.

Background: Human papillomavirus (HPV) infection causes >550,000 cases of cervical cancer worldwide annually. Widespread use of prophylactic HPV vaccine is expected to greatly reduce the incidence of HPV-related cancers. Quadrivalent HPV vaccine (qHPV) is the first HPV vaccine licensed in the US and has been licensed in >80 countries. **Methods**: We reviewed safety data of qHPV from clinical trials and the passive US Vaccine Adverse Event Reporting System (VAERS) and addressed planned studies. **Results**: Prelicensure trials: In 7 clinical trials enrolling 21,464 subjects aged 9-26 years (11,778 qHPV vs. 9,686 placebo), injection site reactions were reported more frequently with qHPV than with placebo (82.9% vs. 73.3%). Serious adverse events (SAEs) were comparable (0.9% vs. 1.0%). No differences in congenital anomalies were observed overall among pregnant women (15 vs. 16); among those vaccinated within 30 days of conception there were 5 abnormalities in the vaccine and none in the placebo group-but no pattern existed. The numbers of deaths did not differ significantly between groups (11 vs. 7); none were considered related to the vaccine. VAERS: During June 2006-July 2007, VAERS received 2,531 reports of adverse events following qHPV after >12.4 million doses distributed in the US; 149 (1.9 per 100,000 doses) were SAEs. Vasovagal syncope (n = 300) was a newly identified adverse event. The diagnosis of Guillain-Barre syndrome was confirmed in 5 vaccinees. None of the 3 confirmed deaths appeared to be vaccine related. Planned studies: Vaccine Safety Datalink is conducting active surveillance. The manufacture established a pregnancy registry in the US to prospectively monitor pregnancy outcomes in vaccinated women. Phase IV studies will (1) enroll ~44,000 vaccinated subjects in a US managed care organization to investigate short-term SAEs and (2) evaluate long-term safety by linking national registries in Nordic countries. **Conclusions**: Review of data involving >30,000 pre-licensure and >12.4 million post-licensure doses provides reassurance regarding the safety of qHPV. VAERS reports should not be used to infer causality. Ongoing safety monitoring especially on syncope, long-term outcomes (e.g. autoimmune diseases), pregnancy outcomes and deaths will support increased global use of HPV vaccines.

Antimicrobial Resistance

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 151. Impact of the New Clinical and Laboratory Standards Institute Nonmeningitis Penicillin Breakpoints on the Incidence of Penicillin Resistance among Invasive Pneumococcal Disease Isolates

M. Deutscher[1], J. Jorgensen[2], B. Beall[1], A. Glennen[3], M. R. Moore[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]University of Texas Health Science Center, San Antonio, TX, [3]Minnesota Public Health Laboratory, St. Paul, MN.

Background: In January 2008, the Clinical and Laboratory Standards Institute (CLSI) will publish new breakpoints for defining susceptibility of *Streptococcus pneumoniae* to penicillin (PEN). The old susceptible (S), intermediate (I), and resistant (R) breakpoints were, respectively, ≤0.06, 0.12-1, and ≥2 µg/ml. The new breakpoints for nonmeningitis isolates are ≤2, 4, and ≥8 µg/ml for intravenous PEN. All meningitis isolates will be considered S (≤0.06 µg/ml) or R (≥0.12 µg/ml). We determined the impact of these new breakpoints on the proportions of pneumococci identified as S, I, and R. **Methods:** Cases of invasive pneumococcal disease (IPD) were defined by isolation of pneumococcus from a normally sterile site in a resident of any of 10 Active Bacterial Core surveillance (ABCs) areas during 2005-2006. Isolates were tested for susceptibility by the CLSI broth microdilution method. **Results:** Of the 7834 cases of IPD identified during 2005-2006, isolates were available for 6800 (87%) of which 6383 (94%) were from nonmeningitis cases. Using the old PEN breakpoints, 4818 (75%), 920 (15%), and 645 (10%) of nonmeningitis isolates were S, I, and R, respectively. Using the new nonmeningitis PEN breakpoints, 5991 (94%), 326 (5%), and 66 (1%) of nonmeningitis isolates were S, I, and R, respectively. Among nonmeningitis isolates, 285 (4.5%) and 68 (1.1%) were cefotaxime intermediate and resistant, respectively, while 426 (6.7%) and 181 (2.8%) were ceftriaxone intermediate and resistant, respectively. By classifying all meningitis isolates as either PEN S or PEN R, 308 (74%) and 109 (26%) were S and R, respectively. **Conclusions:** The new breakpoints markedly reduce the number of reported PEN-resistant isolates. The change in PEN breakpoints could encourage use of PEN for treatment of susceptible nonmeningitis cases of IPD. Microbiologists and clinicians should be aware of the new breakpoints when reporting and using susceptibility results for clinical management.

Board 152. Use of Antibiotics among Dairy Veterinarians in Mid-Atlantic States

N. M. M'ikanatha[1], S. C. Rankin[2], D. O. Morris[3];

[1]Pennsylvania Department of Health, Harrisburg, PA, [2]University of Pennsylvania School of Veterinary Medicine, Philadelphia, Philadelphia, PA, [3]University of Pennsylvania School of Veterinary Medicine, Philadelphia, PA.

Background: Public health concerns about antimicrobial resistance in zoonotic pathogens of animal origin have prompted a call for judicious use of antibiotics on the farm. However, current management practices among food-animal veterinarians are largely unknown. **Methods**: During 2007, we administered an online survey of all dairy veterinarians in Delaware, Maryland, New Jersey and Pennsylvania who were members of the American Association of Bovine Practitioners (AABP). The survey sought to assess practices and opinions related to antibiotic use among dairy veterinarians in the Mid-Atlantic States and to optimize future educational interventions. The use of written management protocols, recommendations regarding milk replacement, and antibiotics prescribing practices were documented. Veterinarians' opinions regarding antimicrobial use by non-veterinary staff on dairy farms and the emergence of antimicrobial resistance were also assessed. **Results:** A total of 35 AABP members (20%) participated in the study. The majority (83%) spend most of their time on dairy calls. Eight-nine percent spend less than 10 minutes per visit discussing antimicrobial use with farmers. Forty percent of the respondents indicated they had provided written disease management protocols to clients and 48% of those thought farmers followed these protocols. Twenty-nine percent recommend colostrum replacer for newborn heifer calves in the first 24 hours and 38% reported the milk replacer contained oxtetracycline

with neomycin. While respondents' choice for treating common conditions included a range of antibiotics, they most commonly cited ceftiofur and oxytetracycline. Forty-nine percent of the respondents thought that more than 50% of their clients used unprescribed antibiotics. Over sixty percent of the respondents were concerned about antimicrobial resistance. The majority of the respondents thought that availability of antibiotics for use by non-veterinarians was among the contributing factors to antimicrobial resistance. **Conclusion:** Most veterinarians surveyed were concerned about antimicrobial resistance. Most veterinarians surveyed use ceftiofur as their preferred antibiotic. Continuing education is necessary to address prescribing patterns in the face of emerging antimicrobial resistance.

Board 153. Prevalence and Antimicrobial Resistance of *Campylobacter* from Retail Meats: Results of the National Antimicrobial Resistance Monitoring System (NARMS): 2002-2006

P. McDermott, L. English, E. Hall-Robinson, S. Friedman, J. Abbott, S. Zhao;

Food & Drug Administration, Laurel, MD.

Background: *Campylobacter* is a leading cause of foodborne bacterial pathogen in the United States. Since 2002, the U.S. National Antimicrobial Resistance Monitoring System (NARMS) has investigated the prevalence and the antimicrobial susceptibility of *Campylobacter* present in the retail meat supply. **Methods:** *Campylobacter* were recovered from a monthly sampling of chicken breasts, ground turkey, ground beef, and pork chops purchased from grocery stores in 10 states (CA,CO, CT, GA, MD, MN, NM, NY, OR, TN). A total of 20,294 meat samples taken from 2002-2006 were screened for presence of *Campylobacter*. In 2002-2003, susceptibility testing included four antimicrobials (CIP, ERY, GEN, and DOX) using agar dilution. After 2004, nine antimicrobials were tested (CIP, NAL, ERY, GEN, TET, FFN, AZI, TEL, and CLI) using broth micro dilution. *Campylobacter* isolates were also analyzed by PFGE. **Results:** Chicken showed the highest *Campylobacter* contamination rate: 47% in 2002, 52% in 2003, 60% in 2004, and 46% in 2005 and 49% in 2006. Other meats had contamination rates < 2.5%. Overall, *C. jejuni* constituted 71.1% of strains, *C. coli* 28.6% and *C. lari* 0.3%. Overall Cip^R (MIC $\geq$ 4 μg/mL) increased significantly (p=0.0158) from 2002 (13.8%) to 2005 (19.6%), and dropped slightly in 2006 (18.9%) following the ban of fluoroquinolone use in poultry production. In *C. jejuni* from chicken breast, however, Cip^R was present in 15.1% of isolates from 2005 and 16.9% in 2006. During the five year testing, Tet^R increased from 27.6% to 47.8% overall. Ery^R each year was present in <1% *C. jejuni*, and decreased steadily in *C. coli* from 18.9% in 2002 to 5.7% in 2006. The most common MDR pattern among strains resistant to $\geq$ 5 antimicrobials was AZI-CLI-ERY-TEL-TET. *C. coli* showed higher proportion of MDR than *C. jejuni*. The PFGE results showed that *Campylobacter* genetically were very diverse, however certain clones were widely dispersed in different meat brands from different store chains in all five years. **Conclusions:** *Campylobacter*, including antimicrobial resistant strains, persist in retail chicken meats and provide a reservoir of resistant strains in the food supply.

Board 154. Decreasing Prevalence of Antimicrobial Resistance in Non-Typhoidal Salmonella Isolated from Children with Bacteraemia in a Rural District Hospital, Kenya

S. Kariuki[1], G. Revathi[2], J. Kiiru[1], J. Mwituria[1];

[1]KEMRI, Nairobi, KENYA, [2]Aga Khan University Hospital, Nairobi, KENYA.

Background: In sub-Saharan Africa community-acquired non-typhoidal Salmonella (NTS) is a major cause of high morbidity and death among children under 5 years of age especially from resource poor settings. The emergence of multidrug resistance is a major challenge in treatment of life threatening invasive NTS infections in these settings. **Methods:** We analysed 336 Non-Typhoidal Salmonella (NTS) isolated from children less than 10 years of age with bacteraemia admitted to a rural District Hospital in Kenya from 1994 to 2005 by pulsed field gel electrophoresis to determine genetic relatedness of strains and antimicrobial susceptibility testing. **Results:** Most NTS were either *Salmonella* Typhimurium 114(33.9%) or *S.* Enteritidis 128(38.1%), with minimal genotypic diversity over the study period. The NTS showed a remarkable decrease in levels of resistance especially to three commonly available antimicrobials - amoxicillin, co-trimoxazole and gentamicin from highs of 69.2%, 68.4% and 12% during 1994-1997 to 11%, 13% and 4%, respectively in 2002-2005 (P value <0.01). In contrast, the prevalence of NTS multiply resistant to all commonly available drugs including ampicillin, streptomycin, co-trimoxazole, chloramphenicol and tetracycline from children in an urban setting rose from 31% in 1994 to 42% at present, with concomitantly higher MICs of each drug. However, all NTS remained fully susceptible to cefotaxime and ciprofloxacin. **Conclusions:** Our findings show that commonly available drugs may still be useful for treatment of invasive NTS infections in this rural population, which is in sharp contrast to the situation in major urban centres. With the introduction of free healthcare in Government facilities and at a major research site in Kilifi, it is plausible that more of the rural population is accessing healthcare facilities for treatment thus minimising over-the-counter sales of antibiotics. Sustained surveillance of NTS in the community will be required to monitor if these levels of susceptibility to antimicrobials are maintained.

Board 155. Multi-Drug Resistant Non-Typhoidal *Salmonella* in New York State's Foodborne Diseases Active Surveillance Network (FoodNet) Counties

S. M. Solghan[1], S. M. Zansky[1], N. B. Dumas[2], T. P. Root[2], T. M. Quinlan[2], L. R. Armstrong[2], N. L. Spina[1];

[1]New York State Department of Health, Albany, NY, [2]New York State Department of Health - Wadsworth Center, Albany, NY.

Background There are an estimated 1.4 million non-typhoidal (NT) *Salmonella* cases in the United States annually, resulting in over 16,000 hospitalizations and 580 deaths. Most cases are self-limiting, but severe cases may require antibiotic treatment. With the emergence of multi-drug resistant NT *Salmonella*, knowledge of current resistance patterns is key to determine appropriate treatment. **Methods** The NYS Department of Health Wadsworth Center public health laboratory tested all *Salmonella* isolates from cases residing in NYS's 34 county Foodborne Diseases Active Surveillance Network (FoodNet) catchment area between May 2003 and September 2007 for antimicrobial susceptibility to ampicillin, chloramphenicol, streptomycin, sulfisoxazole, tetracycline and ciprofloxacin. Isolate susceptibility results were linked to their corresponding demographic and clinical data and analyzed. Multi-drug resistant isolates were defined as resistant to ampicillin, chloramphenicol, streptomycin, sulfisoxazole and tetracycline (R-type ACSSuT). **Results** Antimicrobial susceptibility for 2,050 FoodNet cases (94.8% of total cases) showed 80.1% pansusceptible, 19.7% resistant to at least one agent, and 6.7% R-type ACSSuT. Only 7 (0.3%) isolates were resistant to ciprofloxacin. Cases with R-type ACSSuT were older (median age, 46 years) compared to pansusceptible cases (median age, 35 years) (p<0.01). Over 14% of African American cases (19/135) had R-type ACSSuT isolates, compared to 6.5% of Caucasian cases (114/1761) (p<0.01). R-type ACSSuT cases were hospitalized (33.6%) more frequently than pansusceptible cases (24.0%) (p<0.05). Length of hospitalization was not significantly different. Serotypes with the highest proportion of R-type ACSSuT included *S.* Typhimurium, 17.6% (73/415) and *S.* Newport, 27.8% (44/158). From 2003 to 2007 cases with R-type

ACSSuT significantly decreased from 12.9% (40/310) to 3.4% (12/356) (p<0.01). **Conclusion** Although R-type ACSSuT NT *Salmonella* has decreased since 2003 within the NYS FoodNet catchment area, monitoring resistance patterns remains important in identifying emerging resistant strains, vulnerable populations and determining appropriate treatment regimens. The higher rate of R-type ACSSuT among African American cases requires further study.

Blood, Organ, & Other Tissue Safety

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 156. Prospective Surveillance of Invasive Fungal Infections (IFIs) among Solid Organ Transplant (SOT) Recipients in the U.S. 2001-2006: Review of TRANSNET

T. M. Chiller[1], C. Kauffman[2], B. Alexander[3], D. Andes[4], S. Hadley[5], T. Patterson[6], R. Walker[7], V. Morrison[8], L. Brumble[9], A. Freifeld[10], B. J. Park[1], K. Wannemuehler[1], P. G. Pappas[11];

[1]CDC, Atlanta, GA, [2]Univ. of Michigan, Ann Arbor, MI, [3]DUMC, Durham, NC, [4]Univ. of Wisconsin, Madison, WI, [5]NEMC, Boston, MA, [6]UTXSAMC,, San Antonio, TX, [7]Mayo Clinic, Rochester, MN, [8]Univ. of Minnesota, Minneapolis, MN, [9]Mayo Clinic, Jacksonville, FL, [10]University of Nebraska, Omaha, NE, [11]Univ. of Alabama, Birmingham, AL.

Background: IFIs are a major cause of morbidity and mortality among SOT recipients, although multicenter prospective surveillance for these infections is generally lacking. A better understanding of the epidemiology of these infections could significantly improve the prevention and treatment of this important post-transplant complication. **Methods**: TRANSNET consists of 16 US transplant centers that have prospectively collected detailed data on all IFIs among their SOTs from 2001-2006. Total number of transplants performed at each site was also collected. **Results**: From March 2001-Oct 2005, 17,115 SOTs were performed at TRANSNET sites and a total of 1,222 incident IFIs were reported; these consisted of invasive candidiasis (55%), invasive aspergillosis (19%), cryptococcosis (9%), zygomycosis (2%), other molds (9%), endemic fungi (5%), and pneumocystosis (1%). One-year cumulative incidences, based on first IFI, were: small bowel 17.5%, lung and heart/ lung 8%, liver 4%, and kidney 3.5%. The IFI with highest incidence was candidiasis (1.95%), followed by aspergillosis (0.65%). Reported incidences of IFIs varied across sites. **onclusions**: TRANSNET is the most detailed prospective assessment of IFIs following organ transplantation. Insights from these data will be valuable in understanding the incidence and risk factors for IFI in populations at greatest risk, and designing comprehensive preventive and other interventional strategies to improve outcomes among these patients.

Board 157. Robustness of Solvent/Detergent Treatment of Plasma Derivatives: A Data Collection of PPTA Member Companies

H. O. Dichtelmueller, L. Biesert, F. Fabbrizzi, R. Gajardo, A. Groener, I. von Hoegen, J. I. Jorquera, C. Kempf, T. R. Kreil, D. Pifat, G. Poelsler;

PPTA, Annapolis, MD.

Background: Seven member companies of the Plasma Protein Therapeutics Association (PPTA) participated in collection of data to demonstrate the reliability, efficacy and robustness of solvent detergent (S/D) treatment of plasma-derived therapies. PPTA is the international trade and standards-setting association for manufacturers of plasma-derived therapies and their recombinant analogs. **Methods**: Data on the inactivation of enveloped viruses by S/D treatment was collected from seven PPTA member companies. The data of 308 studies at production conditions (n = 129) and beyond production specifications (robustness; n= 179) were evaluated. Studies comprise different procedures of S/D treatment (TNBP/ Cholate, TNBP/Tween 80, TNBP/Triton X-100) and different products (Factor VIII, Factor IX and iv. and im. immunoglobulins). **Results**: Product class, pH, protein concentration or temperature, did not appear to have significant impact on virus inactivation. The only parameter that did appear to be critical was the concentration of solvent/detergent compounds. The data presented here, employing a broad range of process parameters, demonstrate the robustness of virus inactivation by S/D treatment with regard to a wide spectrum of enveloped viruses by S/D treatment, when the solvent/detergent concentration was within the defined production conditions. **Conclusions**: The results confirm the virus safety of S/D treated plasma derivatives with regard to enveloped viruses and the data substantiate that since introduction of S/D treatment no transmission of viruses like HIV, HBV, HCV or other enveloped viruses by plasma derivatives was reported.

Board 158. Prospective Surveillance for Invasive Fungal Infections (IFIs) in Hematopoietic Stem Cell Transplant Recipients (HSCTs), 2001-2006: Overview of the TRANSNET Database

B. J. Park[1], D. P. Kontoyiannis[2], K. Marr[3], J. Ito[4], W. Brown[5], E. Anaissie[6], T. Perl[7], M. Schuster[8], J. Wingard[9], T. Walsh[10], T. Chiller[1], P. G. Pappas[11];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]MD Anderson Cancer Center, Houston, TX, [3]FHCRC, Seattle, WA, [4]City of Hope, Duarte, CA, [5]Stanford University, Palo Alto, CA, [6]Univ of Arkansas, Little Rock, AR, [7]Johns Hopkins University, Baltimore, MD, [8]University of Pennsylvania, Philadelphia, PA, [9]University of Florida, Gainesville, FL, [10]National Cancer Institute, Bethesda, MD, [11]University of Alabama at Birmingham, Birmingham, AL.

Background: Understanding current epidemiologic trends and the burden of IFIs, a leading cause of death among HSCTs, may lead to improved outcomes. Incidence and epidemiology of IFIs in this population has previously been derived mainly from single-institution studies. **Methods:** 21 US transplant centers (TRANSNET) prospectively enrolled all IFIs occurring in HSCTs. Demographic, diagnostic, clinical, therapeutic, immunosuppression, and outcome data were collected. Only proven or probable IFIs (EORTC/MSG criteria) were included. **Results:** Between March 2001 and October 2005, 16,872 HSCT transplants (42% allogeneic, 58 % autologous) were performed at TRANSNET sites; complete data are available on 995 IFIs occurring in HSCTs. Median age was 50 yrs; 59% were male. Invasive candidiasis (IC) accounted for 30% of IFIs, invasive aspergillosis (IA) 44%, other or unspecified moulds 12%. 90-day all-cause mortality with IC and IA was 52% and 58% (p=0.15), respectively. One-year cumulative incidences, based on first IFI, were: unrelated allo 8.6%, mismatched-related allo 8.4%, matched-related allo 6.1, and autologous 1.4. The IFI with highest incidence was aspergillosis (1.7%), followed by candidiasis (1.2%). Reported incidences of IFIs varied across sites. **Conclusions:** We report the results of the first national surveillance program on IFIs in HSCTs. Invasive aspergillosis represents the major challenge and occurs late post HSCT, although other moulds are emerging. These

data could be of value towards a better understanding of prevention and treatment strategies for IFIs in HSCTs, and the design of future studies.

Board 159. A Prospective Study of Multiple Donor Exposure Blood Recipients (PSBR)

K. Dorsey[1], Y. Wu[2], R. Cable[3], C. Hapip[1], Y. Tang[1], J. Trouern-Trend[1], D. De Stefano[2], R. Melmed[3], M. Champion[2], S. Zou[1];

[1]American Red Cross, Rockville, MD, [2]Yale University School of Medicine - Yale-New Haven Hospital, New Haven, CT, [3]American Red Cross, Farmington, CT.

Background Study of blood recipients is important for evaluating the safety of the blood supply, especially for new or re-emerging pathogens. In order to study transfusion transmitted infectious outcomes in chronic blood recipients, a linked donor-recipient repository has been established and four pathogens of interest have been studied to date. **Methods** Consented recipients are interviewed with a questionnaire to assess risk factors, demographic and clinical data; a blood sample is also collected from recipients at baseline and each follow up visit. Samples were tested for *Chlamydia pneumoniae* (Cp), cytomegalovirus (CMV), parvovirus B19 (B19) and *Babesia microti* (BM), for antibodies and nucleic acids. Donors are informed about the study at the blood collection site and can opt-out. All study units are leukoreduced and the retention tubes from the transfused units are collected and stored in the repository; if necessary, they are tested to investigate possible infections in the recipient. If the recipient of a transfused unit(s) seroconverts or shows other signs of becoming infected further follow up of the donor(s) will occur. **Results** As of the end of recipient recruitment, December 2006, the final total of recipients enrolled is 120, with 4596 donor exposures. Since the beginning of the study, 44 case investigations were initiated. The majority of the cases were opened for CMV investigations (19), followed by CP (13), B19 (11) and BM (1). Of the cases investigated, 30 cases were closed and 14 were open as of October 2007. The investigations were closed for a variety of reasons, 10 seroconversions were due to passive transfer of antibodies, 4 were determined to be real infections with a possibility of transfusion transmission (1 CMV PCR+), 2 were determined to be true infections but not transfusion related and 14 were closed for other reasons. Of the 4 closed determined to be real infections, 2 were for CP and 2 for CMV. Of the 14 opened cases, 3 are CMV PCR + and 1 is PCR + for *Babesia microti*. **Conclusion** Among 120 transfusion recipients with 4596 for donor exposures, there have been confirmed infections for CP , CMV and Babesiosis. Transfusion transmission can not be confirmed or ruled out for these cases. Four CMV PCR + cases and one *Babesia microti* PCR + case are currently being investigated.

Foodborne & Waterborne Infections

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 160. Resistance of *Salmonella* isolates to predation by *Acanthamoeba polyphaga*

J. R. McQuiston[1], R. M. Hoekstra[1], B. R. Levin[2], J. M. Logsdon, Jr.[3], R. V. Tauxe[1];

[1]CDC, Atlanta, GA, [2]Emory University, Atlanta, GA, [3]University of Iowa, Iowa City, IA.

Background: Serotype-based variation in protozoan predation has been observed for *Salmonella*. While studying whether protozoa can distinguish between mono- and diphasic strains of *Salmonella*, we identified two lineages, one of *S. enterica* ser. Typhimurium, and one of the monophasic variant I 4,5,12:i:- that appeared to be completely resistant to predation by *Acanthamoeba polyphaga*, unlike all other *Salmonella* tested. **Methods:** Protozoan predation was measured by comparing surface density of *Salmonella* in a linear predation assay. Briefly, *Salmonella* strains were grown on LB plates. *Acanthamoeba polyphaga* was added to one end of the plate and allowed to advance through the plated bacteria. Agar plugs from locations behind the advancing *Acanthamoeba* predation lines were taken and evaluated by *Salmonella* colony counts. **Results:** Predation of susceptible isolates on an agar surface caused a visible, $\geq \log_{10}$ decrease in cell density, while no difference was observed in the resistant lineages. In the absence of *Acanthamoeba*, isolates that appeared to be resistant grew to a lower cell density in surface but not liquid culture when compared to predation sensitive isolates ($p<0.0001$). Filtered growth media supernatant exchange did not alter the susceptibility of the isolate. Mixing of the isolates resulted in decreased predation of the susceptible isolate when the proportion of the resistant isolate cell density was greater than 80%. **Conclusions:** Our experiments to explore the properties of this phenomenon indicate: i) contact with the "resistant" strains changes neither amebic motility nor appetite for subsequent susceptible *Salmonellae*, ii) predation is not accounted for by a toxin or other agent released by these bacteria, and iii) in mixtures containing more than 80% of resistant bacteria, susceptible bacteria do not appear to be preyed upon. This apparent complete resistance to a natural protozoan predator has not previously been described, and the mechanism that makes amoebae refractory to these bacteria remains to be clarified.

Board 161. Surveillance of salmonelosis and O157 E. coli in Poland during 1995 - 2005 years

G. Madajczak;

National Institute of Public Health – National Institute of Hygiene, Warsaw, POLAND.

Background Salmonelosis is the most commonly reported infectious intestinal disease. During last ten years (1995 - 2005) number of salmonelosis cases rapidly decreased. E. coli O157 surveillance in Poland began in 1999 year. Almost all O157 strains are confirmed in reference laboratory - National Institute of Public Health - National Institute of Hygiene (NIZP- PZH). **Methods** All the Salmonella isolates are serotyped at Regional Sanitary Laboratories and only selected isolates (e.g. untypical or non-typable) are sent for further typing to NIZP-PZH. Regional Sanitary Laboratories use Salmonella isolation and identification methods developed also in NIZP-PZH. O:157 E. coli surveillance system basing on identification of sorbitol fermenting and serotyping. All O:157 strains independently of sorbitol fermentation are reported. All isolated strains are reidentified in NIZP-PZH. Moreover enterohemolysine and shiga toxins detection by fenotypical methods are performed. Also stx, eae and flic genes are detected. **Results and Conclusion** During 10-years period Salmonella cases decrease from more then 30000 to 16000 cases per year. Most common Salmonella serotype is Enteritidis, then Typhimurium. Only in 2003 year in Poland Salmonella Infantis and Virchow were more common then Typhimurium, because of two outbrakes. Every year during ten-years period 350 to 200 outbrakes caused by Salmonella are notified. It is 60 to 80 % of all Salmonella cases per year. Number of salmonelosis cases going down every year, because of a few reasons. First of all reason is health and sanitary standards improvement during last years. From 1995 to 2005 from 10000 to 25000 people with diarrhea are examinated to O:157 E. coli presence in stool samples. Every year form 7 to 14 O:157 E. coli are detected, but only single cases are verotoxic strains. The low rate of VTEC isolated in Poland is caused because of imperfect VTEC detection procedures - only O:

157 E. coli are looked for. All O:157 strains isolated in Poland were identified as E. coli O:157:NM but with genotype O157:H7. Most O:157 strains, isolated from human diarrhea cases, belong to EPEC group. It was confirmed by eae gene typing. All researched non-VTEC strains have eae gene type characteristic for EPEC strains.

Board 162. International Travel Associated Salmonellosis: Foodborne Diseases Active Surveillance Network (FoodNet) 2004-2006

K. L. Ong[1], S. Shin[2], A. Cronquist[3], R. Marcus[4], S. Thomas[5], D. Blythe[6], S. Meyer[7], D. Hoefer[8], P. Cieslak[9], S. Hanna[10], E. Scallan[11], FoodNet EIP Working Group;

[1]Atlanta Research and Education Foundation, Atlanta, GA, [2]California EIP, Oakland, CA, [3]Colorado Dept of Public Health and Environment, Denver, CO, [4]Connecticut EIP, New Haven, CT, [5]Georgia Division of Public Health, Atlanta, GA, [6]Maryland Dept of Health and Mental Hygiene, Baltimore, MD, [7]Minnesota Dept of Health, Minneapolis, MN, [8]New York State Department of Health, Albany, NY, [9]Oregon Public Health Division, Portland, OR, [10]Tennessee Dept of Health, Nashville, TN, [11]Centers for Disease Control and Prevention, Atlanta, GA.

Background: Foodborne infections diagnosed in the United States may be acquired abroad. Knowing the proportion attributable to international travel helps focus efforts to characterize domestic sources and informs food safety policy. Here we describe data on travel-related salmonellosis infections from the Foodborne Diseases Active Surveillance Network (FoodNet). **Methods:** FoodNet conducts active, population-based surveillance for laboratory-confirmed salmonellosis in 10 sites. Data have been collected on international travel since 2004; cases with international travel in the 7 days before illness onset were considered 'travel-related.' **Results:** From 2004-2006, 19,692 laboratory-confirmed cases of *Salmonella* were reported to FoodNet. Data on international travel were available for 13,276, of which 1,567 (12%) were travel-related (10% in 2004, 13% in 2005, and 13% in 2006). Overall, *S.* Typhi (66%) and *S.* Paratyphi A (69%) had the highest proportion of travel-related illnesses. Among the 15 most commonly identified serotypes, the proportion of travel-related illnesses was highest for *S.* Enteritidis (26%) and *S.* Oranienburg (21%), while cases of *S.* Heidelberg, *S.* I4[5]12:i- and *S.* Typhimurium var 5- were less likely to have traveled internationally (2.1%, 2.5% and 2.9% respectively). Persons >80 years had the lowest proportion of travel-related cases (2%); the highest rate was in persons 20-29 and 30-39 years (18%). The proportion of travel-related cases ranged from 5% to 12% each month, with the highest percentage of cases seen in July (11%) and August (12%). **Conclusions:** The likelihood that a case of salmonellosis was acquired from domestic food sources varies by serotype, season and age. Understanding which serotypes are more likely to be acquired during international travel improves our estimates of the burden of illness acquired domestically. Country-specific data on the distribution of *Salmonella* serotypes, along with information from cases on countries visited and specific food and water exposures during travel may inform more targeted prevention activities for travel-related salmonellosis.

Board 163. Novel Food Implicated in an Outbreak of Orally-transmitted Acute Chagas Disease in an Urban Area of the Amazon Region, Brazil, 2007

G. D. Freitas[1], A. A. Nobrega[1], A. P. Romano[1], E. G. Costa[2], J. M. Tinoco[3], M. D. Pontes[3], L. S. Leite[3], J. Sobel[4];

[1]Field Epidemiology Training Program, SVS, Brazilian Ministry of Health, Brasilia, BRAZIL, [2]Para State Chagas Disease Control Program, Belem, BRAZIL, [3]Secretariat of Health, Santa Izabel do Para, BRAZIL, [4]Office of Global Health, CDC, Atlanta, GA.

Background: Outbreaks of orally transmitted Acute Chagas Disease (ACD) are identified with increasing frequency in Brazil, attributed to contaminated açaí fruit and sugar cane juices. A group of municipal employees in the greater metropolitan area of Belem shared meals, and several of them developed ACD over a short period of time. **Methods:** We conducted a retrospective cohort study of municipal welfare secretariat workers and other persons who shared at least one meal served at the secretariat between August 1 and September 14, 2007. Diagnosis was by direct examination (blood or buffy coat) or serology (ELISA, indirect immunofluorescense and hemagglutination) at the state reference laboratory, Para. An entomologic survey sought triatomines in locations frequented by case-patients. **Results:** Of 31 cohort members, 3 were confirmed cases-patients: 2 by direct blood examination and one by serology and clinical findings. Illness onsets were August 23 to September 1. The median age was 34 (34-43); two patients were female. Three (100%) case-patients reported fever, weakness, headache, retro-orbital pain, cough and backache; two reported nausea, vomit, and facial and peripheral edema. All were treated; no deaths occurred. Two resided in urban, and one in rural settings. All three denied having had Chagas Disease, an infected relative, blood transfusion or organ transplant. All denied ever seeing or being bitten by a triatomine. Of food exposures at shared meals, there was no association between illness and: açaí (palm fruit), meat, sugar, cassava or tapioca flour, other raw fruits, or fruit popsicles. Consumption of raw, salted shrimp at one meal was the only exposure associated with illness (Relative Risk=13.5; 95%CI=1.56-116.9, p=0.04). The entomologic survey identified no triatomines at case-patient homes, the municipal welfare office, and locations where food served at suspected meals was prepared. **Conclusions:** This outbreak of orally transmitted ACD appears to be associated with a food not previously implicated: raw shrimp. The shrimp may have been contaminated by feces of infected triatomines, marsupials or rodents while in transport, storage or on display in marketplaces. Vigorous investigation of ACD outbreaks should continue, to better understand this emerging mode of transmission of Chagas Disease.

Board 164. Epidemiology of non-O157 Shiga toxin-producing *Escherichia coli* in FoodNet sites, 2000-2006

L. Gould[1], C. Medus[2], S. Hurd[3], D. Hoefer[4], S. Shin[5], T. Hayes[6], N. Comstock[7], K. Edge[8], P. M. Griffin[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Minnesota Department of Health, St. Paul, MN, [3]Connecticut Emerging Infections Program, New Haven, CT, [4]New York State Department of Health, Albany, NY, [5]California Emerging Infections Program, Berkeley, CA, [6]Georgia Emerging Infections Program, Atlanta, GA, [7]Colorado Department of Public Health and Environment, Denver, CO, [8]New Mexico Emerging Infections Program, Santa Fe, NM.

Background: Shiga toxin-producing *Escherichia coli* (STEC) are an important cause of diarrhea and the major cause of hemolytic uremic syndrome. Most clinical laboratories do not routinely test stool specimens for these organisms and practices vary among labs. With an overall increase in testing, non-O157 STEC infections are being recognized with greater frequency by the Foodborne Diseases Active Surveillance Network (FoodNet). **Methods:** The ten FoodNet sites ascertain all laboratory-confirmed non-O157 STEC infections in their catchment areas. A case was defined as isolation of a non-O157 STEC from the stool of a resident of a FoodNet site. Isolates with a known O antigen were included in the analysis. **Results:** During 2000-2006, FoodNet ascertained 629 cases of non-O157 STEC infection, of which 575 (88%) had O serogroup information. Of the 48 O serogroups reported, O26 was the most common (24%), followed by O111 (22%), O103 (22%), O45 (7%), O145 (4%), and O121 (4%). The number of cases reported increased each year during 2000-2006, from 36 in 2000 (0.12 per 100,000 population) to

212 in 2006 (0.42 per 100,000 population). In 2006, the rate of non-O157 STEC infections varied by site, from 0.15 cases per 100,000 population in Georgia to 1.02 cases per 100,000 population in New Mexico. The median age of cases was 12 years and 55% were in females. Sixty-six (12%) patients were hospitalized; no deaths were reported. **Conclusions:** The number of reported non-O157 STEC infections is increasing in FoodNet sites. Six serogroups were responsible for 83% of reported non-O157 STEC infections during 2000-2006. Variations in the number of cases reported by year and in each FoodNet site may be partly due to differences and changes in laboratory practices, including increased use of Shiga toxin testing. Understanding the epidemiology of non-O157 STEC serotypes will inform prevention and food safety efforts. Clinical laboratories should routinely test all stool specimens for STEC.

Board 165. *Salmonella* Serotype Enteritidis Infections among Workers Producing Poultry Vaccine_Maine, 2006

A. K. Yartel, D. Guppy;

Maine Center for Disease Control and Prevention, Augusta, ME.

Background: Most *Salmonella* infections occur through ingestion of contaminated food. However some outbreaks have been associated with environmental contamination. On November 15, 2006 the Maine Center for Disease Control and Prevention (MeCDC) was notified of a case of salmonellosis in a worker of a poultry vaccine production facility. When a second case in a worker from the same facility was reported on November 25, MeCDC began an investigation to identify additional cases, to determine risk factors and to recommend control measures. **Methods**: A standard questionnaire was administered to 67 (91%) of 74 workers. Workers were asked about clinical symptoms, symptomatic contacts, previous *Salmonella* infections, job tasks and locations, hygiene habits, and knowledge of a recent spill of liquid containing a high concentration *Salmonella* Enteritidis (SE). Environmental swabs and water samples were collected and tested. Stool specimens were obtained from ill workers for culture, phage typing and pulse field gel electrophoresis (PFGE). Stock cultures of the four phage types of SE used by the facility were obtained for analysis. **Results**: Twenty-one (31%) of 67 workers met the case definition, five of whom were culture confirmed as SE. Eighteen (55%) of 33 workers in the production area of the facility were ill compared to 3 (9%) of 34 workers in other areas (RR= 6.2, 95% CI 2.0-19.0). When analysis was restricted to workers in the production area, a significant association was found between illness and working in the room where cleaning of equipment used for vaccine production was performed; 18 (69%) of 26 workers who worked in this room became ill, compared to none of 7 employees who did not work in the room (p=0.002). Environmental swabs and water samples were negative for *Salmonella* and *E. coli*, respectively. Isolates of SE from four case-patients as well as one of the four stock cultures from the facility had indistinguishable PFGE patterns and were phage type 8. **Conclusions**: Environmental contamination of the cleaning room following a spill may have served as an ongoing source of SE, although the exact mechanism for how workers became infected remains unknown. MeCDC recommended creation of spill containment procedures, and improvements in hand washing, use of personal protective equipment, and routine disinfection of work areas.

Board 166. A case control study of sporadic human infection with Shiga toxin producing *Escherichia coli* in Australia

M. McPherson[1], J. Raupach[2], M. Kirk[3], B. Combs[1];

[1]OzFoodNet, Adelaide, AUSTRALIA, [2]Communicable Disease Control Branch, Deparment of Health, Adelaide, AUSTRALIA, [3]OzFoodNet, Canberra, AUSTRALIA.

Background: Infections with Shiga toxin producing *Escherichia coli* (STEC), although rare in Australia, can cause significant illness. We conducted a case control study to determine risk factors for sporadic illness of STEC between 2003 and 2007. **Methods:** Patients notified with STEC to health departments were eligible for the study and three controls per case were selected from a bank of controls based on sex and five year age groups. Cases were recruited in South Australia from July 2003, with all other Australian states participating from 2005. A standardised questionnaire was used to collect information regarding demographic data, food, behavioural and environmental exposures. All factors that were associated with cases at the univariate level ($p<0.1$) were included in a categorical logistic regression model. **Results:** There were 114 cases and 304 controls recruited in the study with the majority from South Australia. Mean duration of diarrhoea was 6 days (range 1-22 days), over half (55.1%) were hospitalised and eight cases were diagnosed with HUS. STEC infection was independently associated with animal contact at work (OR=3.2, 95% CI=1.3-7.8), bush camping (OR=3.4, 95% CI=1.1-10.6), eating chicken or turkey deli meat (OR=5.2, 95% CI=2.0-13.5) and eating out of the home (OR=2.1, 95% CI=1.0-4.1). Eating home grown fruit or vegetables (OR=0.4, 95% CI=0.2-0.9), eating raw vegetables (OR=0.4, 95% CI=0.2-0.8) and eating pork (OR=0.4, 95% CI=0.2-0.9) were negatively associated with infection. **Conclusions:** Animal contact at work is an important risk factor for STEC infection, which is consistent with findings from other studies. The association with bush camping is a novel finding and may be linked to poor food preparation skills and lack of washing facilities in this setting. STEC infection can cause serious illness and this study will assist in the development of prevention programmes in Australia.

Board 167. Botulism in the United States, 1997-2006

P. A. Yu, S. E. Maslanka, E. J. Barzilay, J. Sobel, D. L. Swerdlow;

CDC, Atlanta, GA.

Background: *C. botulinum* is an anaerobic, spore-forming bacterium that produces paralysis-causing neurotoxin. Three major types of human botulism occur: infant (first described in 1976), wound, and foodborne. CDC has conducted botulism surveillance since 1973, providing 24/7 consultation and antitoxin. In recent years, the incidence of botulism has increased and outbreaks due to nationally-distributed foods have occurred. **Methods:** Botulism cases reported to CDC from 1997 to 2006 were reviewed. Reports included those from states, antitoxin release data, and the Infant Botulism Treatment and Prevention Program in CA. **Results:** Between 1997 and 2006, a median of 139 cases were reported annually, compared to a median of 103 between 1973 and 1996, mostly due to increased reports of infant and wound cases. The highest number of cases occurred in 2006 (171). Infant cases (66%) were the most frequent type, while wound (19%) and foodborne (14%) cases also occurred. Of 1,452 cases, 54% were male; the median age of infant, wound, and foodborne cases was 12 weeks, 43 years, and 49 years. All but 1% of wound cases (277/281) occurred in western states (mostly attributed to black tar heroin), with most cases male (72%, p-value <0.01). Case fatality rates were <1%, 4%, and 6% for infant, wound, and foodborne cases respectively. Toxin types A (54%) and B (40%) were most common. Nearly all wound cases were type A (92%). Of infant cases, 57% were type B and most type B cases were infants (95%). Alaska had the highest incidence

(11 cases per 100,000 - over 100 times the national incidence) with most due to traditionally fermented Alaskan Native foods. Of 196 foodborne cases, 106 were part of 31 outbreaks with at least two persons ill. Of these, 27 (87%) were due to homemade foods and three (10%) were due to commercial food: canned chicken broth, chili sauce, and pasteurized carrot juice, the last two led to nationwide product recalls. **Conclusions:** The number of botulism cases has steadily increased largely due to the recognition of infant botulism and the marked increase of wound cases. Outbreaks due to widely distributed commercial foods underscore the importance of rapid detection and public health action to prevent cases and deaths. National surveillance is important to identify outbreaks, guide prevention efforts, and monitor for acts of bioterrorism.

Board 168. Foodborne Outbreaks Caused by Salmonella enterica serotype Typhi, Brazil, 2000- 2005

C. Penaforte[1], R. M. Alves[2], G. Madeleine[1];

[1]EPISUS/COVEH, Secretariat of Health Surveillance, Ministry of Health, Brasilia, BRAZIL, [2]COVEH, Secretariat of Health Surveillance, Ministry of Health, Brasilia, BRAZIL.

Background: Typhoid fever is a life-threatening infection caused by *Salmonella enterica* sorotype Typhi. Humans are the definitive host, and approximately 2-5% of infected, untreated persons become chronic carriers. Immunity acquired naturally or by vaccination is transient. Untreated water is an important means of transmission, whether ingested directly, through contamination of vegetables through irrigation or washing, or by mixing with milk. Person-to-person transmission by chronic carriers is a serious public health concern. We describe foodborne/waterborne outbreaks of typhoid fever in Brazil between 2000 and 2005. **Methods:** We analyzed outbreak data reported to the National Foodborne Diseases Surveillance System (VE-DTA) of the Brazilian Ministry of Health. We calculated attack rates and mortality rates. **Results:** During the study period, a total of 14 outbreaks of foodborne/waterborne typhoid fever were reported. Outbreaks occurred in states from every one of Brazil's five geographic regions. The total number of affected persons was 124, and the size of outbreaks ranged from 1 to 58 persons. One death was reported (mortality, 0.8%). The median attack rate among exposed persons was 85% (range, 5%-100%). The most affected age group was persons aged 20-49, accounting for 66% of cases, followed by persons aged >50 years (40%). Fifty-one percent of cases were male. Of 13 outbreaks with information available about the source, 9 (70%) were caused by contaminated water, 2 (15%) by a sandwich, 1 (8%) by mayonnaise and 1 (8%) by multiple foods The majority (63%) of outbreaks were related to group meals consumed in restaurants, cafeterias, church dining facilities, and hospitals. Of 7 outbreaks in which the criteria for establishing etiology were reported, the diagnosis was determined in 6 (86%) by clinical and laboratory criteria. **Conclusions:** Conclusions Typhoid fever remains a health problem in Brazil. The most common setting of reported outbreaks is group meals consumed outside the home. Underreporting of outbreaks may occur. We recommend completion of standard investigative forms for typhoid fever outbreaks and routine collection of laboratory samples to faciliated adequate investigation and reporting.

Board 169. Enteric Bacterial Infections Among Infants and Children, California FoodNet 1996-2006

N. E. Perez-Licona[1], S. Shin[1], D. J. Vugia[2];

[1]California Emerging Infections Program, Oakland, CA, [2]Infectious Diseases Branch, California Department of Public Health, Richmond, CA.

Background: In the United States, infants and children have higher rates of enteric bacterial infection than adults. Since 1996, the California Emerging Infections Program (CEIP) conducts active population-based laboratory surveillance for foodborne infections in three counties as part of the national Foodborne Disease Active Surveillance Network (FoodNet). **Methods:** CEIP FoodNet data for 1996 through 2006 were analyzed for laboratory-confirmed infections with *Campylobacter, Salmonella, Shigella, and E.coli* O157 among infants and children <18 years of age, by age group, gender, race/ethnicity, hospitalization, and trends. **Results:** During 1996-2006, the incidence rates (IR) per 100,000 population for all bacterial enteric infections among infants <1, 1-4, 5-9, and 10-17 years old were 221.0, 168.7, 76.5, and 41.3 respectively. Rates for *Salmonella* and *Campylobacter* were highest among infants were with IR of 127.0 and 66.4, correspondingly, while rates for *Shigella* and *E.coli* O157 (IR 32.0 and 7.3) were highest among children aged 1-4. By race/ethnicity, IR was highest among Asian/Pacific Islander, 101.0, followed by Hispanic, 60.0. Rates were not significantly different between gender among infants and children. The proportion hospitalized was highest, 16%, among infants, particularly for infants with *Salmonella*. By year, IR of all infections among infants and children significantly decreased from 138.0 in 1996 to 77.0 through 2006. **Conclusions:** Infants and children are substantially affected by enteric bacterial infections. Infants have the highest rate of infection and the highest rate of hospitalization, particularly due to *Salmonella*. Overall infection rates are decreasing since 1996. Strategies to further prevent bacterial enteric infections among children should take into account the different pathogens affecting different age groups as well as special outreach to minorities.

Host & Microbial Genetics

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 170. Genomic Characterization of Human Rotavirus G8 Strains from The African Rotavirus Network (ARN): Relationship to Animal Rotaviruses

M. D. Esona[1], A. Geyer[2], N. Page[3], M. Aminu[4], I. Fodha[4], T. Kerin[1], G. Armah[5], A. Steele[6], R. Glass[7], J. Gentsch[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Diarrhoeal Pathogens Research Unit, University of Limpopo, Pretoria, SOUTH AFRICA, [3]Viral Gastroenteritis Unit, National Institute for Communicable Disease, Johnnesburg, SOUTH AFRICA, [4]African Rotavirus Network, Pretoria, SOUTH AFRICA, [5]Noguchi Memorial Research Institute Accra, Accra, GHANA, [6]WHO, Department of Immunization, Vaccines and Biologicals, Geneva, SWITZERLAND, [7]Fogarty International Center, National Institutes of Health, Bethesda, MD.

Background: Serotype G8 rotavirus (RV) strains are common in cattle. The first human G8 RV strain was isolated from the diarrhea specimen of a child in Indonesia. The prototype strain 69M had a P serotype P4[10] and a supershort RNA migration pattern not previously seen among human rotaviruses (HRV). Since then, few reports of G8 HRV have been published, except in African countries where the detection frequency increased since 1997. Recent G8 HRV exhibited short or long RNA migration patterns and a wide diversity of P types including P[6], P[8], P[1], P[2], P[4], and P[14]. While G8 HRV diversity has been studied in some detail through hybridization, sequencing of a few genes and serologic methods, complete genome characterization by nucleotide (nt) sequencing of gene fragments or entire genes has rarely been done. The aim of this study was to elucidate the genetic and evolutionary relationships of all 11 gene segments of G8 HRV from African Rotavirus Network (ARN). **Methods**: Gene fragments (RT-PCR amplicons) of all 11 gene segments of 6 P[8],G8 and 2 P[6],G8 HRV from ARN were

sequenced on an ABI 3130 sequencer. Phylogenetic relationships were inferred using aligned nt sequences by the neighbor-joining method. The similarity percentages were calculated using the OldDistances program. **Results**: Phylogenetic and sequence analyses of each gene segment of ARN strains revealed high similarities (88%-100% nt and 91%-100% aa) except for gene 4 encoding VP4 proteins P[8] and P[6]. However, for most strains, almost all of the genes of the ARN strains other than neutralizing antigens are related to typical human strains of Wa genogroup.VP7, NSP2 and NSP5 proteins were closely related to cognate genes of animal strains (97-99% aa identity). **Conclusions**: This study suggests that the ARN G8 strains might have arisen in part through VP7 or VP4 gene reassortment events and most of the gene segments resemble those of common HRV. However, VP7, NSP2 and NSP5 genes are potentially derived from animals suggesting a zoonotic introduction. Although these findings help elucidate RV evolution, there is the need to sequence more animal strains.

Board 171. The Role of IS 1016-bexA Partial Deletion in *Haemophilus influenzae* Serotype a

N. G. Rouphael[1], S. Satola[2], M. Farley[2], E. White[3], K. Rudolph[3], P. Gomez de Leon[4], G. Carlone[3], S. Romero-Steiner[3];

[1]Emory University School of Medicine and Centers for Disease Control and Prevention, Atlanta, GA, [2]Emory University School of Medicine, Atlanta, GA, [3]Centers for Disease Control and Prevention, Atlanta, GA, [4]UNAM, Mexico, MEXICO.

Background: Haemophilus influenzae serotype a (Hia) is being recognized as a cause of invasive disease in selected US populations including Native Americans and Alaska Natives. In Hia, partial IS1016-bexA deletion within the capsule gene locus stabilizes capsule gene duplication and may potentiate capsule production and virulence. This deletion is commonly observed in invasive Hib and has been proposed as a virulence factor in some Hia severe infections. We examined 12 Hia isolates from GA and AK for morphologic, genetic, and immunologic differences. **Methods:** Hia strains were divided into group I (n=3 with the IS*1016-bexA* deletion from invasive disease) and group II (n=9 lacking the IS*1016-bexA* deletion from invasive disease and colonization) . Capsule was assessed by Quellung reaction and electron microscopy (EM). Quantification of capsular polysaccharide was tested using orcinol. Southern blot was used to estimate the number of cap loci. Functional assays (7 normal adult and 12 cord blood sera) including serum bactericidal assay (SBA), opsonophagocytosis assay (OPA) and adherence to nasopharyngeal (NP) cells were performed. **Results:** Evidence of greater encapsulation (Quellung reaction = 4+) was found in group I compared with group II (67% and 11%). EM results are pending. However, variation in the number of cap loci was noted between groups. Strains 512 and 513 containing the bexA deletion had the highest copy number (exact number to be determined) where as strains 151, 341 and 491 without the IS1016 had lower and variable copy numbers. Among these strains, the Quellung reaction matched the number of cap loci. Additional polysaccharide determinations are ongoing to associate copy number and polysaccharide content. There was no significant difference in SBA (p=0.82) or OPA (p=0.27) titers using different sources of complement and sera. Only one colonization strain from Group II adhered to NP cells. **Conclusions:** Despite genetic and morphologic evidence of increased encapsulation in Hia strains with IS*1016-bexA* partial deletion, no functional advantage was observed using *in vitro* immunoassays An animal model is being investigated to better understand the role of the partial deletion within the capsule locus in the pathogenesis of invasive Hia infections.

Board 172. Human Genetic Determinants of Infectious Diseases: an Overview of the Current Research Lines and Consortia

S. A. Morré[1], M. Khoury[2], L. Zhang[2], M. Gwinn[2], M. Reichler[2], C. Bruggeman[3], E. Stobberingh[3], P. Wolffs[3], F. Stassen[3], S. Ouburg[1], P. Arora[4], R. Duncan[4], M. Karmali[4], J. Scheres[5];

[1]VU University Medical Center, Amsterdam, THE NETHERLANDS, [2]Centers for Disease Control and Prevention, Atlanta, GA, [3]University Hospital Maastricht, Maastricht, THE NETHERLANDS, [4]Public Health Agency of Canada, Ottowa, ON, CANADA, [5]University Hospital Maastricht & ECDC Management Board, Maastricht, THE NETHERLANDS.

Background: Identification of Human Genetic Determinants of Infectious Diseases (HGDoID) can potentially be very relevant to public health. However a clear overview of the current activities in the infectious disease field is missing. The aim of the current study was to provide such an overview and describe the potential public health relevance. **Methods:** Via PubMed and other data bases an overview was made of research focusing on Human Genetic Determinants of Infectious Diseases in the following 4 fields: 1) Infectious Diseases, 2) Chronic inflammatory diseases with an infectious component, 3) Infection and cancer and 4) Consortia working on the above three topics. In addition, topics of public health relevance were collected for the 4 field investigated. **Results:** A selection of the findings is described. Infection: Malaria, Tuberculosis, HIV, *Chlamydia trachomatis* (Sexually Transmitted Disease (STDs) and Ocular disease), HCV, *Helicobacter*, and sepsis. European Union Framework Programme (FP) funded Consortia: EpiGenChlamydia (FP6 CA). Chronic inflammatory disease with an infectious component: Periodontitis, Inflammatory bowel disease (IBD: Crohn's Disease & Ulcerative colitis), and Pouchitis. European Union Framework Programme (FP) funded Consortia: IBD-Chip (FP6 STREP), INFOBIOMED (FP6 NoE). Infection and cancer: HPV & Cervical Cancer, Helicobacter & Gastric Cancer, and EBV & Lymphoma. European Union Framework Programme (FP) funded Consortia: EUR-GAST (FP5 IP). Public health relevance: identification of genetic biomarkers relevant to the susceptibility to and severity of infectious diseases, relevant host pathway identification helpful for vaccine strategies, treatment efficiency markers, progression markers, and tailor-made treatment options. **Conclusions:** We have made an overview in the field of HGDoID (much more extended than presented in this abstract) Many studies are being performed in different fields, some of them in large funded consortia. The interaction between the different groups studying different microorganism studied is limited, but the public health relevance seems promising. Consorted actions are needed to forward the field of Human Genetic Determinants of Infectious Diseases.

Board 173. Host Genetic Determinants for *E. coli* Susceptibility during Probiotic Prophylaxis for Urinary Tract Infections in Post-menopausal Women

O. Karimi[1], M. A. Berepoot[2], S. E. Geerlings[2], S. Nys[3], S. Ouburg[1], P. Wolffs[3], J. B. Crusius[1], A. S. Peña[1], E. E. Stobberingh[2], S. A. Morré[1];

[1]VU University Medical Center, Amsterdam, THE NETHERLANDS, [2]Academic Medical Center, Amsterdam, THE NETHERLANDS, [3]Academic Hospital Maastricht, Maastricht, THE NETHERLANDS.

Background: The leading causative microorganism of common urinary tract infections (UTIs) is *Escherichia coli.* Human functional genetic variation (single nucleotide polymorphisms (SNPs)) may be responsible for the variable clinical outcome of UTI. Interestingly, colonization with lactobacilli protects against infection with *E. coli.* We studied SNPs in two genes important in *E. coli* recognition: CD14 (binds LPS) and TLR5 (detects flagellin)

to determine if host genetic variation influences the efficacy of probiotic prophylaxis. **Methods:** From our prospective 15 month follow-up study (the 'Non-antibiotic versus antibiotic prophylaxis for recurrent urinary-tract infections' (NAPRUTI) study) of n=473 women randomized to prophylaxis with probiotics, antibiotics or cranberries we have studied 76 postmenopausal women with a history of recurrent UTIs, receiving lactobacilli twice daily orally (>10e9 *Lactobacillus Rhamnosus GR-1* and *L. Reuteri RC-14)* for the first 3 months. *E. coli* presence was assessed by urine culture. Human DNA was isolated from vaginal swabs to genotype two SNPs (CD14-260C>T and TLR5+1174C>T). **Results:** Three analyses were performed (cumulative for t=0, 1, 2, and 3 months): 1) Symptomatic *E. coli* infections: 0-1 (n=40) vs ≥ 2 (n=36). 2) Asymptomatic bacterial infections (ABU): 0-2 (n=29) vs ≥ 3 (n=47). 3) *E. coli* associated ABU (n=26) vs non-*E. coli* associated ABU (n=23). Analysis 1: Carriers of the CD14-260*T allele had fewer symptomatic *E. coli* infections (0-1 vs ≥ 2: p=0.025, OR: 3.4, CI: 1.2 - 9.6). Analysis 2: No relation between the SNPs studied and ABU. Analysis 3: In the non-*E. coli* ABU group, the CD14-260*T allele was more frequently found (83.3%) as compared to the *E. coli* ABU group (57.7%) (p=0.067, OR=3.7, CI: 1.0-14). In neither analyses the TLR5+1174 C>T was linked to either *E. coli* susceptibility or ABU incidence. **Conclusions:** Postmenopausal women carrying of the CD14-260*T allele had significantly fewer *E. coli* infections as compared to carriers of the A allele. Since CD14 T-allele carriers have higher expression of the CD14 linked to clearance of *E. coli* infection, it will be worth-while to further study the effect of probiotics in the resolution mechanism of *E. coli* infection. Further studies from 3-15 months in the different groups of prophylaxis and a wider range of SNPs are underway.

Board 174. Stepwise Replication Identifies a Low-Producing Lymphotoxin-Alpha Allele as A Major Risk Factor for Early-Onset Leprosy

A. Alter[1], A. Alcaïs[2], G. Antoni[2], M. Orlova[1], N. Van Thuc[3], M. Singh[4], P. Vanderborght[5], K. Katoch[6], M. Mira[7], V. Thai[3], N. Thu Huong[3], N. Ngoc Ba[3], M. Moraes[5], N. Mehra[4], L. Abel[2], **E. Schurr**[1];

[1]McGill Centre for the Study of Host Resistance, McGill University, Montreal, QC, CANADA, [2]Laboratoire de Génétique Humaine des Maladies Infectieuses, Institut National de la Santé et de la Recherche Médicale, Paris, FRANCE, [3]Hospital for Dermato-Venereology, Ho Chi Minh, VIET NAM, [4]Department of Transplant Immunology and Immunogenetics, All India Institute of Medical Sciences, New Delhi, INDIA, [5]Leprosy Laboratory, Tropical Medicine Department Oswaldo Cruz Institute, Rio de Janeiro, BRAZIL, [6]Central Jalma Institute of Leprosy and Other Infectious Diseases, Agra, INDIA, [7]Centro de Ciências Biológicas e da Saúde, Pontifícia Universidade Católica do Paraná, Curitiba, BRAZIL.

Background: Leprosy is a chronic infectious disease caused by *Mycobacterium leprae*. In 2006, 259,017 new cases were reported. Here we dissected a linkage peak on chromosome region 6p21 (lod=2.7) identified in a previous genome-wide linkage scan. **Methods:** A 10.4 Mb interval underlying the linkage peak and including the HLA class II and class III genes (224 genes, *BAT1* → *CCND3*) was selected for a low-density association scan (307 SNPs) in 194 single-case Vietnamese leprosy families. Subsequently, a 90 kb interval around the *lymphotoxin-alpha* (*LTA*) gene (10 genes, *PPIAP9* → *NCR3*) was selected for a high-density association scan (29 SNPs). All SNPs showing evidence for association were tested in a second independent sample of 104 Vietnamese single-case leprosy families and a third sample of 364 cases and 371 controls from Northern India. **Results:** All SNPs in the bin (r^2>0.8) containing the functional *LTA*+80 5'-UTR variant (AA/AC vs. CC *P*=0.007; OR=1.74[1.16-2.60]) were associated with leprosy. The association of *LTA*+80A was replicated in the second independent Vietnamese sample (*P*=0.003; OR=2.34[1.27-4.31]). When stratifying on age at diagnosis, the association of *LTA*+80 was captured almost entirely by cases diagnosed before age 16 (*P*=0.00004), reflecting significant genetic heterogeneity of the *LTA*+80 effect between cases <16 years and those ≥16 years (*P*=0.00054). In the second sample, the odds-ratio increased in cases <16 years (OR=5.31[1.19-23.60]) resulting again in significant evidence for heterogeneity (*P*=0.04). When both Vietnamese samples were combined, the evidence for association overall and in cases <16 years was very strong (*P*=0.000024 and *P*=0.0000004, respectively). In the third sample of 364 cases and 371 controls from Northern India, the association of *LTA*+80A was replicated (*P*=0.01; OR=1.60[1.10-2.33]) using multivariate analysis to adjust for differences in linkage-disequilibrium structure. The strength of association increased in the youngest age group (*P*=0.004; OR=2.95[1.32-6.58]) replicating the age-effect and genetic heterogeneity (*P*=0.003) observed in the Vietnamese samples. **Conclusions:** Our results, replicated in three samples from two ethnically diverse populations, show that the low-producing *LTA*+80 A-allele is a strong risk factor for early-onset leprosy.

Influenza

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 175. DoD Global Influenza Surveillance Program At The Air Force Institute For Operational Health: Enhancements And Support Of Global Partners In Pandemic Preparedness

M. C. Johns, A. B. Owens;

Air Force Institute for Operational Health, Brooks City-Base, TX.

Background: In an effort to monitor and prevent outbreaks of influenza attributable to newly emerging strains, the US Air Force has conducted influenza surveillance of US military forces and their families since 1976 in a program called Project Gargle. In accordance with the Department of Defense (DoD) *Implementation Plan for Pandemic Influenza*, the Air Force Institute for Operational Health (AFIOH) has begun enhancing existing influenza surveillance to rapidly identify and respond to a pandemic. Emphasizing the importance of surveillance and early detection, AFIOH has instituted a multi-phased plan for program enhancement, modernization and operational flexibility. **Methods**: Historically, military training sites, international military ports, and overseas installations have been chosen as sentinel sites. In the interest of expanding the overall "footprint" of surveillance, AFIOH has considered a number of factors in evaluating new participants. New site prioritizations will be determined by geographical risk, where a pandemic threats exists as well as where troop concentrations are greatest. Health care providers at surveillance sites collect specimens from individuals presenting with a fever and either a cough or sore throat. These specimens are sent to AFIOH for viral isolation and identification. Sentinel sites are requested to submit 6-10 respiratory specimens per week, throughout the year. **Results:** AFIOH is in the third phase of a multi-phased approach to building a more robust surveillance network. The phases involved have provided the framework for a versatile system of year-round detection, identification and response to a pandemic threat. Enhanced efforts have provided AFIOH and global partners a more timely and reliable way to identify influenza viruses of epidemiologic and public health significance. **Conclusions:** Close monitoring and investigations are needed to evaluate variance from endemic levels of disease activity.

Surveillance and disease investigations remain the cornerstones of proper pandemic preparedness. Risk communication and awareness play an important role given the anticipated enormity of such an event. Through these enhancement efforts, the US military is working to address these needs while maintaining operational relevance and flexibility during a time of war.

Board 176. Influenza Virus in Human Exhaled Breath

M. P. Fabian[1], J. J. McDevitt[1], W. H. Dehaan[2], R. O. Fung[3], B. J. Cowling[3], K. H. Chan[3], G. M. Leung[3], D. K. Milton[1];

[1]University of Massachusetts Lowell, Lowell, MA, [2]Pulmatrix Inc., Lexington, MA, [3]The University of Hong Kong, Hong Kong, HONG KONG.

Background Recent studies suggest that humans exhale fine particles during tidal breathing but little is known about where the particles are generated or their role in infection transmission. We conducted a study of influenza infected patients to characterize particle and influenza virus concentrations in their exhaled breath. **Methods** We recruited patients with influenza-like illness presenting for medical care at three clinics in Hong Kong, China. We collected two nasal swabs per subject, one for rapid testing and a second one for analysis via quantitative PCR (qPCR). Patients breathed with a steady regular pattern through a mouthpiece supplied with HEPA filtered air. Exhaled breath flowed through a 22 mm diameter and 40 cm long tube to an Exhalair (Pulmatrix, Inc, Lexington, MA), which monitored flow rate, and counted particles between 0.3 and 5 um in diameter using an optical particle counter. After three minutes of particle counting, we collected exhaled breath particles by sampling for 20 minutes on Teflon filters. We assayed each filter for influenza A and B using qPCR. **Results** Thirteen of the 51 screened patients tested positive for influenza using the QuickVue rapid test (7 for influenza B, 6 for influenza A). Twelve rapid test positive patients completed the exhaled breath test (7 influenza B subjects and 5 influenza A subjects) and we recovered influenza virus in the exhaled breath of 4 (25%) subjects. Three (60%) of the five patients with influenza A infection and one (14%) of the seven with influenza B infection had detectable influenza virus in their exhaled breath. Exhaled breath virus concentrations ranged between 21 and 312 virus copies per sample, corresponding to a generation rate between 1 and 16 virus particles per minute. Preliminary particle data analysis indicated that 50% of subjects exhaled more than 500 particles per liter of air, a suggested threshold for identification of high particle producers. **Conclusions** We recovered influenza virus from the exhaled breath of 4 out of 12 influenza patients, three of whom tested positive for influenza A. The results provide evidence that influenza virus is contained in fine particles generated during tidal breathing.

Board 177. Epidemiology of 1918 Pandemic Influenza in Japan

T. Kamigaki, N. Fuji, H. Oshitani; Tohoku University Graduate School of Medicine, Sendai, JAPAN.

Background: Currently the thread of next pandemic influenza is more concerned and lessons from past pandemic are important for pandemic preparedness. In Japan there were 385,000 deaths reported in 1918 pandemic but this involved only peak periods that was potentially underestimated. So its impact as well as epidemiology remained unclear. This study was conducted to estimate the mortality impact and to describe epidemiology of influenza during 1918-20 pandemic in Japan. **Methods:** National census data as well as national vital statistics were obtained from 1913 to 1922. Monthly mortality data were divided by its causes and pneumonia and influenza (P&I) data were assumed as a combination of influenza and pneumobronchitis. Both pandemic and seasonal epidemic period were excluded for baseline estimation. Serfling model were applied to estimate baselines with all cause mortality and P&I mortality data. Secular and seasonal parameters were involved with semi seasonal parameters in this model. Excess mortality was calculated as the difference between observed mortality data and baseline mortality data. Since census data were available on annual basis, interpolated monthly values were calculated between each year to obtain rates. Monthly Age stratified P&I data as well as prefectural P&I data were obtained for further analysis. **Results:** First wave was observed from October with following smaller secondary peak in Feburuary,1919 and large recurrence wave was observed in 1919/20 winter period. 316,588 (95% C.I. 205,030-614,300) and 444,232 (95% C.I. 408,716-489,539) excess deaths were estimated in all cause and P&I deaths respectively. P&I excess deaths were higher than officially reported but all cause deaths were not. less number for all cause may reflect overfitting of baseline thoreshold. Age distribution of excess deaths indicated peak deaths among young adult age group as well as younger children and elders age groups. **Conclusions:** The large recurrence peak in 1919/20 followed the first peak. In total, 0.72 per 100 person-years excess mortality rate were estimated in P&I deaths and 0.56 for all cause deaths, that is, Japan had a certain impact in terms of excess mortality during 1918 pandemic influenza. Age distribution trend of excess mortality in Japan was similar to that in the US and Europe studies.

Board 178. Revisiting the Classical W-shape of 1918 Pandemic Influenza Mortality: The True Meaning of Catastrophe

L. Simonsen[1], V. Andreasen[2], D. Olson[3], K. Molbak[4], C. Viboud[5];

[1]George Washington University, Washington DC, DC, [2]Roskilde University Center, Roskilde, DENMARK, [3]New York City Department of Health & Mental Hygiene, New York, NY, [4]Statens Serum Institute, Copenhagen, DENMARK, [5]National Institutes of Health, Fogarty International Center, Bethesda, MD.

Introduction: Recent studies have brought attention to the fact that the age-specific mortality caused by the Spanish flu-pandemic of 1918-19 is not "W-shaped" as previously thought. The complete sparing of seniors in the pandemic has been demonstrated in two recent studies of age-stratified monthly mortality data from New York City and Copenhagen. Here we extend these studies to further quantify the pandemic mortality risk elevation across the entire age spectrum. **Methods:** We compiled 4-week moving averages of deaths from pneumonia and influenza (P&I) and all causes for 7 age groups for 1910-1921, based on the historic Copenhagen surveillance system "Ugelisterne". We applied a Serfling-type regression model to create a winter-seasonal background of death and attributed deaths during October 1918-March 1919 in excess of this baseline to pandemic influenza. To estimate the relative pandemic mortality risk in the different age groups, we compared pandemic excess death rates with average mortality rates for a reference 6-month period during 1912-1917. We also explored age variations in mild illness based on weekly data on influenza-like illness (ILI) incidence in Copenhagen. Lastly, we compared age-specific pandemic mortality patterns in Copenhagen with those of New York City. **Results:** Data from both cities demonstrated the well established extreme pandemic mortality risk elevation in young adults. Children aged 1-19 years and the adults aged 45-64 experienced a less pronounced elevation than adults aged 20-44. Infants had little relative risk elevation; the two senior age groups had no detectable pandemic excess mortality. When plotting the relative pandemic risk against age we revealed a "Λ"-shape in both countries, with both extreme age groups approaching RR=1. For Copenhagen, all age groups except seniors ≥65 experienced dramatically elevated respiratory morbidity during the pandemic period. **Conclusions:** The true meaning of "catastrophe" during the 1918 Spanish influenza takes on a new light when considering the age-specific experience. The demonstrated lack of increased mortality risk in infants and seniors

has important implications for priority setting for vaccine allocation. So far, pandemic planning in most countries focus on a 1918-like risk scenario yet favor vaccination of extreme age groups.

Board 179. Impact of Household Crowding on the Risk of Being Hospitalised With Influenza and Pneumonia in a Large Cohort Study

M. G. Baker, J. Zhang, K. Venugopal, CDC funded Pandemic Influenza Research Team;

University of Otago, Wellington, Wellington, NEW ZEALAND.

Background: Plans for prevention and control of pandemic influenza make virtually no mention of measures to reduce transmission within households. Yet this setting is arguably one of the most important for pandemic virus spread. This research therefore aimed to investigate whether the risk of seasonal influenza was associated with the level of household crowding. **Methods:** We used a prospective longitudinal cohort study of public housing applicants and tenants to investigate the risk of hospitalisation for influenza and pneumonia in relation to housing conditions. The cohort consisted of 212,224 social hosing applicants and tenants followed for a median of 34 months. They were linked to their hospitalisation records and anonymised. This analysis included hospitalisations over the 44-month period from May 2003 to December 2006. We extracted hospitalisations for influenza (ICD.10 codes J10 and J11) and pneumonia and influenza (P&I) (ICD.10 codes J10-J18). We calculated hospitalisation rates, rate ratios and 95%CI for individual level and household level variables. We then carried out a survival analysis using Cox proportion hazard model in which we treated household crowding and tenure status as time varying covariates. **Results:** P&I hospitalisation rates were markedly higher in the cohort population (435.2 /100,000) compared with other New Zealanders not in the cohort (209.9/100,000) across all age and ethnic groups. Both influenza and P&I hospitalisation rates were strongly influenced by individual-level factors of age, and to a lesser extent ethnicity and socio-economic position. Influenza numbers were too small to investigate other important associations. P&I hospitalisation rates were marginally higher for those living in the most crowded households (RR= 1.20 95%CI 1.05-1.37 for those with a 2+ bedroom deficit) and for households containing children (RR=1.28 95%CI 1.03-1.60 for single adult plus 1 or more children). **Conclusions:** Household crowding was associated with an increased risk of being hospitalised with P&I in the univariate analysis only. The effect of this exposure was relatively small compared with the influence of age, ethnicity and poverty and disappeared in the multivariate analysis.

Board 180. Serological Evidence for Influenza A H3N8 Virus Circulation in Canines from 1999 to 2004

T. C. Anderson[1], L. Grimes[2], J. Pompey[3], C. Osborne[1], C. Bromfield[1], W. J. Dodds[2], J. M. Katz[3], C. H. Courtney[1], P. C. Crawford[1];

[1]University of Florida College of Veterinary Medicine, Gainesville, FL, [2]Hemopet/Pet Life-Line, Garden Grove, CA, [3]Immunology and Viral Pathogenesis Section, Influenza Branch, Centers for Disease Control and Prevention, Atlanta, GA.

Background: Canine influenza A subtype H3N8 virus (CIV) is an emerging, highly contagious respiratory pathogen for dogs. This novel virus was first isolated from racing greyhounds during respiratory disease outbreaks at Florida tracks in 2004. Subsequently, CIV has been associated with respiratory disease outbreaks involving thousands of racing greyhounds and non-greyhound dogs in 28 states in the U.S. Molecular analyses of the CIV isolates show that this virus forms a monophyletic group closely related to equine influenza H3N8 viruses (EIV), suggesting the interspecies transmission of EIV from horse to dog at some point in the recent past. Limited testing of archived tissue and serum samples from racing greyhounds has suggested that influenza A H3N8 virus may have circulated in dogs prior to 2004. To further investigate this possibility, serum samples collected from dogs from 1999 to 2004 were tested for antibodies to CIV and EIV. **Methods:** Serum samples collected from 549 racing greyhounds and 288 shelter dogs from 1999 to 2004 were tested for antibodies to CIV (A/canine/FL/04) and EIV (A/equine/NY/99) using the hemagglutination inhibition (HI) assay. The EIV isolate was used in case viruses infecting dogs prior to 2004 were more antigenically similar to EIV than CIV. Prior racing history was traced using unique ear tattoos carried by all racing greyhounds and a corresponding database housed at www.greyhound-data.com. **Results:** The numbers of seropositive greyhounds by year were: 33% in 1999 (n=174), 38% in 2000 (n=71), 19% in 2001 (n=43), 1% in 2002 (n=74), 44% in 2003 (n=126), and 28% in 2004 (n=61). Many of the seropositive dogs in 1999 to 2001 were detected by higher reactivity to the 1999 EIV isolate than the 2004 CIV isolate. Seropositive dogs were at tracks or farms in AR, AZ, CO, FL, IA, KS, OK, TX, and WI during respiratory disease outbreaks in 1998, 1999, and 2003. One of the shelter dogs, which entered a FL shelter in 2004, was seropositive for CIV and EIV. **Conclusions:** Based on the serological evidence, we conclude that influenza A H3N8 virus was circulating in the racing greyhound population as early as 1999. The seropositive dogs were located at tracks involved in respiratory disease outbreaks of unknown etiology, suggesting that influenza A H3N8 virus may have been the causative agent of those outbreaks.

Board 181. Clinical Experience of Military Service Members and Their Dependants Who Received an Influenza Anti-Viral Prescription

A. K. McCabe, A. K. Goodin, G. Kubiak, R. Moseley, Jr., C. Rennix;

Navy Environmental Health Center, Portsmouth, VA.

Background: EpiData Center is pursuing the development of a Department of Defense Pandemic Influenza (PI) surveillance model based on HL7 laboratory results and pharmacy transaction data and clinical encounter data. The study evaluates the value of the pharmacy data for PI surveillance and describes its relationship to laboratory and encounter data. The study evaluates the association between influenza-specific anti-viral (AV) outpatient (OP) prescriptions and influenza laboratory tests, as well as influenza-like illness (ILI) or influenza specific diagnoses in the encounter data. **Methods:** All influenza specific AV medications prescribed during the 2006-2007 influenza season were selected from the OP data, and matched to the laboratory and encounter data to find tests or diagnoses within (±) 7 days of the pharmacy transaction date. Laboratory records for each patient were evaluated for influenza testing and results. Prescriptions were matched to encounter records to establish if the patient had encounters within (±) 7 days, and if so then diagnoses were evaluated for ILI and/or an influenza specific diagnosis within (±) 7 days of the pharmacy transaction. **Results:** There were 1,040 people who received 1,083 AV prescriptions during the 2006-2007 season. A third of all prescriptions had an influenza test or an ILI, and half of them had an influenza **positive** test result or an **influenza-specific** diagnosis. A fourth of all prescriptions had an influenza **positive** test result or an **influenza-specific** diagnosis. About half of all prescriptions had at least one lab test or an encounter within (±) 7 days of the pharmacy transaction, and two thirds of those were influenza tested or had an ILI **Conclusions:** The prescriptions may suggest a suspicion of influenza infection by the clinician. Using pharmacy records as indicators, lab or encounter data surveillance would not have identified two thirds of potential influenza cases. Physicians may rely on clinical presentation for diagnosis, which would account for patients who received no lab tests. It does not account for the patients who were prescribed an

influenza AV, but had non-influenza tests or diagnoses. Influenza treatment is not indicative of disease. Pharmacy records appear to be useful in the surveillance of influenza by identification of additional potential cases.

Board 182. A Review of Influenza-like Illness Symptoms Among Laboratory-Confirmed Respiratory Results

A. B. Owens, M. C. Johns;

Air Force Institute for Operational Health, Brooks City-Base, TX.

Background: The DoD Influenza Surveillance Program requires patients meet the ILI case definition of a temperature at least 100.5°F and cough and/or sore throat. Utilizing these symptom indicators allows healthcare providers to administer care days earlier than would be based on laboratory confirmation. Due to seasonal variations in influenza strains and the potential for differences in the symptoms associated with these illnesses, the need exists to regularly evaluate the sensitivity and specificity of the DoD ILI case definition. **Methods:** A sample of patients with this criteria are requested to submit a nasal wash specimen and a questionnaire. The questionnaire is used to gather demographic information, including symptom and travel history. ILI symptoms were reviewed by coupling lab-confirmed results with surveillance questionnaires. **Results:** A total of 1,361 individuals met the criteria: 14% had both an influenza infection and a questionnaire. The most commonly reported symptoms were cough (n=171, 91.0%), fever (n=160, 85.1%), fatigue (n=145, 77.1%), runny nose (n=134, 71.3%), chills (n=126, 67.0%), headache (n=126, 67.0%), body ache (n=120, 63.8%) and sore throat (n=120 63.8%). 57% of the individuals in the review met the ILI criteria. Of these, confirmed influenza was isolated among 152 (19.6%), corresponding to a positive predictive value of 19.6 (16-22). The negative predictive value, sensitivity, and specificity of the current DoD ILI case definition were 93.9 (91-95), 80.9 (74-86) and 47.0 (44-49), respectively. **Conclusions:** Among ILI cases, the average highest recorded temperature was 102.0°F (median 101.9°F, range 100.5-106.3°F) compared to 101.8°F (median 102.0°, range 98-106.2°F) among influenza cases. Although cough and fever appear to be the strongest predictors of influenza infection, several symptoms appear to be better indicators than sore throat. This finding is in agreement with the patterns previously observed among DoD personnel during the 2005-6 influenza season. Although modification to the inclusion of sore throat in the DoD ILI definition may be warranted, future studies should assess whether adding fatigue, runny nose, chills, headache or body ache to the criteria truly provides greater predictive capabilities.

Molecular Epidemiology

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 183. Detection of Human Bocavirus in Children with Lower Respiratory Tract Infection in Taiwan

Y. Lin[1], K. Lin[2], S. Chiu[3], P. Hou[4], J. Lin[3];

[1]Departments of Medical Research, Pingtung Christian Hospital, Pingtung City, TAIWAN, [2]Department of Clinical Laboratory,Kaohsiung Medical University, Kaohsiung City, TAIWAN, [3]Research and Development Division, Central for Disease Control, Taipei City, TAIWAN, [4]Department of Laboratory Medicine,Pingtung Christian Hospital, Pingtung City, TAIWAN.

Background: Human influenzavirus, parainfluenzavirus, respiratory syncytial virus, human metapneumovirus and adenovirus are viruses that cause upper and lower respiratory tract infections (URTI and LRTI) in children. A new virus related to LRTI was isolated in Sweden, in 2005 and denominated to Human bocavirus (HBoV), the family *Parvoviridae*, genus *Bocavirus*. To date, HBoV has not been successfully cultured. To understand the prevalence rate of HBoV in Taiwan we design this retrospective analysis. **Methods:** A total of 533 throat swab collected from LRTI patients in Kaohsiung Medical University Hospital from Oct. 2006 to Mar.2007 were included. The age of patients ranged from 0 to 16 years old. Virus DNA was extracted using QIAamp DNA Blood mini Kit (Qiagen) and stored at -70°C. In this study we used real-time PCR targeting the HBoV NP1 for the detection of HBoV. We also perform the phylogenetic analysis based on VP2 region to reveal more epidemiologic information of bocavirus in Taiwan. **Results:** HBoV was detected in 30 (5.6%) of the 533 specimens. The ratio of male to female was 2:1. The positive rate peaked in October (30%) and November (23.3%) 2006. The age distribution analysis revealed that all the HBoV-positive cases were under the age of 8 years old, and peaked at the age of 2 years old (33.3%). Direct sequencing of PCR products of the VP2 gene showed that most strains had similar sequences. The Taiwanese strains clustered into two groups depicted by phylogenetic analysis. **Conclusions:** This is the first report of detection of HBoV in Taiwan in patients with LRTI. Our results provide the evidence that HBoV is involved in acute lower respiratory tract infections in Taiwan. Two groups of HBoV was found in Taiwan. Seroepidemiology and complete genome of the Taiwanese HBoV will be further studied.

Board 184. Emergence of Coxsackievirus A24 as the Etiologic Agent for the Recent Outbreak of Acute Hemorrhagic Conjunctivitis in Taiwan

C. Yang, C. Huang, Y. Li, C. Hsu, J. Yang, L. Lee, H. Wu, T. Lin;

CDC Taiwan, Taipei, TAIWAN.

Background: There were more than 16,000 cases of acute hemorrhagic conjunctivitis (AHC) reported through the Taiwan Sentinel Surveillance System between September 27 and October 30, 2007. The outbreak started in the north (Keelung) and west (Yunlin), and soon spread to Taipei City,Taipei county (north), and Chiayi (west). Clinical symptoms are characterized by photophobia, watering, foreign body sensation, eyelid edema, conjunctival hemorrhages, and superficial punctuate keratitis, with symptoms usually lasting between 10 and 14 days. **Methods**: Conjunctival swabs were collected from 91 patients for laboratory testing. Virus isolation on cell lines including Rhabdomyosarcoma (RD), HeLa, and Hep-2C cells were used. Direct determination of the serotype from clinical specimens by employing a molecular method (CODEHOP) also used. Indirect immunofluorescence antibody (IFA) staining and neutralization test were used to identify the isolate after appearance of cytopathic effect (CPE). Phylogenetic analysis by using a MEGA program was conducted to determine the genetic make-up and evolution of the virus isolates. **Results**: The virus isolation rate from cell cultures was 65.9 % (60/91) of the specimens. The IFA test using a CVA-24 antiserum confirmed that the etiologic agent Coxsackievirus A24 was present in 98.3% (59/60) of the isolates. Determination of the serotype directly from clinical swabs by examining the partial VP1 gene sequences revealed 72/91 (79.1%) was CVA 24. Phylogenetic analysis of partial 3C protease genome (511 bps) from these isolates showed 99-100% of nucleotide identity among them, indicating the outbreak might have been initiated from a single focus. When compared to the sequences from other countries, our strains are closer to the strains from Singapore (2005) but more distinct from China (2002),

Korea (2002), and Taiwan (2000-2002). Our isolates are forming a new lineage (3) in cluster 6 with strains from Singapore (2005) and belonging to genogroup III. **Conclusions**: We have determined, by using different laboratory methods including cell culture, IFA staining, neutralization, and molecular techniques, that the etiologic agent which caused the recent acute hemorrhagic conjunctivitis in Taiwan was a Coxsackievirus A24 variant.

Board 185. Phylogenetic Analysis of *Influenza A virus* Subtype H5N1 Strains from Egypt 2006-2007

M. D. Saad[1], K. C. Earhart[1], M. M. Mansour[1], S. L. Yingst[1], N. M. Elsayed[2], A. Ismail[2], A. Abdelghani[2], H. Essmat[2], M. Abdelhakam[3], S. Nassef[3], M. Taha[3], M. R. Monteville[1], J. A. Tjaden[1];

[1]U.S. Naval Medical Research Unit No.3, Cairo, EGYPT, [2]Ministry of Health and Population, Cairo, EGYPT, [3]Central Laboratory for Evaluation of Veterinary Biologicals, Cairo, EGYPT.

Introduction: The first detection of highly pathogenic avian influenza (HPAI) subtype H5N1 in Egypt was in February, 2006. Four foci were detected in four governorates extending from northern to mid southern Egypt. Infection at that time was mainly in domestic poultry. Human cases began to appear in March. Poultry vaccination plus other control measures were employed in May 2006. Both human and poultry infections subsided in the summer but reappeared in October, and between Jan-May 2007. Most human infections were due to contact with backyard poultry. **Methods:** The hemagglutinin gene (HA) was sequenced from all poultry, wild birds and human cases made available to NAMRU-3. Strains were phylogentically analyzed with GenBank selected strains from Africa, Europe, and Asia. **Results:** HPAI strains from Egypt were closely related, and formed one cluster with a 98% bootstrap support value. A strain from a common teal showed a parental relationship to all Egyptian strains with a bootstrap support value of 96%. All strains from Egypt were phylogentically related to the Qinghai 2005 strain (clade 2.2) and distant from clade 1 strains from Vietnam. Three main geographical clusters were evident among the Egyptian strains: the Nile Delta region, Lower Egypt (North) and Upper Egypt region (South). Strains from Egypt recovered in December 2006 had mammalian polymorphisms in the HA gene, and a low level resistance to Oseltamivir. Amino acid mutations at the antigenic sites were present in some strains. **Conclusions:** Egypt had only one introduction of HPAI H5N1, possibly from a migratory bird. Mutations in the HA gene indicate ongoing transmission. Vaccine pressure may be contributing to virus mutations. In-vivo vaccine challenge experiments are indicated for proper vaccine selection. Continued viral surveillance and phylogenetic analysis is important in monitoring, detecting and characterizing avian influenza in Egypt.

Board 186. *Salmonella* Typhimurium Variant Dt104 In Colombia, Costa Rica And Argentina, An Emergent Pathogen In Latin America

A. Salve[1], R. Terragno[1], N. Muñoz[2], E. Campos[3], F. Duarte[3], M. Pichel[1], A. Tijerino[3], L. Sánchez[3], M. Caffer[1], E. Perez[4], N. Binsztein[1];

[1]Instituto Nacional de Enfermedades Infecciosas ANLIS, Buenos Aires, ARGENTINA, [2]Instituto Nacional de Salud, Bogotá, COLOMBIA, [3]INCIENSA, San José de Costa Rica, COSTA RICA, [4]Salud Pública Veterinaria-Inocuidad de Alimentos (FOS), PAHO-WHO, Rio de Janeiro, BRAZIL.

Background: The epidemic strain *Salmonella* Typhimurium DT104 was first isolated in England and recognized as human and farmed animals´ pathogen in 1990. This strain is identified by its phage type DT104 and the resistance to ampicillin, chloramphenicol, streptomycin, sulfonamide and tetracycline. This international study was done in the frame of WHO Global Salm Surv and PulseNet in Latin America (LA). **Methods**: *S.* Typhimurium isolates were serotyped (Kauffmann-White scheme) and the antimicrobial susceptibility was assayed following CLSI. Phagetyping was done according to Anderson *et al*. The isolates were subtyped by pulse field gel electrophoresis (PFGE) with *Xba*I, following PulseNet protocol and analyzed with BioNumerics software. **Results**: In Costa Rica, 16 strains of mutiresistant (MR) *S.* Typhimurium (15 human and one from porcine origin), isolated between 2004-2006, were confirmed as DT104; all of them showed the same PFGE pattern. This profile was compared with *S.* Typhimurium PFGE patterns stored in Argentina and Colombia PulseNet Databases. In Argentina, three human MR DT104 isolates in 2005-2007 were identified, with PFGE patterns identical or differing in only one band to the Costa Rica profile. In Colombia, eight human MR DT104 isolates from 2000-2003 showed PFGE patterns identical or closely related to the Costa Rica-Argentina ones. **Conclusions**: Up to our knowledge this is the first report of *S.* Typhimurium variant DT104 in LA. The PFGE profiles identified were compared with those of the epidemic strains from Europe and USA and it could be seen that they were identical to the predominant profile found in LA, suggesting that the same strain has disseminated to this region. The relation of these strains should be further analyzed. It is mandatory to prevent the dissemination of this pathogen by enhancing the surveillance in humans, animals and food, in order to reduce the risk of contamination in all the steps of the chain "from farm to fork".

Board 187. Characterization of the Measles Virus after Declaration of The Nation-Wide Measles Elimination in Republic of Korea, 2007

Y. Chung, S. Choi, W. Lee, K. Kim, J. Choi, H. Oh, H. Oh, H. CHO, C. Kang;

Korea Center for Disease Control and Prevention, Seoul, REPUBLIC OF KOREA.

Background: Measles virus (MV), which causes serious public health problem world wide, is seologically monotypic virus; however, diversity within the complete hemagglutinin gene and nucleoprotein gene has allowed the classification of MV into eight clades, A to H, 22 genotypes. After the Korea declared nation-wide measles elimination in November 2006, detected outbreak of measles re-emerged in 2007 by the enhance surveillances. **Methods:** During the outbreak, 45 cases were confirmed by RT-PCR followed by sequencing analysis. In addition, 8 isolates were obtained from urine, blood, throat swab samples from 45 patients through inoculation onto Vero-SLAM monolayer cell line. All cases amplified PCR products of nucleoprotein (N) gene were sequenced and their characteristics were compared with prototype or sequences from Genbank to clarify leading genotype of the outbreak. **Results:** According to the phylogenetic analysis using Clustal-W, all cases belong to H1 except one D5 and two A, which might be derived from imported and post-vaccination, respectively. Eight isolates of MV, which were recovered from clinical specimens, were also confirmed as H1. The homogeneity of the target sequenced was ranged from 98% to 99%. **Conclusions:** In summary, most of genotype of MV from outbreak in 2007 belongs to H1, except one possible imported case. Even though genetic diversity of MV is rather stable than other RNA viruses, our results indicate that the outbreak in 2007 might share the origin and further epidemiological investigation should be performed.

New or Rapid Diagnostics

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Baord 188. A Rapid, High Throughput Vaccinia Virus Neutralization Assay for Testing Smallpox Vaccine Efficacy Based on Detection of Green Fluorescent Protein

M. C. Johnson, I. Damon, K. Karem;

Centers for Disease Control, Atlanta, GA.

Background: Virus neutralization remains a vital tool in assessment of vaccine efficacy for smallpox in the absence of animal smallpox models. In this regard, development of a rapid, sensitive, and high throughput vaccinia neutralization assay has been sought for evaluating alternative smallpox vaccines, use in bridging studies, as well as understanding the effects of anti-viral immunotherapeutic regimes. The most frequently used method of measuring vaccinia virus neutralization by plaque reduction is time, labor, and material intensive, and therefore limiting in its utility for large scale, high throughput analysis. Recent advances provide alternative methods that are less labor intensive and higher throughput but with limitations in reagents needed and ease of use. **Methods**: Here we describe an innovative neutralization assay based on a modified Western Reserve vaccinia vector expressing green fluorescent protein (WR-GFP) and an adherent cell monolayer in multi-well plate format. Individual cell nuclei are identified via Hoechst staining, and nuclear localized GFP is measured via a Cellomics HCS Arrayscan automated fluorescent microscope. Antibody-mediated reduction in virus activity relative to controls (neutralization) is observed via two methods: as a reduction in the mean average GFP intensity per cell, per well, and as a reduction in the percentage of cells reporting GFP. **Results**: When tested with vaccinia immunoglobin (VIG), poxvirus naïve serum, and vaccinee (primary and tertiary) serum, the HCS-GFP neutralization assay produces neutralization titers similar to a traditional plaque reduction neutralization assay, and is dramatically less time, labor, and material intensive. **Conclusions**: The assay is quick, accurate, provides a large dynamic range and is well-suited for large-scale vaccination studies using standard adherent cell lines.

Board 189. Evaluation and Validation of a Real Time Fluorescence RT-PCR for the Detection and Differentiation of Noroviruses in Genogroups I and II

T. P. Fabrizio, II[1], H. Deng[2], T. Gao[2], Z. Zhao[2], C. Daniels[2], R. Owens[3];

[1]APHL/CDC EID Fellow, Arkansas Department of Health, Public Health Laboratory, Molecular Diagnostic Unit, Little Rock, AR, [2]Arkansas Department of Health, Public Health Laboratory, Molecular Diagnostic Unit, Little Rock, AR, [3]Arkansas Department of Health, Public Health Laboratory, Director of Biological Sciences Section, Little Rock, AR.

Background: Noroviruses, of the family *Caliciviridae*, consist of at least 5 genogroups and are responsible for at least 50% of all foodborne gastroenteritis in the United States. Three genogroups (I, II, and IV) are known to infect humans. Due to the large number of norovirus infections, it is important to clinically diagnose and differentiate norovirus cases to provide essential data to locate outbreaks and their sources. With the spread of antibiotic resistance it is crucial to rapidly and accurately identify norovirus infections in public health laboratories to prevent the improper administration of antibiotics. Due to its sensitivity and accuracy real time RT-PCR has become a principle diagnostic tool. **Methods:** RNA specimens were obtained from the Arkansas Public Health Laboratory, and 6 raw stool samples were obtained from CDC. RNA was extracted by making a 20% wt/vol suspension of stool in 50 mM Tris buffer. The samples were centrifuged at 3000 x g for 20 min to clarify. RNA was extracted from 400 µL of supernatant using the Qiagen Magattract® Virus Mini M48 Kit and the Qiagen M48 BioRobot. Real time RT-PCR was performed on the Cepheid SmartCycler® II platform. Samples were tested using the Quantitect™ SYBR® Green RT-PCR Kit and results were verified on a 1.2% Agarose Flash Gel DNA Cassette run at 275 V on the Lonza Flashgel® System. The samples were also tested using the Ambion Ag-Path ID™ One Step RT-PCR Kit and the Quantitect™ Probe RT-PCR Kit. **Results:** The Arkansas results matched the 6 CDC Panel results with zero discrepancies. Preliminary results from the initial SYBR Green data (5/2006-5/2007) indicate a 100% similarity between the Ambion data and the Quantitect Probe kit data. However, recent SYBR Green testing of the stored samples (10/2007-Present) resulted in 27 NV positive and 6 NV negative samples which is a 12.9% discrepancy of the recent SYBR Green test results compared to the Taqman kits and the initial SYBR Green data. **Conclusions:** The results indicate that the Ambion kit and the Quantitect Probe kit procedures are as accurate and more sensitive in the detection of noroviruses when compared to the SYBR Green kit. In addition, they distinguish between GI and GII. Further data will be collected on specificity and precision in order to validate these new procedures and utilize them in the Arkansas Public Health Laboratory.

Board 190. Comparison of Reverse Transcriptase Loop-Mediated Isothermal Amplification (RT-LAMP) Tests for H5 Influenza

R. G. Coon, C. A. Myers, D. Metzgar, D. J. Faix, K. L. Russell;

NHRC, San Diego, CA.

Background: The Department of Respiratory Disease Research at the Naval Health Research Center has been tasked by the US Department of Defense Global Emerging Infections Surveillance (DoD-GEIS) to evaluating promising technologies for the detection of pandemic influenza strains. One such technology, the reverse transcriptase loop-mediated isothermal amplification (RT-LAMP), allows for detection of H5 influenza subtypes in approximately an hour. The need for expensive equipment is obviated by RT-LAMP due to the isothermal reaction temperature as well as the ease of visual detection. **Methods:** A commercially available H5 RT-LAMP kit and two isothermal primer sets previously published were evaluated for sensitivity and specificity against a collection of avian influenza samples (n=42) from NAMRU3 in Cairo, Egypt, including 24 H5N1 patient samples. The three sets of primers were also tested with a standardized clinical sample panel (n=100) consisting of 20 seasonal influenza A, 20 influenza B, 20 adenovirus, 15 parainfluenza, 5 RSV, and 20 Negative samples as determined by PCR and/or culture for these pathogens. This panel was collected as part of our DoD-wide febrile respiratory illness surveillance at all US military basic training centers. **Results:** Sensitivity of the published primers approaches 100%. False negatives were observed with the commercially available kit. Specificity of both the kit and the published primers approaches 100%. **Conclusions:** RT-LAMP offers a rapid, inexpensive, easily-deployable diagnostic tool for the detection of H5 influenza. The use of multiple primer sets appears to overcome specificity problems that may occur with any one group of primers. This technology can be adapted to many other pathogens with the development of specific primers appropriate for isothermal reactions.

Board 191. Rapid, Point of Care Avian Influenza Diagnostic Evaluation

C. A. Myers[1], E. McDonough[1], K. Butler-DeRose[1], C. De Mattos[2], C. De Mattos[2], D. J. Faix[1], K. L. Russell[1];

[1]NHRC, San Diego, CA, [2]NAMRU3, Cairo, EGYPT.

Background: The Department of Respiratory Disease Research at the Naval Health Research Center (NHRC) conducts surveillance for respiratory diseases in large-population recruit training centers. The US Department of Defense has been tasked with several objectives in the National Pandemic Preparedness Plan, including furthering the development of point-of-care diagnostics for avian influenza (HPAI) strains. In support of these tasks, NHRC has been leveraging its archive of well-characterized clinical respiratory samples to evaluate promising new technologies. The Arbor Vita Corporation (AVC) has developed a rapid-antigen strip test to detect strains of HPAI. This test differs from other rapid-antigen assays in that it detects the NS1 protein, as opposed to the nucleoprotein (NP). Antigen capture is mediated through a PDZ protein, which binds the C-terminal region of the NS1 protein. As the C-terminal region of the NS1 protein differs for each influenza sub-type, a PDZ protein with high affinity to NS1 protein of H5 strains was chosen for assay development. **Methods:** The AVC rapid antigen assay was tested against a standardized panel of 100 clinical samples previously characterized by molecular and culture methods at NHRC. This sample consisted of 20 influenza A samples, 20 influenza B samples, 20 Adenovirus samples, 15 PIV samples, 5 RSV samples and 20 samples negative for the previously-mentioned pathogens. To evaluate the assay against its intended target, the assay was also evaluated against amniotic fluid from eggs inoculated with 29 different H5N1-postive samples collected by Naval Medical Research Unit 3 (NAMRU3) in Cairo, Egypt. **Results:** The AVC assay showed no false positives against the respiratory clinical panel. Of the 29 H5N1 cultures tested, 26 were gave positive results on the assay (specificity = 89%). **Conclusions:** True H5 rapid diagnostic tests with potential for point-of-care clinical use are few. This unique AVC technology shows promise. NHRC & NAMRU3 will continue to collaborate to evaluate this assay against other grown strains (H7, H9 etc.) as well as with clinical specimens in actual outbreak situations.

Outbreak Investigation: Lab & Epi Response

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 192. Identification of Factors (Environmental And Human) Responsible for the Endemicity of Cholera in Ajegunle and Amukoko Districts (Ajeromi/Ifelodun Local Government Area - LGA), 1990 - 2007 in Lagos State, Nigeria

O. S. Badaru[1], C. E. Egbom[1], A. J. Onoja[1], E. Ademuson[1], N. Njepuome[2], E. B. Coker[2], J. Scharff[3], P. Nsubuga[3], S. Gwarzo[4];

[1]Federal Ministry of Health, Lagos, NIGERIA, [2]Federal Ministry of Health, Abuja, NIGERIA, [3]Centre for Disease Control and Prevention, Atlanta, GA, [4]Centre for Disease Control and Prevention, Abuja, NIGERIA.

Background: Cholera epidemics have been reported from several Local Government Areas (LGAs) of Lagos State, including Surulere, Mushin, Ajeromi-Ifelodun, Ikeja and other LGAs. The disease has continuously caused high mortality and morbidity within the populace in the State. The disease is common among the children and young adults, who are not economically viable and sometimes affects all ages due to economic hardship in the country. The major objectives are to study the environmental and human factors responsible for the recurrent or periodic cholera epidemics and proffer control measures for containing the epidemics. **Methods**: A total of 224 data of standard questionnaires corroborated with stool and water specimens were collected from traders, civil servants and students of colleges found within Ajegunle and Amukoko districts of Ajeromi-Ifelodun LGA, Lagos State during the period of the investigation. **Results**: Data analysis revealed that among the 41 (20.1%) of the individuals that had experienced cholera infection. Of those who experienced cholera, the male (73.2%) had significantly more experience than the female (25.8%) ($p \leq 0.0001$). The most affected age group is 18 - 25 group (19) where the male (17) in this age group had the overall highest. Among those that experienced cholera, none boiled nor treated their water before drinking while majority (37.5%) had just any water for drinking. The commonest method of refuse disposal was that done indiscriminately by individuals (38.3%). To control the spread of cholera in this environment, sources of water should be inspected and those with low chlorine content should be treated. Environmental sanitation of the districts should be improved through intensive public health education and enforcement of sanitation laws in the LGA. Building structures that lack waste management facilities should be mandated to have such facilities with stiff penalty for defaulters. Government in a long term, should plan out ways of resettling the inhabitants of most part of the LGA for safety of life. Immediate surveillance should be set in place for imminent cholera outbreaks in the LGA. **Conclusion**: Human and environment factors have been identified as the major factors responsible for the endemicity of cholera in the area.

Board 193. Using Molecular Identification Methods in Investigating an Apparent Outbreak of *Rhodococcus equi* Infections --- New Jersey, 2007

A. J. Langer[1], K. Feja[2], H. P. Hinrikson[3], B. A. Lasker[3], R. Morey[3], G. J. Pellegrini, Jr.[3], T. L. Smith[3], C. Robertson[4];

[1]Epidemic Intelligence Service assigned to the New Jersey Department of Health and Senior Services, Centers for Disease Control and Prevention, Atlanta, GA, [2]Saint Peter's University Hospital, New Brunswick, NJ, [3]Division of Foodborne, Bacterial, and Mycotic Diseases, National Center for Zoonotic, Vector-Borne, and Enteric Diseases, Centers for Disease Control and Prevention, Atlanta, GA, [4]New Jersey Department of Health and Senior Services, Trenton, NJ.

Background: *Rhodococcus equi* is a facultative intracellular Gram-positive aerobic coccobacillus commonly associated with respiratory infection among foals. Rarely, immunocompromised humans are infected, typically as pneumonia. During January-April 2007, three patients with *R. equi* bacteremia were treated at one children's hospital, where *R. equi* had not been identified in >15 years. Two patients had catheter-associated infections; one infant was hospitalized after prolonged apnea. All isolates were identified as *R. equi* by using commercial test kits. We investigated this apparent outbreak to confirm the diagnosis and to identify the source of the infections. **Methods**: We reviewed all patients' medical records to ascertain their immune status and any common exposures. We interviewed two patients' families to identify possible sources of infection; language barriers prevented interviewing the third family. We submitted the isolates to the Centers for Disease Control and Prevention's Special Bacteriology Reference Laboratory for identification, using biochemicals and 16S rRNA gene sequencing, and for multilocus sequence typing (MLST). **Results**: Two patients were immunocompromised; the third had no known immune disorder. We identified no common exposure. A patient aged 17 years had potential contact with horses; we identified this patient's isolate as

Gordonia polyisoprenivorans. We identified isolates from the other patients, one aged 5 years and the other 6 months, as *R. equi*. The *R. equi* were not identical by MLST. **Conclusions**: This investigation established that all patients in this apparent outbreak were infected from different sources. One isolate was initially misidentified as *R. equi*. *Gordonia* species belong to the same suprageneric group of actinomycetes as *R. equi*, and available commercial tests cannot differentiate them. Further characterization of unusual isolates is important, particularly during suspected outbreaks.

Board 194. *Clostridium perfringens* Foodborne Intoxication Outbreak Associated with Consuming Chili Beans Prepared at a Correctional Facility

J. Ward[1], N. Comstock[2], W. Ray[2], C. Nevin-Woods[1], J. Carrillo[1], M. Klaber[3], M. Miller[4], J. Ludwig[1], H. Maio[1], V. Carlton[1], B. Montoya[1], C. Wolgram[1], D. Aragon[2], S. Bruestle[1], K. Williams[1];

[1]Pueblo City-County Health Department, Pueblo, CO, [2]CDPHE Communicable Disease Epidemiology Program, Denver, CO, [3]El Paso County Health Department, Colorado Springs, CO, [4]Otero County Health Department, La Junta, CO.

Background: In September 2007, the Pueblo City-County Health Department (PCCHD) investigated a gastrointestinal illness outbreak at a correctional facility. Approximately 125 of 500 (25%) inmates reported onset of gastrointestinal symptoms, primarily diarrhea and abdominal pain, within a 24-hour period after a lunch meal. **Methods**: PCCHD initiated a prompt investigation. A case-control study was conducted among a proportion of the ill and well inmates. Cases and controls were interviewed about symptoms and exposures during the week before the onset of illness. Environmental health specialists performed an onsite kitchen inspection. Twenty-four stool specimens collected from ill inmates and leftover food were sent to the state public health laboratory for viral, bacterial, and toxin analysis. **Results**: The case-control study included 36 cases and 40 controls. A case was defined as an inmate experiencing diarrhea with three or more episodes in a 24-hour period and onset after lunch on September 4, 2007 or on September 5, 2007. In addition to diarrhea, 33 (92%) cases reported abdominal pain. Less than one-third of cases reported fever, bloody diarrhea, or vomiting. Symptom onset for cases occurred between 1:00 pm September 4 and 2:00 pm September 5. Duration of illness ranged from two to 72 hours (median 24 hours). No cases were hospitalized. Several food exposures were statistically significant; however chili beans served for lunch on September 4 had the largest odds ratio (OR = 12.50, p = 0.0066). An onsite kitchen inspection found several violations including food holding temperature violations. Laboratory analysis found 18 of 24 (75%) stool specimens positive for *Clostridium perfringens* toxin. Chili bean culture results found 11,000 *C. perfringens* colonies per gram. According to the Centers for Disease Control and Prevention, the presence of the *C. perfringens* toxin in stool specimens of two or more ill individuals confirms a *C. perfringens* outbreak. **Conclusions**: *C. perfringens* intoxication was determined to be the cause of the outbreak and is an important cause of foodborne illness worldwide. This outbreak demonstrates the importance of prompt public health response to reported outbreaks and the importance of collecting stool and food specimens to assist in determining the etiology.

Prevention Effectiveness, Cost Effectiveness, & Cost Studies

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 195. Effectiveness of Hygiene Control Measures for Containing an Outbreak of Norovirus

P. Teunis[1], J. Heijne[1], G. Morroy[2], C. Wijkmans[2], S. Oostveen[2], E. Duizer[1], M. Kretzschmar[1], J. Wallinga[1];

[1]RIVM, Bilthoven, THE NETHERLANDS, [2]Municipal Health Services "Hart voor Brabant", 's Hertogenbosch, THE NETHERLANDS.

Background: Norovirus is one of the most common causes of gastroenteritis. Almost half of all gastroenteritis outbreaks in the Netherlands are caused by norovirus. Little is known about the effectiveness of control measures to contain an outbreak of norovirus. However, improved hygiene measures like hand washing, surface cleaning, use of paper towels and separate toilets for sick persons are often implemented to contain norovirus outbreaks. Little is known about the effectiveness of these improved hygiene measures in limiting further spread of norovirus infections. **Methods:** We studied the effectiveness of improved hygiene measures during norovirus outbreaks, by estimating key transmission parameters from data obtained during an outbreak of norovirus at an international scouting camp in the Netherlands in July/August 2004. We measured the epidemic potential of norovirus by its effective reproduction number: the number of secondary cases caused by each infectious subject in this outbreak. **Results:** We estimated that implementation of improved hygiene measures was associated with an 83% decrease in effective reproduction number; from 13.3 secondary cases before hygiene advice to 2.2 secondary cases after hygiene advice was issued.**Conclusions:** Our results confirm high transmissibility of norovirus and suggest that improved hygiene measures can have a substantial impact on transmission of norovirus; however improved hygiene measures themselves may not suffice to stop transmission. It is thinkable that a combination of improved hygiene measures with more rigorous control measures like quarantine of sick persons can stop transmission completely. Causal relations between improved hygiene measures and decrease of virus transmission must be studied by analysis of other outbreaks in different settings.

Board 196. Information Collection and Utilization at Clinical Microbiology Laboratories: Chongqing, China, 2006

H. Zhong[1], H. Ma[1], Q. Li[1], R. Fontaine[1], B. P. Zhu[1], L. Ran[2];

[1]China CDC CFETP, BEIJING, CHINA, [2]China CDC, BEIJING, CHINA.

Background: Clinical microbiology laboratories (CMLs) are an important component of the "National Laboratory Surveillance Network", and can provide vital information for infectious disease surveillance. To assess laboratory capacities and evaluate what information is collected and utilized at CMLs, in 2006, we conducted a survey of CMLs in Chongqing, one of the four Municipalities in China, with a population of approximately 30 million. **Methods**: We asked all CMLs in Chongqing to complete a self-administered questionnaire, covering information on the geographic location of the CML, basic equipments, tests performed, numbers of specimens submitted, and microorganisms identified. These data were compared with the data in the Disease Reporting System to

determine their usage. **Results**: Of the 144 CMLs in Chongqing, 142 (103 hospital CMLs and 39 local CDC CMLs) responded to the survey (response rate=98.6%). Of the hospital CMLs, 18% had a laboratory information system; 55% had high-pressure sterilizers, and 51% had biosafety cabinets. The CML at Chongqing CDC is the only one capable of conducting viral isolation; the other CMLs can only conduct bacterial culture. There were no BSL-3 laboratory in Chongqing; fewer than 20% of the CMLs can conduct antibody testing for viruses such as measles, rubella, Japanese encephalitis, or hemorrhagic fever; whereas over 80% of the CMLs were equipped to isolate Salmonella or Shigella spp. In 2006, of the 78,048 specimens submitted for bacterial isolation, 41.3% were sputum, 19.3% were blood, and 11.3% were stool specimens. The median number of specimens cultured at all CMLs in 2006 was 293. Common pathogens identified in 2006 included M. tuberculosis (2369 strains), Shigella spp (208 strains), Salmonella spp(140 strains), and Vibrio cholerae(111 strains). All 111 strains of Vibrio cholerae appeared in the surveillance data system; whereas only 26% of Shigella spp strains and 23.6% of Salmonella spp strains appeared in the system. **Conclusions**: CMLs in Chongqing are a rich, yet underutilized, information source for infectious diseases surveillance. Establishing an electronic laboratory information system as well as microorganism banks should be an important part of the "National Laboratory Surveillance Network".

Board 197. Observational Study Regarding Incorporation of Measures to Prevent Disease Associated with Animals in Public Settings

S. L. Singleton[1], S. Poole[1], J. Scheftel[2], K. Smith[2], J. B. Bender[1];

[1]Univeristy of Minnesota, St. Paul, MN, [2]Minnesota Department of Health, St. Paul, MN.

Background: Since 2001, 50 outbreaks associated with animal contact venues in the United States have been documented. Agents responsible for outbreaks include *Escherichia coli* O157:H7, *Salmonella*, *Campylobacter*, and *Cryptosporidium*. The National Association of State Public Health Veterinarians has published broadly distributed recommendations to prevent illnesses and injuries associated with animal contact venues. The purpose of this study was to evaluate compliance with these recommendations at petting zoos at county fairs (and the state fair) in Minnesota. **Methods:** County fairs within a 100 mile radius from Minneapolis/St. Paul were identified. A convenience sample of these fairs were selected and visited between July-August 2007. A standard questionnaire was used to collect information about signage, availability of hand washing facilities, supervision, type of animals, and patron behavior. The number of visitors over a 1-hour period was estimated. **Results:** Eighteen county fairs and one state fair were evaluated. The mean number of people visiting the petting zoo over a 1-hour period was 435 (range 42 to 4,446). There were a number of different animals displayed including goats (78%), calves (56%), chickens (28%), chicks (33%) and cattle (17%). Less frequently displayed animals included kittens, dogs, monkeys, iguanas and ostriches. The public was not allowed to contact primates, wild animals or reptiles. Twelve (63.2%) of the 19 petting zoos provided handwashing facilities to the public. Six (31.6 %) of 13 facilities had hand sanitizer stations. Two facilities had neither a handwashing station nor hand sanitizer, while one facility had both. 50% of facilities allowed people to feed the animals, 63% instructed visitors to wash their hands after handling animals, 47% instructed individuals not to bring food or pacifiers into the petting zoo area, and 37% provided information about the risk of acquiring infection from contact with animals. **Conclusions:** Higher risk animals such as chicks and calves were frequently displayed. Many facilities instructed individuals to wash their hands and not to bring in food into animal contact areas, however, further education and encouragement is needed to attain a higher level of compliance with published guidelines.

Board 198. Cost of Public Health Response to an Outbreak of Malaria among Recently Resettled Refugees, July 2007

S. Bagga, M. I. Meltzer, A. Casano, P. Arguin, B. Kapella;

CDC, Atlanta, GA.

Background: From a group of 1,805 refugees resettled to 34 U.S. states from Tanzania between May 8 and July 9, 2007, 29 symptomatic cases of *Plasmodium falciparum* malaria were reported. These refugees had been given presumptive treatment for malaria with pyrimethamine/sulfadoxine prior to departure. Because clinical cases indicated treatment failure, CDC recommended that those refugees without clinical symptoms be re-treated with atovaquone/proguanil. To guide future recommendations regarding pre-departure presumptive treatment for malaria, we calculated the costs of the re-treatment and additional interventions for these refugees. **Methods:** We collected, from the perspective of the health care system, cost data in the following categories: (1) *Personnel Costs:* We sent questionnaires to relevant state refugee health coordinators, federal and state health departments, and voluntary agencies to collect hours of personnel time spent in the response. Work hours were valued using information from the results of an earlier cost-of-outbreak -questionnaire and the Bureau of Labor Statistics. *(2) Cost of re-treatment:* We used age-weight charts to calculate the drug dosage given to each refugee. Prices of atovaquone/proguanil were obtained from a wholesale drug price database *(3) Hospitalization Costs:* The length of stay for each of the 25 hospitalized cases was obtained from the admitting hospitals. The average per-day cost of an inpatient stay was derived from the Nationwide Inpatient Sample (NIS). **Results:** The measured response costs totaled to $363,700 (average $201/refugee), with personnel costs accounting for $118,222 (32%), re-treatment costs $104,687 (29%), and hospital costs $140,792 (39%). The average cost of re-treatment (drugs only) was $60/ refugee. **Conclusions:** This analysis shows that it can be costly to treat malaria cases and repeat presumptive treatment of refugees upon arrival in the United States.. These costs can largely be averted by using a more effective pre-departure presumptive treatment. Since July 2007, all refugees from Tanzania receive artemisinin-based combination therapy as pre-departure treatment.

Board 199. The Economic Cost of Guillain-Barré Syndrome in the United States

P. D. Frenzen;

Economic Research Service, USDA, Washington, DC.

Background: Guillain-Barré syndrome **(**GBS) is a postinfectious autoimmune reaction triggered by *Campylobacter jejuni* and certain other pathogens, as well as some vaccines. This study estimated the annual cost of GBS in the United States in 2004, including the direct costs of medical care and the indirect costs due to lost productivity and premature death. **Methods:** The lifetime economic cost of GBS for society was estimated. The cost-of-illness method was used to determine the costs of medical care and lost productivity, and a modified value of a statistical life approach was used to determine the cost of premature deaths. The estimated medical costs included inpatient care in community hospitals, rehabilitation facilities, and nursing homes, and outpatient care by physicians and therapists after patients were discharged. The estimated productivity costs included earnings foregone due to temporary or permanent disability. Data were obtained from the Nationwide Inpatient Sample, the Medical Expenditure Panel Survey, the Compressed Mortality File, a survey of adult GBS patients, and other sources. **Results:** The estimated annual cost of GBS was $1.6 billion (95% CI , $1.5-1.7 billion), including $0.2 billion (16%) in direct medical costs and $1.4 billion (84%) in indirect costs due to lost productivity and premature death. Most of the medical costs were for community hospital care. Most of the indirect costs were due to

premature deaths, which accounted for 62% of the total cost of GBS. The mean cost per GBS patient was $293,410 (95% CI, $255,588-331,232). The health burden due to GBS included approximately 6,000 admissions to community hospitals, 1,900 admissions to other inpatient facilities, 10,100 person-years of employment lost due to temporary or permanent disability, and 247 deaths. **Conclusions**: The cost estimate summarizes the lifetime health burden due to GBS from a societal perspective, expressed in monetary terms. The estimated cost of GBS provides some of the information needed to assess the cost effectiveness of food safety measures that reduced the incidence of *Campylobacter* infections that might trigger GBS, or vaccines that inadvertently increased the risk of GBS.

Surveillance: International and New Strategies

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 200. Detection of Emerging Disease Outbreaks through a Regional Network in the Former Soviet Union: ProMED-RUS

L. Madoff[1], N. Psenichnaya[2], A. Stepanyan[3], V. Melnik[4], N. Rakhmanova[5];

[1]ProMED-mail, ISID, Harvard Medical School, Boston, MA, [2]ProMED-RUS, Rostov-on-Don, RUSSIAN FEDERATION, [3]ProMED-RUS, Yerevan, ARMENIA, [4]ProMED-RUS, Donetsk, UKRAINE, [5]ProMED-RUS, Tashkent, UZBEKISTAN.

Background: The breakup of the Soviet Union left a gap in the availability of information on emerging infectious diseases as communication among health professionals in the countries of the Commonwealth of Independent States (CIS) was disrupted. ProMED-mail, an emerging disease reporting system that operates a collection of e-mail lists and websites, has employed regional networks in Latin America and Southeast Asia to improve detection and reporting of outbreaks in underserved areas. Despite cultural and linguistic diversity in the CIS, Russian is a language shared by many in the region. Thus, a Russian-language ProMED regional network was established in the CIS to improve communication regarding microbial threats within the region. **Methods:** A team of 4 bilingual experts in infectious diseases was recruited from member countries of the CIS. Initially, relevant reports from Russian-language sources were translated into English and disseminated via the English-language ProMED systems. Second, a Russian-language e-mail listserv was established using Mailman software and reports were circulated to participants who enrolled in a free subscription to ProMED-RUS. Finally, a Russian-language website was established where the same reports sent by e-mail could be viewed and also archived in a fully-searchable Oracle database. Selected reports continue to be translated into English and disseminated on other ProMED lists. **Results:** During the first 21 months of operation (through July 2007), over 150 participants have joined ProMED-RUS, mostly from CIS countries (Russia, Ukraine, Uzbekistan, Armenia, Kyrgyzstan, Belarus). Subscribers include WHO and UN agency staff, and members of Research Institutes and Medical Associations from CIS. Sources of information include Internet, media and official reports. For the first 6 months of 2007, 424 reports were posted. The most common reported diseases during this 6-month period were hemorrhagic fever (41 reports), tick-borne encephalitis (33), rabies (32), avian influenza (24), botulism (22), and foot and mouth disease (20). **Conclusions:** ProMED-RUS, the Russian-language regional network of ProMED-mail, has been established and is actively reporting infectious disease outbreaks, improving outbreak detection within the region of the former Soviet Union.

Board 201. Epidemiological analysis of influenza by laboratory surveillance in Gyeongnam province, Korea, 2004/2005 ~ 2006/2007

H. Jeong, W. Kim, G. Ha, M. Jang, J. Kim, K. Lee, H. Choi, J. Park, Y. Kim, H. Kim;

Gyeongnam institute of health and environment, Gyeongnam Province, REPUBLIC OF KOREA.

Background: Influenza virus classified into orthomyxoviridae is contagious and can easily cause respiratory disease especially in winter season. New viruses developed by mutation of antigen showed high infection rate in the aged and lead to fatal complications from respiratory disease. **Methods:** Epidemic aspect of influenza was investigated for patients with influenza-like illness (ILI) who visited hospital in South Gyeongsang area from October to May for 2004/2005 ~ 2006/2007 influenza seasons. Respiratory specimens were collected and used for genetic detection and isolation of virus by cell culture. **Results:** 187 influenza viruses were isolated from 1125 specimens in 2004/2005 season and it was identified as one A/H1N1, 123 A/H3N2 and 63 B type influenza viruses. During 2005/2006 season, from 520 specimens we isolated 85 influenza viruses. A/H1N1 were 19, A/H3N2 were 10, and the rest of them were B type. 361 influenza viruses were isolated from 1000 specimens during 2006/2007 season, and of which 87 were A/H1N1, 210 were A/H3N2, and 64 were B type. According to our results, A/H3N2 was dominant during 2004/2005 and 2006/2007 seasons in South Gyeongsang area. On the other hand, B showed similar distribution during all observed periods, 2004/2005~2006/2007. Influenza viruses appeared in 4-15 years of age. In particular, A/H3N2 was usually found in specimens from children or juveniles. While influenza viruses were isolated up to 30.4% from testing group in which people were vaccinated, the isolation rate was 39.1% for unvaccinated group. There was difference between their subtype's distributions. Sensitivity and peculiarity of kit test for antigen were 85.9% and 78.9% of virus isolation, respectively. **Conclusions:** These results will be good information to predict the effect of vaccine and epidemic appearances of influenza viruses and to plan measures for influenza control and management.

Bord 202. A Field Method for Surveillance of Yellow Fever Adverse Events Following Mass Vaccination Campaigns in Togo, 2007

G. Breugelmans[1], G. Napo-Koura[2], A. Kpinsaga[3], S. Kroman[1], S. Yactayo[4], M. Lourd[1], S. Briand[4], A. Aplogan[1], W. Perea[4], M. Niedrig[5], B. D. Gessner[1], D. I. Nassoury[6];

[1]Agence de Médecine Préventive, PARIS, FRANCE, [2]Lome Medical University, LOME, TOGO, [3]World Health Organization, LOME, TOGO, [4]World Health Organization, GENEVE, SWITZERLAND, [5]Robert Koch Institute, BERLIN, GERMANY, [6]Ministry of Health, Lomé, TOGO.

Background: During 2007-2010, the Global Alliance for Vaccines and Immunization will provide funding to deliver the highly effective attenuated 17D yellow fever (YF) vaccine to 48 million people in 12 African countries. Although this vaccine is safe, some rare but serious adverse events following immunization (AEFI) have been reported. The importance YF vaccine associated AEFIs is poorly understood, in large part because of difficulty in conducting systematic field surveillance and collecting biological specimens in developing countries. **Methods:** During February 2007 a reactive mass YF vaccination campaign was conducted in Northern Togo. A passive surveillance system based on the national notification process was established. This experience was then used

to develop a systematic surveillance system for implementation during a mass vaccination campaign during September 2007 in Southern Togo. **Results:** In Northern Togo, training and technical discussions were held with relevant field staff. All were given case definitions, detection and notification procedures, procedures for biological specimen collection and transport, guidelines on completion of clinical case reports, and the serious adverse events investigational process. Clinicians reported 72 AEFI cases (58 severe) but no biological specimens were collected. Based on the experience gained, a detailed study protocol, operational guide, and tools were developed that then were implemented in Southern Togo. Additionally, an active surveillance component was added that included visiting randomly selected health care centers to review medical records and sensitize clinicians that might manage potential AEFI cases. Clinicians subsequently reported 256 AEFIs (45 severe), obtained serology for 16 severe cases, and performed autopsy evaluations for 4. An expert committee reviewed all 45 severe cases. Laboratory analysis and committee deliberation are ongoing. **Conclusions:** Following implementation of a standardized protocol for YF AEFI surveillance in Togo, clinical staff obtained numerous biological specimens that - along with expert committee review - may help ascertain the causative role of vaccine. Training of health personnel and experts is critical in the success of YF AEFI surveillance and the investigation of AEFI cases.

Board 203. MN Medical Examiner (ME) Infectious Deaths Surveillance

C. Lees, J. Rainbow, R. Lynfield;

Minnesota Department of Health, St. Paul, MN.

Background: In 2006, the MN Department of Health (MDH) began an ME infectious deaths surveillance program (MED-X). This supplemented an existing Unexplained Deaths (UNEX) program targeted at young healthy people. MED-X was conducted at the MN Regional ME Office, which covers 7 counties (14.3% of state population). **Methods:** The ME reported possible cases to MDH, and MDH reviewed all death certificates to identify additional cases. The case definition was any death with active ante or postmortem infectious signs/symptoms, or an unexplained death in someone <50 years. MDH distributed specimen kits containing collection and transport materials, to increase and improve diagnostic specimens obtained at autopsy. Specimens were tested by the ME, MDH, and in some cases at CDC. **Results:** Of 1,563 deaths, 61 (4%) were MED-X cases, and 10 of these were UNEX cases. 12 cases were reported by the ME, and 49 additional cases were found by MDH through death certificate review. There were 18 (30%) confirmed infectious disease deaths (7 reported by ME and 11 from death certificates), 33 (54%) possible infectious disease deaths, 8 (13%) had no specified cause of death, and 2 (3%) were determined not to be infectious-related. Of the 18 confirmed infectious disease deaths, 3 were vaccine preventable (2 *S. pneumoniae*, 1 *N. meningitidis*). In addition, there were 2 CJD, 2 HIV/AIDS, 1 HSV, 1 metapneumovirus, and 1 norovirus-related death. The rate of infectious-related deaths was 12 per 1,000 for confirmed cases and 33 per 1,000 for both possible and confirmed cases. In the 4 cases that used specimen collection kits, all had pathogens identified as potential or confirmed causes of death. **Conclusions:** Surveillance for infectious deaths through MED-X provided a specific etiology in almost a third of eligible cases. Diagnoses included pathogens of public health importance. Providing resources such as a specimen collection kit, improved the ability to diagnose a specific pathogen. Cases identified by the ME were more likely to have a confirmed infectious cause than cases found by death certificate review, although additional cases were detected by the latter. Enhanced surveillance of infectious deaths with ME can strengthen infectious disease surveillance systems and improve the accuracy of data regarding the burden of infectious diseases.

Board 204. Sero-epidemiology as a Novel Approach to Estimate the Incidence of *Campylobacter* and *Salmonella* Infections in the Human Population

G. K. Falkenhorst[1], J. Simonsen[1], D. Krüger[1], T. Hansen[1], K. Krogfelt[1], P. Teunis[2], W. van Pelt[2], Y. T. van Duynhoven[2], K. Mølbak[1], for the MedVetNet Workpackage 32 Project Team;

[1]Statens Serum Institut, Copenhagen, DENMARK, [2]National Institute for Public Health (RIVM), Bilthoven, THE NETHERLANDS.

Background: Reports on the incidence of human infections with *Campylobacter spp.* and *Salmonella enterica* ssp. *enterica* are mostly based on laboratory-confirmed cases, which constitute only a small fraction of all clinical cases occurring in the community. The degree of underascertainment is influenced by health seeking behaviour, by clinical practices and by diagnostic practices in clinical laboratories. It differs between countries or states, which makes comparison of reported incidence rates problematic and potentially misleading. As a novel approach to estimate the incidence of these infections, we propose sero-epidemiology. A pilot study including six European countries is being conducted by Workpackage 32 of "MedVetNet", a zoonosis research network funded by the European Commission. **Methods**: Decay profiles of IgG, IgA and IgM antibodies against campylobacter and salmonella have been determined in sequential sera from culture-confirmed cases by in-house-developed ELISAs. Based on this data, we developed a stochastic backcalculation model, which allows to estimate the probable time since infection for any combination of IgA, IgG and IgM values in a single serum sample of an individual with unknown infection history. We measured antibody concentrations in sera collected from the general adult population in different countries. Estimates of the population incidence were then generated with the model. **Results**: Serology-based incidence estimates for salmonella were ~100 and ~125/1000 person-years for Denmark (DK) in 2006 and The Netherlands (NL) in 2000, respectively. For each notified laboratory-confirmed case, there were 360 (DK) and 830 (NL) persons with serological evidence of infection within the previous 12 months. Analysis of sera from more countries and for campylobacter is ongoing. **Conclusions**: Laboratory-based surveillance captures less than one percent of serologically diagnosed salmonella infections in the community. Sero-epidemiology provides estimates of the population incidence independent of surveillance artefacts. In the future, this method may complement existing laboratory-based surveillance of salmonella, campylobacter and potentially other organisms.

Board 205. Pregnancy-associated Listeriosis in the United States, 2004-2007

K. Jackson, M. Iwamoto, D. Swerdlow;

CDC, Atlanta, GA.

Background. Listeriosis is caused by *Listeria monocytogenes*, a gram-positive bacillus transmitted to humans primarily through food; it is more likely to result in death than other bacterial causes of foodborne illness, particularly in vulnerable populations including pregnant women. Infection in pregnant women may result in amnionitis, premature delivery, fetal loss, or invasive disease in the newborn. As part of the Listeria Initiative, launched in 2004, a standardized questionnaire about consumption of high-risk food items is administered to aid in investigations of listeriosis outbreaks. **Methods.** We examined pregnancy-associated cases that were reported to CDC through the Listeria Initiative during January 1, 2004-October 15, 2007. A case was defined as the isolation of *L. monocytogenes* from a normally sterile site, including blood or CSF samples, or from placenta or other products of conception. Cases were classified as pregnancy-associated if illness occurred in a pregnant woman or an infant less than 31 days old. **Results.** Of 526 reported *Listeria* cases, 78 (14.8%) were pregnancy-associated.

Median age of mothers was 28 years (range 15-45 years). Of those who reported ethnicity, 28 (41.2%) of 68 pregnant patients were Hispanic compared with 33 (8.9%) of 371non-pregnant patients (odds ratio=7.2; CI=3.8-13.7). Mothers most often reported no symptoms of illness (34.7%) or non-specific flu-like illness (20.8%). Maternal infection resulted in two neonatal deaths and 19 (24.4%) stillbirths. Invasive illness seen among newborns (n=51) were meningitis (37.3%) and sepsis (35.3%). Common food exposures during pregnancy were ham (47.4%), and hotdogs (44.2%), Mexican-style cheese (17.3%), and turkey deli meat (16.2%). **Conclusions.** Pregnant woman were a large proportion of reported listeriosis cases, and almost half of pregnancy-associated cases occurred among Hispanic women. Common exposures included previously recognized foods associated with *Listeria* infection. Further declines in pregnancy-associated listeriosis will require education about dietary measures to reduce the risk of infection, particularly among Hispanic populations, and regulatory and industry efforts to decrease the prevalence of *Listeria* in foods.

Board 206. Operationalizing Climate-based Epidemic Prediction Models

J. Chretien[1], A. Anyamba[2], J. Small[2], C. Tucker[2], J. Gaydos[1], K. Linthicum[3];

[1]DoD-Global Emerging Infections Surveillance & Response System (DoD-GEIS), Silver Spring, MD, [2]NASA-Goddard Space Flight Center, Greenbelt, MD, [3]USDA-ARS Center for Medical, Agricultural, and Veterinary Entomology, Gainesville, FL.

Background: There is considerable optimism that climate data and predictions will facilitate early warning of infectious disease epidemics. Interest in climate-based epidemic forecasting stems from climate-disease associations and global climate change (rising temperatures may extend arthropod vector habitats and enhance vectorial capacity, bringing infections to susceptible populations, and increase the frequency or severity of El Nino/Southern Oscillation, which has precipitated epidemics). Currently, though, there are few operational climate-based epidemic early warning systems. **Methods:** We qualitatively assess 10 years of operation of our climate-based epidemic early warning system to identify key considerations in system development. Our system was designed originally using satellite observations, epidemiological data, and field experiments to forecast Rift Valley fever (RVF) epidemics in East Africa, and operationalized in a global epidemiological surveillance-response network. **Results:** The system enabled model development and epidemic forecasts for various diseases, including East Africa RVF alerts beginning in September 2006, 3 months before a regional epidemic. Guided by geographical risk assessments, field partners in Kenya identified infected vectors and likely human cases in December, facilitating rapid international response. Other applications included warnings preceding yellow fever and RVF epidemics in Sudan, and retrospective identification of precursors to a chikungunya fever epidemic in Kenya which spread widely. **Conclusions:** In our experience, key factors in successful system implementation are organizations bridging model developers and end-users, and epidemiological surveillance programs for model validation and public health response.

Board 207. Trained district health personnel and the performance of Integrated Diseases Surveillance and Response (IDSR) in the WHO African region

I. Sow; World Health Organisation, Harare, ZIMBABWE. *I. Sow(1); W. Alemu(1), N. Ndayimirije(1), M. Nanyunja(2), N. Eseko(1), L. Ouedraogo(1); A. Yada(1);* Sambe Duale(3); H. Perry (4); P. Gaturuku(1)

Background: African countries have intensified in-service training on IDSR for district and health facility personnel to strengthen national surveillance system. Selected countries documented experiences and lessons in the implementation of IDSR. An analysis of the evaluation reports was conducted to assess the impact of training of district health personnel on the performance disease surveillance systems. **Methods**: Districts and health facilities were selected using either a multi staged or random sampling for the evaluation. Data were collected on core (detection, report, analysis, investigation, response and feedback) and support (training, supervision and communication) activities. Indicators on timeliness and completeness in reporting, data analysis, supervision and feedback were used for this review. **Results**: Approaches included cascade, on-job,fast track and pre-service training on detection, reporting and data analysis . The proportion of health facilities with 1 to 2 personnel trained varied from 52 to 89% and the knowledge of the health personnel for epidemic prone diseases ranged from 52 to 78%. In countries where all districts had trained personnel, timely reporting and completeness of health facilities is respectively 70 and 92 %. The increase in timely reporting varied from 47 to 100% and evidence of regular data analysis at district level reached 71%. In countries where 50 to 90% of districts had trained health personnel, evidence of data analysis at district level is 62 %. Supervision of health facilities ranged from 75 to 100% however feed back was less regular. In one country, despite the training in 88 % of the districts, reporting was neither complete nor timely. **Conclusions**: Trained district personnel are a key factor in the performance of IDSR through improvement of timeliness, completeness in reporting and analysis of data at the lower level. The experience shows that training of district personnel coupled with other components such as sustainable supervision and feedback, reliable communication and availability of simplified reporting tools is critical for the performance of national diseases surveillance systems.

Board 208. Health Seeking Patterns in a Population-Based Surveillance System Offering Free Health Care in Western Kenya

G. Bigogo;

KEMRI/CDC, Nairobi, KENYA.

Background We are conducting population-based surveillance for pneumonia, diarrhea, febrile illness and jaundice in rural western Kenya. Information on health-seeking patterns of the population is needed to extrapolate our case detection data to more precisely define disease burden. **Methods** Between September 2006 and August 2007 data were collected during biweekly household visits, as well as clinic visits. At household visits, a structured questionnaire enquiring about illnesses in the last 2 weeks was administered using PDAs. Participants reporting illness were asked if and where they sought care. Care was free to participants at the study's referral health facility, Lwak Hospital, within 5 km of all participants' homes. For clinic visits, standardized sick-patient visit forms were filled by clinic staff, enquiring about health-care seeking and medications taken prior to coming to the referral clinic. **Results** At the household visits, 75% of participants reporting fever, 62% reporting cough/difficulty breathing and 72% reporting diarrhea, sought care outside the home. Only 17%, 16% and 18% of the respective proportions above sought care at Lwak. The most common sites for care seeking were drug-sellers/chemists (35%), clinics other than Lwak (21%) and shops (16%). Children were more likely than adults to visit Lwak or other health clinics when ill (OR=2.3, 95% CI, 1.25-4.27). Reasons that participants cited for not going to Lwak for care were that the distance was too far (65%), some diseases not treated at Lwak (11.2%), and dissatisfaction with care at Lwak (7%). Based on Lwak clinic data, 43% of both children and adults making sick visits sought prior care. Forty-four percent took medication before visiting Lwak, most often from a chemist/drug seller - 14% took an antimalarial and 20% took an antibiotic. **Conclusions** Despite care being free at Lwak, a considerable proportion of sick participants did not seek care outside the home

or sought care at other sites before visiting the designated referral facility. Other factors besides cost influence care seeking. Defining the burden of infectious diseases in this rural African setting might require extending surveillance beyond health facilities, or making extrapolations based on health utilization data.

Board 209. Virological Surveillance of Enteroviruses in North India: A vital assessment before global Polio eradication

R. Chowdhary, Jr., T. N. Dhole, Sr., A. Sakaya, IV;

Sanjay Gandhi PGI, Lucknow, INDIA.

Background: This study is an overview of Enterovirus (EV) circulating in North India studied from the perspective of Poliomyelitis eradication. Wild polio cases decline due to intensive oral polio vaccine (OPV) immunization by World Health Organization. Monitoring NPEV is essential, as we approaches towards global eradication of poliovirus, NPEV causing AFP are equally cause of concern. **Methods:** A total of 28,854 Acute Flaccid paralysis (AFP) samples (National Polio Surveillance Project) and apparently 1000 healthy contacts living in same geographical area studied (2004-06). Serological identification of NPEV was done using RIVM specific pools (National Institute of Public Health and Environment, Bilthoven, The Netherlands). Untyped (UT) NPEV were sequenced directly from Reverse Transcription-Polymerase Chain Reaction (RT-PCR) using Pan-Enterovirus (Pan-EV) primer (CDC, USA) targeting highly conserved 5'un-translated regions (5'UTR) of the EV. **Results:** 9741 NPEV were isolated from the collected stool samples accompanied by high seasonal temperature and humidity. Seroneutralization had identified 67% of NPEV isolates, 32.6% remain as UT- NPEV. In typed NPEV, Coxsackie-B (Cox-B) accounted 32.3%; followed by Echoviruses-11, 12, 13, 7 between 8%- 28%. In sequenced UT-NPEV; Echovirus-30, 11 and 18 identified in high percentages. This is the first report from India that has to identify newly classified Human Enteroviruses (HEV); HEV-86(EU079026), HEV-97(EU071767), HEV-B isolate (EU071768) in AFP samples. **Conclusion:** Study provided definitive information about circulation, prevalence and new emerging NPEV in the polio endemic region of India. As the spectrum of NPEV causing AFP continues to expand, they should be considered in AFP surveillance to check for new emerging EV's. This would help in planning of strategies to be adopted in post poliovirus eradication in the country. This is the right time to prepare for the future tasks ahead as we are heading towards polio free region.

Vector-Borne Diseases

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 210. Evaluation of Five Formulations of *Bacillus Thurigiensis* For Dengue Control In The Municipality of Caicó - Rn

F. Gaiger, C. V. Assis-Pujol, I. A. Braga, G. E. Coelho;

Ministry of Health, Brasilia, BRAZIL.

Background: Detection of resistance of *Aedes aegypti* to organophosphates in Brazilian cities led the Ministry of Health (MS) to search for control alternatives. One of these options is the use of *Bacillus thurigiensis* sorovar *israelensis* (Bti). Even though the efficiency of this biolarvicide was confirmed in several studies, its application on large scale in dengue control programs is pioneering in Brazil, as an initiative of the MS, through the National Dengue Control Program (PNCD), in face of the need of insecticide substitution in the municipalities where resistance was detected. **Methods:** Five different commercial formulations were analyzed, herein designated as A, B, C, D e E. An area of approximately 6.000 premises, with occurrence of *Ae. Aegypti*, was selected. The total area was divided in four sub-areas. Formulations C and D were applied in the same sub-area since one is intended to treatment of human consumption water, while the other is used only for non-potable water. The House Index (HI) was assessed, prior to treatment, based on a larval survey of 30% of the study area premises. Each sub-area was treated with one of the tested larvicides. All water-filled recipients were inspected and treated according to PNCD's directives. All treated containers were tagged. In each sub-area blocks were selected with approximately 750 premises, of these 1/3 were weekly inspected during the two cycles of the test. The HI, Breteau Index (BI) and Recipient Index (RI) were used to evaluate the efficiency and persistence of each formulation. **Results:** Results revealed that the recipients treated with formulation A displayed a positivity of 10,0% in the eighth week of both cycles, the ones treated with formulation B showed 10,0% and 12,0% in the first and second cycle respectively, those treated with formulation C and D had 11,0% in the first cycle and 13,0% in the second cycle and the ones in which formulation E was applied showed 25,0% and 41,0% in the first and second cycle respectively. **Conclusions:** The results indicate that formulation A is the one that has the best persistence on field conditions.

Board 211. Marked increase in the incidence of Dengue and Dengue Hemorrhagic Fever in Brazil, 2007

A. C. Simplicio[1], G. Coelho[1], G. H. Moraes[2];

[1]Secretariat of Health Surveillance, Ministry of Health, Brasilia, BRAZIL, [2]Secretariat of Health, Federal District of Brasilia, Brasilia, BRAZIL.

Background: Dengue fever is an important health, environmental and economic concern in the Americas. Brazil has accounted for approximately 70% of reported dengue fever (DF) cases in this region. We analyzed national surveillance data for DF and dengue hemorrhagic fever (DHF) in Brazil during 2006 and 2007. **Methods:** National Dengue Surveillance System data from January 2006 to September were analyzed. Case definitions for suspected DF and confirmed of DHF followed Pan-American Health Organization guidelines. **Results:** Between January-September 2007, 510,117 cases of DF were reported. The incidence during this period was 267.4 cases/100,000 inhabitants; this was the highest incidence since a 2002 epidemic, when 794,219 cases occurred and the incidence was 454.8 cases/100,000 inhabitants. In 2007 cases were reported throughout the country; however the highest incidence occurred in the central state of Mato Grosso do Sul state, where the incidence reached 3,100 cases/100,000 inhabitants due to a DEN 3 epidemic in the beginning of the year. Comparing the first nine months of 2006 and 2007, the incidence of DF increased by 55%, and southern Brazil experienced the greatest increase (838%), mostly in the state of Parana. Confirmed cases in 2007 increased by 74% compared with 2006 (1,191 vs. 82 cases). DHF deaths in 2007 (136) increased by 79% compared with 2006, but the mortality increased by only 2.5% (from 11.1% to 11.4%). Regions reporting high numbers of DFH cases were already affected by outbreaks of serotypes 1, 2 and 3 during the past 20 years. There were no changes in the gender distribution of cases. **Conclusions:** Cases and deaths from DF/DHF increased in Brazil during 2007. The main affected areas were central and southern Brazil. Possible explanations may include climate changes, weakness of healthcare services, and challenges in vector control and mobilization of the population for prevention actions. These results led the National Dengue Control Program to invest in surveillance system enhancements and to promote improved diagnosis and treatment of DF.

Board 212. Lyme Disease in New York City - Is It Locally Acquired?

A. J. Abdool[1], R. Fernandez[2], C. Addei-Maanu[1], S. Slavinski[1], A. Fine[1];

[1]New York City Department of Health and Mental Hygiene, New York, NY, [2]Lincoln Medical and Mental Health Center, Bronx, NY.

Background: Little evidence has been found of local transmission of Lyme Disease (LD) in New York City (NYC). Incidence rates of LD are much lower in NYC than in surrounding highly endemic regions. Tick surveillance has rarely detected the vector, *Ixodes scapularis*, in NYC and few deer are present to host adult ticks. An investigation was conducted among NYC residents reported with early LD to determine where infections were likely acquired and to characterize the population at risk. **Methods:** The NYC Health Department attempted to phone all patients reported with onset of physician-diagnosed erythema migrans (EM) between April and November of both 2005 and 2006 (n=349). EM is the characteristic sign of early LD and the only sign or symptom with a relatively well-defined incubation period. Case patients were asked about travel outside NYC during the 30 days prior to EM onset. Incidence rates and median annual income for zip code of residence were calculated. **Results:** Of 196 (55%) subjects interviewed, most (61%) were aged 31-60 years, and 88% were Caucasian. Nearly all cases (95%) reported travel outside NYC during the incubation period, most frequently to the Hudson Valley region (28%) of NY or Long Island (20%), followed by CT, NJ, and MA. There was no clustering among locally-acquired cases. Cases with travel history appeared to cluster geographically. 59% resided in the borough of Manhattan. Incidence rates were highest in 17 zip codes which comprised five neighborhoods, four in Manhattan and one in Brooklyn (14.9/100,000 compared to 1.3/100,000 in the remainder of NYC). These zip codes also had an average median annual income twice that of the rest of the City ($71,994 vs. $35,822). **Conclusions:** Most NYC residents diagnosed with early LD likely acquired their infection while traveling to known endemic areas outside NYC. Demographic and residential characteristics, and travel history indicate that the population at risk likely has higher socioeconomic status. Prevention efforts should be targeted to neighborhoods with higher LD incidence. Although local transmission is likely to occur rarely if at all, further tick surveillance is needed to evaluate this possibility, particularly in areas of NYC which may have more suitable *I. scapularis* habitats.

Board 213. Etiology of Fever of Unknown Origin in a Selected Group of Sri Lankan Patients with Prompt Responses to Doxycycline

G. A. Dasch[1], R. Premaratna[2], R. P. Rajapakse[3], T. G. Chandrasena[2], M. E. Eremeeva[1], H. J. de Silva[2];

[1]Centers for Disease Control, Atlanta, GA, [2]University of Kelaniya, Ragama, SRI LANKA, [3]University of Peradeniya, Peradiniya, SRI LANKA.

Background: Most patients with long duration of fever go undiagnosed in settings where diagnostic facilities are inadequate. Untreated rickettsial infections cause extended fevers; while both scrub typhus and tick typhus are re-emerging diseases in Sri Lanka, laboratory facilities to specifically diagnose rickettsial infections in Sri Lanka are not available. **Methods:** We collected 2 ml venous blood from febrile patients who had no etiological diagnosis after 7 days of hospital admission, but who showed rapid clinical response to doxycycline, to verify whether they had experienced a rickettsial infection. Acute serum samples were analysed using IFA for rickettsial infections caused by *Orientia tsutsugamushi*, *Rickettsia conorii* and *Rickettsia typhi*. A positive IgG IFA titer ≥1:128 was used to define a probable case of rickettsial infection. **Results:** 28 patients [15 males, mean age 32.5 (SD 9.2 yrs)] were studied. Mean duration of fever at admission was 6.1 days (SD 3.1). Two patients had features suggestive of encephalitis and two had erythema nodosum. Others had no specific clinical features. Routine investigations were inconclusive and blood cultures were negative. IgG-IFA titer of ≥128 was found in 10 for *R. conorii*, 6 for *O. tsutsugamushi* and 6 for both *R. conorii* and *O. tsutsugamushi*. None were positive for *R. typhi*. Six were negative for all tests. One patient with encephalitis and one with erythema nodosum had high titers for *R. conorii*. **Conclusions:** The majority of Sri Lankan patients with undiagnosed fever responding promptly to doxycycline had a rickettsial etiology. Patients with rickettsioses exhibit varied clinical presentations so greater use of doxycycline for patients with extended fevers in rickettsial-endemic settings with inadequate diagnostic facilities appears warranted. The high proportion of patients with tick typhus and antibodies against both spotted fever and scrub typhus rickettsiae was unexpected based on previous studies of patients from the same region who were confirmed to have scrub typhus by serology and by the presence of the classic eschar. It is unknown whether the etiology of tick typhus and vector(s) transmitting this agent on the Western lowland region of Sri Lanka are the same as those responsible for spotted fevers in the central hill country of Sri Lanka.

Board 214. Dengue Virus Infections in Patients suspected of Malaria/Typhoid fever in Nigeria

M. M. Baba[1], M. Saron[2], A. V. Vorndam[3], J. A. Adeniji[4];

[1]University of Maiduguri, Maiduguri, NIGERIA, [2]Institut pasteur, Dakar, SENEGAL, [3]CDC, San Juan, PUERTO RICO, [4]University of Ibadan, Ibadan, NIGERIA.

Introduction: Dengue viruses (DENs) are etiologic agents of Dengue fever and hemorrhagic fever/shock syndrome. Since the prodromal phase of these diseases mimics malaria/typhoid which are highly endemic in Nigeria, this study was designed to determine the significance of these viruses in febrile illnesses. **Materials**: About 1948 serum samples from suspected cases of malaria and typhoid were collected in June 2001 to July 2002 from six ecological zones. In addition, 973 sera were collected from the same group of patients at different seasons from Sahel savanna zone. 295 *Aedes Spp* from Rain forest were identified and pooled by species. MAC- ELISA was used to test all the sera for IgM and IgG while Reverse Transcriptase-Polymerase Chain Reaction (RT-PCR) was used to analyze each mosquito pool and IgM positive sera. Each mosquito pool was also tested for virus isolation. **Results:** Thirteen (0.67%) of the1948 sera were positive for DEN 1and 2 IgM from 4 zones. Six (33.3%) of 18 of the IgM positive sera had detectable RNA to DENs. Two (0.2%) of the 973 patients had mixed infections of DEN and WNV. DEN IgM was significantly higher during the rainy season (1.3%) than harmattan (0.3%). No DEN IgM was detected in the hot dry season. A high proportion (>59%) of the study population in four ecological zones had IgG to DENs but was slightly lower in Sudan (32.6%) and Grass savanna (38.1%). No virus was isolated from mosquitoes after two passages in AP61. However, DENs RNA was detected in *Aedes species* from the rain forest. **Conclusion:** The prodromal phase of DEN infection could be mistaken for malaria/typhoid. There is need to include DENs and probably other endemic arboviruses routinely in the differential diagnosis of febrile illness in Nigeria.

Zoonotic & Animal Diseases

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 215. Molecular Epidemiology of Cross-Species Transmission of Rabies in the Central Great Plains

H. D. Barton[1], S. M. Wisely[1], R. Davis[2];

[1]Kansas State University, Manhattan, KS, [2]Kansas State University College of Veterinary Medicine, Manhattan, KS.

Background: Rabies is a generalist mammalian pathogen that has emerged multiple times in different reservoir species. Emergence in a novel host requires that a transmission network be established. One model of emergence posits that viruses adapt to new hosts upon infection, while an alternate model suggests that viruses must already contain the requisite mutation necessary to invade the novel host, i.e. they are pre-adapted. We conducted a molecular survey of rabies viral isolates from two strains of skunk rabies found in the Midwest. We compared diversity and sequence divergence in isolates from the reservoir host, striped skunk, and spillover hosts to determine the model of emergence to which rabies conforms. **Methods:** We isolated rabies RNA from 50 striped skunks, and 7 spillover hosts (cows, horses, dogs and cats). We sequenced 516 bp of N gene to compare viral characteristics among reservoir and spillover isolates. **Results:** We found lower dN/dS ratios in reservoir than in spillover isolates (skunk: 0.005/0.01, spillover: 0.006/0.008). Minimum spanning networks showed that southern strain spillover haplotypes were found both in the network interior and at tips. Six of 7 spillover hosts contained viral isolates that were also found in reservoir hosts, although these skunks were located more than 260 km from spillover hosts. **Conclusions:** The dN/dS ratios suggest that although stabilizing selection is occurring in both sets of isolates (dN/dS < 1), selection pressure is relaxed in isolates found in spillover hosts suggesting that some adaptation in new hosts may be occurring. Isolates which were found in both spillover and host species were the most broadly geographically distributed of all isolates. Cross-species transmission of rabies in North America is poorly understood. In the Midwest, transmission is thought to occur mainly through chance encounters between striped skunks and livestock, but transmission to companion animals is expected to increase as human landscape alteration leads to increasing numbers of striped skunks in urban areas.

Board 216. Comparison of Pig and Ferret Models for Respiratory versus Alimentary Transmission of H5N1 High Pathogenicity Avian Influenza Viruses

A. Lipatov[1], Y. Kwon[1], D. L. Suarez[1], K. Lager[2], D. E. Swayne[1];

[1]USDA, Agricultural Research Service, Athens, GA, [2]USDA, Agricultural Research Service, Ames, IA.

Background: H5N1 high pathogenicity avian influenza viruses (HPAIV) have caused over 300 human infections and over 200 deaths since 2003. The majority of the cases have involved close direct or indirect contact with infected poultry but a few cases have incriminated consumption of uncooked poultry products. This study compares transmission of H5N1 HPAIV in pig and ferret models via the respiratory and alimentary exposure routes. **Methods**: Groups of pigs and ferrets were intranasally (IN) or intragastrically (IG) challenged with 4 different H5N1 HPAIV in amnioallantoic fluid or given infected poultry meat orally or IG. Individual animals were examined for evidence of infection, clinical signs, gross and microscopic lesions and sites of virus replication. **Results**: IN exposure of pigs with 4 H5N1 viruses produced variable respiratory infection, most severely with Clade 1 and 2.2 viruses. The pigs exhibited bronchiolitis and alveolitis which were less severe, but similar to lung lesions observed in human H5N1 cases. Viral antigen was only visualized in lower respiratory tract in histiocytes and bronchiolar epithelium. IG exposure to virus in liquid failed to produce infection. However, pigs fed infected chicken meat became infected, and virus was isolated from nasal swabs and turbinates, and tonsil. IN exposure of ferrets produced respiratory infection with 2 isolates, systemic and fatal infection with 1 isolate and asymptomatic with 1 isolate. Ferrets feed infected meat developed respiratory and olfactory bulb infection with 1 virus and systemic infection with another. IG exposure to any virus in liquid failed to produce infection. However, IN virus in liquid, or oral feeding or IG exposure to chicken meat infected with 1 isolate produced fatal infection. At the early stage of infection, specific lesions in intestine, liver and pancreas without pulmonary lesions suggested that H5N1 virus could invade through alimentary tracts exposed to infected raw poultry meat. **Conclusions**: Pigs and ferrets were infected with H5N1 viruses by respiratory or alimentary exposure although the outcome was dependent on virus strain and host. Importantly, consumption of infected raw meat produced systemic and fatal infection via pharyngeal exposure and, likely, initial alimentary infection in the ferrets with one H5N1 HPAIV.

Board 217. *Corynebacterium diphtheriae* Among Domestic Cats: A Potential Zoonosis?

A. J. Hall[1], D. Bixler[2], A. P. Isaac[3], B. Keavey[4], C. D. Clark[2], P. K. Cassiday[5], L. C. Pawloski[5], M. L. Tondella[5];

[1]Epidemic Intelligence Service, Centers for Disease Control and Prevention, Atlanta, GA, [2]West Virginia Department of Health and Human Resources, Charleston, WV, [3]Elk Valley Veterinary Hospital, Elkview, WV, [4]West Virginia Department of Agriculture, Charleston, WV, [5]Pertussis and Diphtheria Laboratory, Centers for Disease Control and Prevention, Atlanta, GA.

Background: Diphtheria is a rare disease in the United States, with ≤5 cases reported annually, the majority of which are associated with international travel. Humans are considered to be the sole reservoir of *Corynebacterium diphtheriae*, the primary etiologic agent of diphtheria. In June 2007, the West Virginia Department of Agriculture isolated *C. diphtheriae* from an aural swab of a domestic cat presenting with severe otitis, prompting a public health investigation. **Methods:** We performed a contact investigation of the veterinary staff and household members of the affected cat, including interviews to assess exposure, medical history, vaccination status, and recent travel. We also conducted a carrier study, including oropharyngeal swabs of human contacts and either oropharyngeal, aural, or ocular swabs from a convenience sample of other household animals. Swabs were cultured on selective media, and isolates of *C. diphtheriae* were characterized by using biochemical and molecular assays at CDC. **Results:** Two human household members and eight veterinary staff were interviewed, none of whom had recent respiratory or skin infections or travel to diphtheria-endemic countries. All human samples were negative for *C. diphtheriae*. Including the index case, 11 samples were taken from seven other household animals (four cats, two dogs, and one horse). *C. diphtheriae* was isolated from both ears of the index cat and from the left ear of a second cat. These three isolates, along with the original isolate from the index cat, were identified biochemically as *C. diphtheriae* biovar *belfanti*. On the basis of real-time polymerase chain reaction amplification of the diphtheria toxin gene, *tox*, and the Elek toxin-antitoxin precipitation test, the four isolates all yielded atypical results that were inconclusive for toxin production, with further analyses pending. The four isolates also produced identical patterns by ribotyping, which was markedly distinct from any other *C. diphtheriae* isolate analyzed by CDC.

Conclusions: A novel clone of *C. diphtheriae* was isolated from two domestic cats in the same household in West Virginia, and no apparent human source of infection was identified. Although public health implications are unclear, domestic cats should be considered potential reservoirs of *C. diphtheriae*.

Board 218. Landscape Genetics of White-Tailed Deer and the Implications for the Spread of Chronic Wasting Disease across Kansas

M. Statham[1], A. Mattox[1], S. Wisely[1], L. Fox[2], J. Cully[1];

[1]Kansas State University, Manhattan, KS, [2]Kansas Department of Wildlife and Parks, Emporia, KS.

Background: Chronic Wasting Disease (CWD) is a form Transmissible Spongiform Encephalopathy found in deer and elk in North America. CWD is caused by prions, an unusual isoform of a naturally occurring protein, and leads to loss of body condition, behavioral abnormalities and death. CWD has been documented in free ranging deer in Colorado since the 1980s; however, the first documentation of the CWD in free ranging deer in Kansas occurred in December 2005, within 30 miles of two newly confirmed sites in Colorado. An understanding of the influence of landscape on population connectivity aids in the understanding of disease transmissibility. Using landscape genetic approaches, we estimated gene flow across Kansas to help predict the spread of the disease and assist in developing management plans for susceptible populations. **Methods:** We genotyped 240 white-tailed deer at eight microsatellite loci, in eight different locations across Kansas. We calculated geographic distances among populations to determine if they were isolated by distance. We correlated genetic diversity and inbreeding with independently derived estimates of population density and hunting pressure. **Results:** All eight populations had high levels of allelic diversity (11-13) and observed heterozygosity (>0.70). Global geneflow was high (F_{ST} <0.02), however several values reflected low connectivity between population pairs. Bayesian clustering analysis gave greatest support for 3 populations, suggesting a level of population differentiation. Populations showed no significant effect of isolation by distance. Lower deer density was associated with an increase in the inbreeding coefficient (F_{IS}). **Conclusions:** We detected genetic differentiation between adjacent populations occupying the Arkansas and Smoky Hill River drainages, suggesting that dispersal may be limited by these two major drainages. Populations in these drainages also had greater F_{IS} values, indicating increased inbreeding. High F_{ST} values were detected between drainages, suggesting that control of disease spread should concentrate in these areas. This information will be vital in formulating a management strategy to minimize the transmission of CWD across different populations and watersheds.

H1. Respiratory Diseases

Tuesday, March 18
3:00 PM – 4:30 PM
Centennial I

Novel Adenovirus Serotype Identified in Healthcare Workers at a Military Hospital _ Texas, 2007

F. Lessa[1], P. Gould[1], N. Pascoe[2], D. Erdman[1], X. Lu[1], M. Bunning[3], V. Marconi[4], L. Lott[5], M. Widdowson[1], L. Anderson[1], A. Srinivasan[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Texas Department of State Health Services, Houston, TX, [3]37th Training Wing, Air Force Institute for Operational Health, San Antonio, TX, [4]59th Hospital Wing, Air Force Institute for Operational Health, San Antonio, TX, [5]Epidemic Outbreak Surveillance, Advanced Diagnostics Laboratory, Modernization Directorate, Office of the Surgeon General, San Antonio, TX.

Background: Adenovirus serotype 14 (Ad14), first identified in 1955, is rarely detected in the United States. From March 1 through June 15, 2007, 16 military recruits were hospitalized for Ad14 pneumonia in an acute care facility on a military base in Texas. Subsequent reports of acute respiratory illness among healthcare workers (HCWs) in this facility raised questions regarding nosocomial spread of Ad14 infection. An investigation was initiated to confirm possible Ad14 infections among HCWs, identify risk factors for Ad14 acquisition, and recommend prevention measures. **Methods:** HCWs from the units where recruits had been admitted were offered testing for Ad14 infection. Each tested HCW completed a questionnaire on history of recent respiratory illness and on risk factors for infection, including infection control practices. A case of Ad14 infection was defined as presence of Ad14 antibodies by serum neutralisation or a nasal wash positive for Ad14 by polymerase chain reaction (PCR). We reviewed infection control practices and collected environmental samples from frequently touched surfaces. **Results:** Among the 483 HCWs identified, 218 (45%) were tested; of these, 42 (19%) met the case definition. Thirty-six (85%) were Ad14 positive by serology, 2 (5%) by PCR, and 4 (10%) by both. Median age of cases was 29 years (range: 19–74 years). Forty percent were nurses, 17% were residents, and 14% were respiratory therapists. Thirty-eight percent of cases reported febrile respiratory illness compared with 11% of HCWs with no Ad14 infection ($p<0.001$). Of the 32 cases who reported respiratory symptoms, only 5(16%) stopped working during the course of illness. Direct contact with Ad14 patients was reported by 81% of cases compared with 62% of HCWs with no Ad14 infection (p=0.02). Review of infection control practices revealed that Ad14 patients were not placed on contact and droplet precaution at the time of admission. Of the 47 environmental surfaces sampled, 9 (19%) were positive for Ad14 by PCR. **Conclusions:** Our findings support nosocomial transmission of Ad14 to HCWs from infected patients. Prevention measures should include placing patients with suspected Ad14 infection on isolation precaution at admission, cleaning environmental surfaces daily, and removing HCWs with respiratory symptoms from direct patient contact.

Severity of Invasive Pneumococcal Disease Caused by Vaccine and Nonvaccine Serotypes

T. Pilishvili[1], C. A. Lexau[2], A. S. Craig[3], A. Thomas[4], J. L. Hadler[5], N. M. Bennett[6], M. M. Farley[7], A. Reingold[8], L. H. Harrison[9], B. Beall[1], C. G. Whitney[1], M. R. Moore[1];

[1]CDC, Atlanta, GA, [2]Minnesota Department of Health, St. Paul, MN, [3]Tennessee Department of Health, Nashville, TN, [4]Oregon Department of Human Services, Portland, OR, [5]Connecticut Department of Public Health, Hartford, CT, [6]Monroe County Department of Public Health, Rochester, NY, [7]Emory University School of Medicine and VAMC, Atlanta, GA, [8]University of California, Berkeley, CA, [9]9University of Pittsburgh, Pittsburgh, PA.

Background: Invasive pneumococcal disease (IPD) rates among children aged <5 years declined after introduction of 7-valent pneumococcal conjugate vaccine (PCV7) in 2000. IPD rates caused by non-PCV7 serotypes have increased. We evaluated severity of illness indicators among children with PCV7 and non-PCV7 IPD. **Methods:** IPD cases were defined as isolation of pneumococcus from a normally sterile site in a resident aged <5 years of 8 Active Bacterial Core surveillance areas during 1998-2006. We classified cases as having an underlying illness (UI) if they had an illness listed as a PCV7 indication. We determined serotype and assigned cases to 2 groups: VT (PCV7-types and PCV7-related types, except 19A), and NVT (type 19A and all other types). We compared proportions hospitalized and case-fatality ratios (CFR) during 2005-2006 and 1998-1999 (pre-PCV7) and evaluated predictors of IPD severity

in a multivariable model. **Results:** Overall IPD rates declined from 98.7 in 1998-99 to 22.4 per 100,000 in 2005-06 (P<0.001); NVT rates increased from 9.5 to 20.3 (P<0.001). The proportion of cases with UI increased from 3% to 7% (P<0.001). Although the proportion of cases hospitalized increased from 32% to 52% (P<0.001), hospitalization rates declined from 31.4 to 11.5 per 100,000 (P<0.001). Controlling for serotype group, presence of UI, and time (1998-99 vs 2005-06), case patients with UI were more likely than those without UI to be hospitalized (odds ratio [OR] 7.7, 95%CI 4.5-13.1); hospitalization was not more common among NVT than VT cases (OR 1.2, 95%CI 0.9-1.6). While CFR increased from 0.7% in 1998-99 to 2.2% in 2005-06 (P=0.001), mortality rates declined from 0.7 to 0.5 deaths per 100,000. In 2005-06, CFRs for VT (N=49) and NVT cases (N=433) did not differ significantly (4.1 and 1.9%, respectively; P=0.27). Controlling for presence of UI, serotype group, and time, cases with UI were more likely than those without UI to be fatal (OR 11.1, 95%CI 4.4-27.8), while serotype group did not affect the likelihood of fatal outcome (OR 0.8, 95%CI 0.2-3.0). **Conclusions:** IPD cases caused by NVT are not more severe than VT cases. In 2005-06, IPD cases were more likely to have UIs and the presence of these illnesses, rather than serotype, was an independent predictor of severity of illness.

Impact of 7-Valent Pneumococcal Conjugate Vaccine on Invasive Pneumococcal Disease among Children and Adults, U.S., 2006

M. Moore[1], T. Pilishvili[1], N. M. Bennett[2], J. L. Hadler[3], A. Thomas[4], M. M. Farley[5], A. S. Craig[6], C. Lexau[7], A. Reingold[8], L. Harrison[9], B. Beall[1], C. G. Whitney[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Monroe County Department of Public Health, Rochester, NY, [3]Connecticut Department of Public Health, Hartford, CT, [4]Oregon Department of Human Services, Portland, OR, [5]Emory University Department of Medicine, Atlanta, GA, [6]Tennessee Department of Health, Nashville, TN, [7]Minnesota Department of Health, St. Paul, MN, [8]University of California, Berkeley, Berkeley, CA, [9]University of Pittsburgh, Pittsburgh, PA.

Background: Seven-valent pneumococcal conjugate vaccine (PCV7) was introduced in the U.S. in 2000 for children aged <5 years. We assessed the impact of PCV7 use on invasive pneumococcal disease (IPD) incidence among children and adults. **Methods**: Cases of IPD, defined as isolation of pneumococcus from a sterile site, were identified through 8 Active Bacterial Core surveillance sites under continuous surveillance. We serotyped isolates using the Quellung reaction. We compared percent change in IPD incidence rates in 2006 to rates during the baseline period of 1998-99 using the X^2 test. We determined age-and race-adjusted rates of IPD at baseline and in 2006 to estimate the total number of cases prevented through vaccination. **Results**: Overall incidence of IPD, expressed as cases per 100,000 population, declined among all age groups: <5y: 99 to 22 (-78%, 95%CI -81,-75); 5-17y:, 4.2 to 2.6 (-38%, 95%CI -51, -21); 18-49y: 13 to 8 (-39%, 95%CI -44,-34); 50-64y: 24 to 21 (-14%, 95%CI -22, -5); 65-79y: 46 to 31 (-32%, 95%CI -39,-24); ≥80y: 99 to 57 (-42%, 95%CI -49,-35). These trends reflected declines in incidence of IPD caused by PCV7 serotypes among all age groups: <5y: 82 to 0.5 (-99%, 95%CI -100,-99); 5-17y: 2.4 to 0.5 (-80%, 95%CI -89, -67); 18-49y: 7.6 to 0.9 (-88%, 95%CI -91,-86); 50-64y: 12.7 to 2.1 (-84%, 95%CI -87, -79); 65-79y: 25 to 3 (-88%, 95%CI -91,-83); ≥80y: 57 to 6 (-90%, 95%CI -93,-86). Incidence of IPD caused by non-PCV7 serotypes increased from 8.9 to 12.5 (+40%, 95%CI +21, +46) and reflected increases in serotype 19A from 0.8 to 2.8 (+264%, 95%CI +213, +323). Although serotype 19A IPD rates increased significantly among all age groups, absolute increases were small, ranging from 0.5 cases per 100,000 among 5-17 year-olds to 7.6 cases per 100,000 among <5 year-olds. Overall >30,000 IPD cases were prevented in 2006. As of 2006, 3%, 67%, and 69% of all IPD cases were caused by serotypes included in PCV7, a developmental 13-valent conjugate vaccine, and the 23-valent polysaccharide vaccine, respectively. **Conclusions**: PCV7 continues to provide impressive public health benefits 6 years after introduction. Disease caused by non-PCV7 serotypes, especially 19A, is emerging and accounts for nearly all IPD. Newer conjugate vaccines targeting more serotypes are needed to further reduce IPD.

Adenovirus 14 Illness among Basic Military Trainees, 2007

J. E. Tate[1], M. Bunning[2], X. Lu[1], C. Panozzo[1], L. Lott[3], J. Su[1], M. Prill[1], B. Johnson[4], N. Johns[5], L. Brosch[6], D. Erdman[1], V. Fonseca[7], L. Anderson[1], M. Widdowson[1];

[1]CDC, Atlanta, GA, [2]Air Force Medical Operations Agency, United States Air Force, Kelly Air Force Base, TX, [3]Epidemic Outbreak Surveillance, Lackland Air Force Base, TX, [4]Emory University, Atlanta, GA, [5]Air Force Institute for Operational Health, United States Air Force, Brooks City Base, TX, [6]37th Medical Group, Unites States Air Force, Lackland Air Force Base, TX, [7]Texas Department of State Health Services, Austin, TX.

Background: In 2007 in the United States, several clusters of hospitalizations for respiratory illness associated with a genetic variant of a rare adenovirus, serotype 14 (Ad14) were reported. To determine the spectrum of Ad14 illness and antibody correlates of protection, we investigated a cohort of basic trainees at a military base with ongoing Ad14 transmission. **Methods:** After 6.5 weeks of training, 171 of 216 trainees from 4 training groups (3 male; 1 female) with high rates of febrile respiratory illness (FRI) were interviewed about potential risk factors and symptoms during training. Throat swabs and blood specimens were collected and pre-training sera obtained. Throat swabs were tested for Ad14 by real-time PCR. Sera were tested for Ad14 neutralizing antibodies by micro-neutralization assay. Pre-training sera from Ad14 infected cohort members with mild symptoms and from trainees hospitalized with Ad14 associated pneumonia were obtained to examine any association of Ad14 disease severity with preexisting neutralizing antibodies to adenovirus 7a and 11, known to be cross-reactive with Ad14. **Results:** Of 171 trainees, 85 (50%) had evidence of Ad14 infection during training. The attack rate in males was 63% (79/126) compared to 13% (6/45) in females. Of 126 males, 33 (26%) reported FRI compared to none of the 45 female trainees. The risk of FRI was significantly higher in Ad14 infected trainees (39%) compared to non-Ad14 infected trainees (8%) (risk ratio (RR) = 4.8; 95% CI: 2.2, 10.2). Approximately 40% of trainees reported afebrile respiratory illness (cough plus another respiratory symptom) but this was not associated with Ad14 infection (RR = 0.8; 95% CI: 0.5, 1.1). Ad11 serum neutralizing antibody was not found in any of the specimens tested. Ad7a serum neutralizing antibody was found in 7 (37%) of 19 Ad14 positive trainees with mild illness but was not found in any of the 16 hospitalized patients (p=0.007). **Conclusions:** More than a third of Ad14 infections resulted in FRI. Males had a higher risk of Ad14 infection and of FRI compared to females. The significant association of mild illness with presence of Ad7 serum neutralizing antibody in pre-training sera suggests that an Ad7 vaccine could potentially cross-protect against severe Ad14 disease.

Full Genomic Sequence Analyses of Emerging Human Adenovirus (Ad) 14 Isolates from 2006-2007 Acute Respiratory Disease Outbreaks in the US Military.

H. Houng;

Walter Reed Army Institute of Research, Silver Spring, MD.

Background: Emerging Ad14 caused severe acute respiratory disease (ARD) outbreaks in multiple states during 2006- 2007 (Nov

16, 2007; MMWR, CDC). Though not a frequently reported serotype in humans and rarely encountered in US military basic training where Adenovirus ARD is a common health problem. Ad 14 was isolated in several military training camps during this period. Full genomic sequences of Ad14s are compiled to study the genetic makeup and relationships from various 2006-2007 isolates that caused both severe and mild ARD infections among military trainees. **Methods**: Lab grown Ad14s were obtained by inoculating throat-swabbed samples of infected patients into A549 cells. Fourteen Ad14s isolated from 2007 ARD outbreak at Lackland Air Force Base (LAFB) plus two other Ad14s, one 2006 Ad14 from infected military recruit in San Diego, CA and Ad14 DeWitt prototype were used for genetic sequence studies and analyses. DNA sequences were determined and analyzed using Sanger's dideoxy-terminator sequencing method based on manufacture's protocol and software, such as ABI 3100 DNA sequencing system and MacVector DNA analysis software. **Results**: Consensus Ad14 genome sequences (total of 36,764 base pair nucleotides/virus) of both mild and severe ARD cases at LAFB were determined to be 100% identical. It was found that the recent Ad14s from 2006-2007 outbreaks are closely related with distinctive clonal differences identified from two distinct geographic locations. Comparison between Ad14s of LAFB and San Diego, only one bp mutation within the Fiber plus two minor non-coding mutations, such as poly-Ts region were uncovered. However, there are significant mutations identified, i.e. up to 0.3% or 100s bps differences scattering through out the entire genomes when these isolates are compared to the Ad14 DeWitt prototype. In addition to consensus sequence studies, extensive Ad14 terminal inverted terminal repeat (ITR) deletions were uncovered from all Ad14s. **Conclusions**: Most of recent Ad14s are closely related to each other, but these Ad14 isolates are distinctively different from Ad14 prototype.

Incidence and Etiologies of Hospitalized Pneumonia in Young Children in Rural Thailand

J. C. Rhodes[1], H. Baggett[1], S. Thamthitiwat[1], M. Chittaganpitch[2], P. Areerat[3], D. Areechokchai[4], S. Naorat[1], P. Prapasiri[1], S. Olsen[5], A. Fry[6], L. Peruski[7], S. Maloney[7];

[1]IEIP, Thailand MOPH-US CDC Collaboration, Nonthaburi, THAILAND, [2]Thailand MOPH, National Institute of Health, Nonthaburi, THAILAND, [3]Provincial Health Office - Sa Kaeo Province, Nonthaburi, THAILAND, [4]Thailand MOPH, Bureau of Epidemiology, Nonthaburi, THAILAND, [5]US CDC, Division of Emerging Infections and Surveillance Services, Atlanta, GA, [6]US CDC, National Center for Immunization and Respiratory Diseases, Influenza Division, Atlanta, GA, [7]Thailand MOPH-US CDC Collaboration, IEIP, Nonthaburi, THAILAND.

Background: Pneumonia is the leading infectious cause of child morbidity and mortality worldwide, but detailed data on the burden of disease and specific etiologies among children are limited, especially in Asia. **Methods:** We conducted active, population-based surveillance for community-acquired pneumonia in all 20 hospitals in 2 rural Thai provinces (population 1.1 million; 77,800 <5 years) from 2003 through 2006. Clinical pneumonia was defined as illness in a child age <5 years hospitalized with evidence of acute infection and signs or symptoms of respiratory disease. Children with a chest x-ray within 48 hours after admission were eligible for enrollment in an etiologic study. Enrolled patients provided nasopharyngeal swabs for viral PCR and culture and acute and convalescent blood for serologic studies. Starting in 2005, blood culture capacity was added to the surveillance system to enhance detection of bacterial causes of pneumonia. Cultures were performed when considered clinically indicated by hospital physicians. **Results:** During August 2003 - December 2006, 16,475 children age <5 years had clinical pneumonia requiring hospitalization (annual incidence = 61.1/1,000 persons); 34% (5,616) of cases occurred in children <1 year (142/1,000 persons). Nearly 25% of pneumonia patients received oxygen therapy, 1.4% intubation, and 0.6% (104) died, including 81 children age <1 year (200/100,000). Viral pathogens were detected in 49% of those enrolled in the etiology study (1,492/3,046) and included RSV (21.6%), parainfluenza viruses 1-3 (9.6%), influenza A/B (8.1%), and rhinovirus (20.4% [11.9% as single pathogen]). Blood cultures were also obtained in 42% (1,266/3,046) of enrolled patients and 2.8% (36/1,266) were positive, including *Acinetobacter* (0.7%), *S. pneumoniae* (0.6% [0.2% by isolate and 0.4% by rapid antigen test on blood culture media], *Escherichia coli* (0.3%), *Salmonella* non-typhi (0.3%), and *Haemophilus influenzae* (0.2%). Seasonal peaks in pneumonia incidence corresponded to peaks in RSV and influenza cases. **Conclusions:** Children under 5 years of age in rural Thailand experienced high rates of pneumonia. These data can guide vaccine strategies and other public health interventions to reduce the pneumonia disease burden and provide data on etiologic agents that deserve further study.

H2. Health Communications

Tuesday, March 18
3:00 PM – 4:30 PM
Centennial II

Facilitating Community Action to Prevent Avian Influenza

B. Moore, **W. Pyles**;

CARE USA, Atlanta, GA.

Background In communities at high risk for H5N1 avian influenza virus (AI), limited understanding of AI symptoms and preventive measures are major challenges to preventing transmission. From November 2006 to August 2007, the Strengthening Training, Outreach and Prevention for AI (STOP-AI) project implemented a five-step model addressing these obstacles in 64 communes in four Vietnam provinces where AI is endemic in poultry. The model strengthens vertical and horizontal collaboration between leadership and communities to develop outreach campaigns. Engaging local institutional structures, the model complemented existing interventions and resources. CARE partnered with local organizations, government, and animal and health workers. After providing initial AI training, all partners jointly planned a communications campaign tailored to each commune. Each campaign used a multi-sectoral approach to reach various target audiences, during which time CARE provided monitoring and support. After the two-month campaign, community and district leaders met to evaluate success and propose next steps. **Methods** Two evaluations assessed the relevance, efficacy, and sustainability of the model. One used in-depth interviews and focus groups with involved community members in six communes, while the other used pre- and post-intervention surveys assessing knowledge, attitudes, and practices (KAP) in 10 intervention and 10 control communes. **Results** Both evaluations indicate that the model enhances local capacity, mobilizes the community, and raises awareness of AI. The intervention far exceeded its target due to community-led expansions of outreach campaigns to schools and community meetings. The 58,057 households reached consistently demonstrated more detailed and accurate knowledge of AI and preventive measures than their counterparts. They were more likely to report sick poultry to health officials and seek immediate medical care for AI symptoms. Behavior change among small-flock farmers remained a challenge. **Conclusion** The model's approach effectively raises awareness of AI and prompts further community action when necessary. More can be done to foster long-term behavior change among certain communities. **Partners,** Vietnamese Women's Union, Academy for Educational Development, USAID

Trying to Get the Message Right: Formative Research on Avian Influenza

L. S. Blum[1], A. Yemweni[2], C. Manianga[2], D. Lango[1], L. Flamigni[3], R. F. Breiman[1], N. Muraguri[4], M. A. Katz[1];

[1]CDC, Nairobi, KENYA, [2]University of Kinshasa, Kinshasa, CONGO, DEMOCRATIC REPUBLIC OF THE, [3]CDC, Kinshasa, CONGO, DEMOCRATIC REPUBLIC OF THE, [4]MOH, Nairobi, KENYA.

Background: Social and cultural factors present major challenges to preparedness against Avian Influenza (AI), especially in countries where backyard farming prevails, communication is poor and other diseases are widespread. In Africa, AI communication development has been reactive rather than carried out in a systematic fashion. As a result, messages are often not contextually appropriate and feasible for the population to put into practice. **Methods:** Formative research was carried out in urban and rural sites in Kenya and DR Congo (DRC) to gather information for the development of national communications strategies for AI prevention and preparedness. Qualitative methods entailed in-depth interviews, observations and group discussions and were conducted with a variety of respondents including backyard and commercial farmers, vendors and transporters of poultry, and food service workers involved in raising, processing, and preparing poultry products. **Results:** In Kenya and DRC**,** residents of densely populated, low income areas live and sleep in very close quarters with poultry. Raising poultry provides income critical for daily survival. In all sites, sick poultry are generally treated at home with high doses of human medications, and to avoid an economic loss, are slaughtered for household consumption or sold when poultry are thought to be dying. Dead poultry may also be consumed, depending upon people's religious and economic background. Some backyard farmers expressed suspicions about veterinarians who are known to confiscate animals from households. Farmers generally have little confidence in reporting sick birds to authorities. Small commercial farmers have limited access to health information and fail to follow basic bio-security measures; mechanisms for commercial farmers to report outbreaks are not established. Some restaurant owners working in low income areas in DRC reported serving birds dying of unknown causes. **Conclusions:** Study results identified a wide range of misconceptions and risky practices that could affect the spread of AI among poultry and facilitate the transmission of AI from poultry to humans. These data underscore the need to make avian influenza messages contextually appropriate, taking into account economic and sociocultural conditions affecting human behavior.

Physicians' Knowledge, Attitudes, and Practice Regarding Prevention of Infections During Pregnancy

D. S. Ross[1], S. A. Rasmussen[1], M. J. Cannon[1], B. Anderson[2], K. Kilker[1], A. Tumpey[1], J. Schulkin[2], J. L. Jones[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]American College of Obstetricians and Gynecologists, Washington, DC.

Background: Maternal infection during pregnancy is a well-recognized cause of birth defects, developmental disabilities, and other adverse pregnancy outcomes. Obstetrician-gynecologists (OB/GYNs) are an important source for information for pregnant women about prevention strategies. Increased understanding of the effects of infections during pregnancy and awareness of prevention strategies is important both for pregnant women and their health care providers. **Methods:** To determine obstetrician-gynecologists' knowledge, attitudes, and practices regarding the prevention of infections during pregnancy, we surveyed by mail 606 American College of Obstetricians and Gynecologists members (approximately 2% of membership), sampled to demographically represent ACOG. After three mailings, the response rate was 50% (n = 305). **Results:** The majority of obstetrician-gynecologists knew that pregnant women should avoid cleaning cat litter boxes, be tested for HIV, cook meat until well done, keep up-to-date on vaccines, avoid contact with people who have chicken pox or pertussis, wash their hands after changing a diaper, and avoid rodents. Ninety percent or more of OB/GYNs reported providing specific prevention messages to pregnant women about preventing *Toxoplasma gondii* and hepatitis B infection, about 60% reported providing prevention messages about varicella zoster virus and *Listeria* infection, and <50% reported providing prevention messages about preventing cytomegalovirus, *Bordetella pertussis*, and lymphocytic choriomeningitis virus infection. The majority surveyed reported that they did not have sufficient time to counsel pregnant women about preventing infections, and most reported that educational materials would assist them in this activity. **Conclusions:** Among OB/GYNs, the level of knowledge regarding prevention of infections during pregnancy was high and provision of prevention messages was frequently reported for some infections (e.g. *Toxoplasma gondii* and hepatitis B virus). However, for other infections (e.g. cytomegalovirus, and *Bordetella pertussis*) preventive counseling could be improved. Additional opportunities for prevention might be available through increased educational efforts and further studies aimed at OB/GYNs and pregnant women.

Community Capacity to Implement Non-Pharmaceutical Measures for Pandemic Influenza: An Assessment

B. Burrus[1], B. Stone-Wiggins[2], D. Coombs[2], D. Currivan[2], F. DeStefano[1], A. McCalla[2], S. Wetterhall[1];

[1]RTI International, Atlanta, GA, [2]RTI International, Research Triangle Park, NC.

Background Much recent attention has been focused on the possibility of an influenza pandemic. Due to the anticipated delay in developing an effective vaccine and shortages of antiviral medications, public health officials will rely upon nonpharmaceutical interventions (NPIs) as their first line defense for mitigation. Responsibility for implementation of NPIs will be largely centered at the local levels. Despite the criticality of these NPI strategies, little is known regarding challenges to implementing these recommendations at the local level. With support from the Centers for Disease Control and Prevention, RTI International, partnering with the North Carolina Division of Public Health, has conducted a feasibility assessment of communities' capacity to assess readiness and identify gaps for implementation of NPIs in a pandemic event. **Methods** Nine North Carolina counties participated in the assessment. Site visits included in depth interviews with local public health officials, social service providers, school personnel, religious organizations and private sector representatives (e.g., business leaders, health care providers, and children care providers). Qualitative analysis techniques were used to assess plans, possible barriers, and gaps for topics including communication, lines of authority, and ability to respond/implement plans. **Results** Results suggest a number of challenges to successful implementation of NPIs; these include challenges in communications flow, lack of clarity related to lines of authority, and serious practical limitations on the ability to implement NPIs. In some instances, critical stakeholders, including day care providers and those responsible for special populations (e.g., nursing home residents, institutionalized persons, the incarcerated) have had limited participation in the community planning process. **Conclusions** Local communities will face serious challenges in implementing a coordinated and effective response to a possible pandemic flu event. Some challenges can be mitigated by addressing barriers related to communication and authority as part of the planning process. Our findings will be useful in developing strategies for overcoming barriers and unaddressed gaps in pandemic influenza preparedness planning and response.

Evaluation of a West Nile Virus Prevention Education Intervention Among Organ Transplant Recipients, Colorado, 2006

E. C. Zielinski-Gutierrez[1], M. E. Levi[2], A. F. Hinckley[1], Y. Fitzpatrick[3], J. A. Lehman[1];

[1]CDC/Division of Vector-Borne Infectious Diseases, Fort Collins, CO, [2]University of Colorado Health Sciences Center, Division of Infectious Diseases, Denver, CO, [3]University of Colorado at Denver and Health Sciences Center, Fort Collins, CO.

Background: Transplant recipients may have 40 times the risk of serious West Nile virus (WNV) disease as the general population, should they be infected. We evaluated the effectiveness of a WNV prevention intervention for this high risk population. **Methods**: A survey, consent form and return envelope were sent to ~2000 transplant recipients associated with the University of Colorado Health Sciences Center during summer 2006. The survey covered socio-demographic factors, perceived WNV risk and prevention behaviors. Patients were randomized to receive WNV prevention literature specific to transplant recipients or literature plus insect repellent samples. A follow-up was sent to all respondents to the baseline survey in fall 2006. **Results**: 264 of 2000 patients, 13%, responded to both baseline and follow-up surveys. 90% of respondents had heard about WNV prevention. 60% of respondents were "a little" or "not at all" concerned about becoming ill from WNV during the 2006 season. Reported rare/never use of repellent decreased slightly from 42.2% (baseline) to 37% (follow-up) ($p<.04$, McNemar), although there was no difference by whether respondents had received a sample of repellent. Repellent use was positively associated with increased risk perception. ($p=.000$) Always/often use of long pants/sleeves increased from 39.7% to 51.8% ($p=.000$, McNemar) and always/often/sometimes avoiding the outdoors during peak mosquito biting hours increased, 62.7% to 78.6% ($p<.001$, McNemar). **Conclusions**: Respondents' low risk perception may reflect a mild/focal 2006 WNV season in Colorado, but is still of concern given transplant recipients' susceptibility to severe WNV disease. The small but significant increase in repellent use and other preventive behaviors suggests that targeted educational materials may provide some benefit, though this data does not support an added benefit to providing sample products. Despite high reported rates of exposure to information many transplant recipients are not taking preventive measures, indicating a need to pursue more effective behavior change strategies. Low response may limit the generalizability of this study to other transplant recipients. A second follow-up survey in 2007 may give a better sense of preventive action over a longer period.

Findings from An Evaluation of Malaria Prevention Health Messages Tailored to Travelers Visiting Friends and Relatives in Nigeria and India

S. F. Steele, E. Termilus, E. Stein, I. Ahluwalia, D. Roth Allen, C. Reed, N. Marano, B. Person;

Centers for Disease Control and Prevention, Atlanta, GA.

Background: Of the estimated 1400 malaria cases reported in the U.S. annually, a majority are associated with travel to malarious areas in Africa and Asia. Travelers whose primary reason for travel is to visit friends or relatives (VFR) represent a disproportionately high percentage of these cases. Among all malaria cases with a known country of acquisition, the greatest numbers are from Nigeria and India. In addition, a majority of cases occur among persons who do not adhere to a recommended chemoprophylaxis regimen. Previous CDC formative research about malaria risk perceptions among Nigerian and Indian VFR travelers recommended that CDC develop targeted malaria prevention messages for the two groups. To this end, CDC developed two malaria prevention posters which included images of mothers and children in traditional African attire. An evaluation was conducted to elicit the target audience's perspectives about the posters' design and messages, as well as perceptions about malaria risk. **Methods**: The evaluation consisted of two separate focus groups conducted with first- and second-generation immigrants from Nigeria and India and community canvassing using convenience sampling. Additionally, anecdotal opinions about the posters and perceptions about malaria risk were obtained through conversations with community members at health fairs. **Results**: Focus group findings revealed that most subjects had the following incorrect assumptions: (1) malaria is not a serious threat to their health when they travel home; (2) antimalarial drugs purchased in Nigeria or India are equally as effective as U.S. produced drugs in preventing and treating malaria; (3) risk from malaria is limited to certain areas or seasons in their home country. They also felt that the images in the CDC malaria posters lacked credibility. Other perspectives about the posters obtained through both methods included: a discrepancy between the text and image messages, and a preference for a family image. **Conclusions**: CDC should continue outreach to Nigerian and Indian immigrants about malaria prevention, and collaboratively work with representatives from those communities to develop and improve credible and effective prevention messages. Pilot testing of health education materials with the intended audience is essential to this effort.

H3. Blood, Organ and Tissue Safety

Tuesday, March 18
3:00 PM – 4:30 PM
Centennial III

Fatal Group C Streptococcal Infection due to Transfusion of a Contaminated Pooled Platelet Unit despite Routine Bacterial Culture Screening

F. Lessa[1], G. Leparc[2], K. Benson[3], R. Sanderson[4], C. Van Beneden[1], P. Shewmaker[1], B. Jensen[1], M. J. Arduino[1], M. J. Kuehnert[1];

[1]Centers for disease control and prevention, Atlanta, GA, [2]Florida Blood Services, St. Petersburg,, FL, [3]Hospital Lee Moffitt Cancer Center and Research, Tampa, FL, [4]The Florida Department of Health, Tampa, FL.

Background: Despite implementation of screening methods, bacterial contamination of platelets (PLTs) has remained a public health concern due to continued reports of transfusion-related sepsis. In April 2007, an elderly man with chronic myelomonocytic leukemia developed respiratory distress and died less than 48 hours after transfusion of a pool of eight whole blood-derived PLTs. A transfusion reaction was suspected and an investigation was begun to determine the etiology of the patient's death and the source of infection, and to evaluate blood center's screening process for bacterial contamination of PLT components. **Methods**: We cultured the recipient's blood, remnants from the pooled PLT bag, and residual PLTs from the eight 50 mL individual donor PLT bags. Red blood cell (RBC) co-components made from the same eight donations were traced, quarantined, and cultured. We interviewed the implicated donor, and collected blood and swabs from throat, nose, antecubital skin, and perineal areas for culture. Isolates were sent to the Centers for Disease Control and Prevention for identification and molecular typing by pulsed-field gel electrophoresis (PFGE). We reviewed the blood center's screening procedures for bacterial contamination of pooled PLTs. **Results**: Beta-hemolytic group C streptococci (GCS) were cultured from the recipient's blood and the remnants from the pooled PLT bag. GCS were also recovered from one of the eight RBC co-components, linking the GCS to a single donor. A throat

swab collected from the implicated donor 20 days after donation also grew GCS. All GCS isolates were identified as *Streptococcus dysgalactiae* subsp. *equisimilis* and were indistinguishable by PFGE. The donor denied any illness around the time of donation. The PLT bacterial screening at the blood center comprised liquid media culture of PLT samples before pooling, validated to a threshold of 15 colony-forming units per mL. **Conclusions**: GCS is a known throat colonizer and has been recognized as a cause of invasive disease. Current screening methods for PLTs are not capable to detect low levels of bacteria that might be present in asymptomatic donors with bacteremia. Small volumes of individual PLT units place limits on culturing strategies for pooled PLTs. Efforts to improve detection of bacterial contamination of PLTs should continue.

Risk Reduction for Transfusion Transmissible Emerging Infections: Blood Donor Geographic and Behavioral Risk Deferrals and Their Impact on Blood Availability

S. Zou, E. Notari, F. Musavi, J. Trouern-Trend, K. Dorsey, C. T. Fang;

American Red Cross, Rockville, MD.

Background: Blood safety is ensured through selection of appropriate donor populations, screening of presenting donors and testing of donated blood units. Donor screening consists of basic physical examination and an interview to identify donors who may have increased risk of exposure to transfusion transmissible infections (TTIs). For infections where no test is available, donor screening and deferral is regarded as an important safeguard for the blood supply. **Methods**: Data on deferral of blood donors presenting at all American Red Cross (ARC) regions in 1997-2006 were obtained from the centralized databases. Deferrals included were: traveling to variant Creutzfeldt-Jakob disease (vCJD) areas, malaria, and risk of blood exposure through injection drug use (IDU), receipt of blood transfusion, tissue or organ transplant, and potential parenteral blood exposure. Deferrals for vCJD risk were permanent as was that for IDU; the rest resulted in temporary deferral. Return donation data for temporarily deferred donors were from our previous study. (Zou et al., Transfusion 2005; 45:1593-1600) **Results**: A total of 745,553 deferrals, representing 1% of total donor presentations or 9% of total deferrals, occurred in 1997-2006 relating to potential risk of exposure to emerging TTIs. Among them, 604,718 deferrals (81%) were temporary and 140,835 (19%) were permanent. Traveling to malaria endemic areas and potential parenteral blood exposure respectively accounted for 53% and 36% of the temporary deferrals whereas traveling to vCJD countries in 2000-2006 contributed to 82% of the permanent deferrals. By applying the return donation rates of temporarily deferred donors, the permanent and temporary deferrals combined resulted in an estimated loss of 546,098 donors to ARC in 1997-2006. In view of the non-specific nature of such deferrals, most of those lost are expected to be safe donors **Conclusions**: A significant number of blood donors have been lost in order to reduce the already low risk of potential TTIs. While indicative of the regulatory effort to ensure blood safety, the impact on blood availability and the frustration such deferrals may have caused, e.g. among those deferred for traveling to vCJD or malaria areas, warrant continuous monitoring and assessment for the necessity and effectiveness of such deferrals.

Transplantation-Transmitted Tuberculosis in Oklahoma, 2007

E. Piercefield[1], L. Smithee[1], M. J. Kuehnert[2], T. Harrington[3];

[1]Oklahoma State Department of Health, Oklahoma City, OK, [2]CDC, NCPDCID, Division of Healthcare Quality Promotion, Atlanta, GA, [3]CDC, NCHHSTP, Division of Tuberculosis Elimination, Atlanta, GA.

Note: The findings and conclusions in this presentation have not been formally disseminated by the Centers for Disease Control and Prevention and should not be construed to represent any agency determination or policy. **Background:** The incidence of tuberculosis among organ transplant recipients is up to 74-fold higher than that of the general population and is most often caused by activation of latent tuberculosis infection after immunosuppression. In 2007, however, after an Oklahoma organ donor's cerebrospinal fluid grew *Mycobacterium tuberculosis* postmortem, we investigated the possibility of transplantation-transmitted tuberculosis. **Methods:** Medical records of the donor were reviewed for risk factors for tuberculosis; donor contacts were investigated; recipients were evaluated for clinical evidence of tuberculosis; and confirmatory testing for *M. tuberculosis* and tuberculosis genotyping were conducted on donor and recipient specimens. **Results:** The donor had a history of homelessness and alcohol use and was hospitalized for progressive neurologic illness attributed to cerebral vasculitis. Although he recently had pneumonia, he had no known history of tuberculosis, and prior tuberculin skin tests were negative. Three organs (liver and two kidneys) were transplanted to three recipients. Disseminated tuberculosis was diagnosed in both kidney recipients and one died. *M. tuberculosis* isolates from the donor and kidney recipients had matching genotypes. The liver recipient had no evidence of tuberculosis. Approximately 100 close contacts of the donor, predominantly healthcare workers, were assessed for tuberculosis infection, and no new cases were identified. **Conclusions:** Organs transplanted from a donor with disseminated tuberculosis resulted in confirmed disease transmission to two of three organ recipients. Although donor medical and social history might reveal risk factors for tuberculosis, no standard screening exists for evaluating potential organ donors for tuberculosis. Although the risk for transplant-transmitted tuberculosis infection is low, the consequences can be devastating. Organ procurement organizations and transplant teams should consider the possibility of transplantation-transmitted tuberculosis from donors with known risk factors.

Amotosalen and UVA Illumination Inactivate Influenza H5N1 and Chikungunya Virus in Platelet Concentrates and Plasma

L. Sawyer[1], K. Dupuis[2], J. Kinsey[1], D. L. Vanlandingham[3], K. Tsetsarkin[3], S. Higgs[3], A. Sampson-Johannes[1];

[1]Cerus Corporation, Concord, CA, [2]California Public Health Department, Richmond, CA, [3]University of Texas, Medical Branch, Galveston, TX.

Background: The INTERCEPT Blood System for platelets and plasma was developed to prevent transfusion-transmitted infections by inactivating pathogens in donor blood. This proactive approach utilizes amotosalen HCl and UVA illumination and has been demonstrated to inactivate blood-borne pathogens in platelet and plasma components, including a broad spectrum of both cell-free and cell-associated, enveloped and non-enveloped viruses, gram negative and gram positive bacteria, and protozoan parasites. High levels of inactivation have been shown for those organisms for which blood is routinely tested (e.g. HIV, HBV, HCV, HTLV, and Treponema pallidum) as well as organisms that have recently emerged as transfusion concerns (e.g. WNV, SARS-CoV, Borrelia, Plasmodium, Trypanosoma, Babesia and Leishmania). Recent studies evaluated the efficacy of this treatment for inactivation of two additional viruses of emerging concern in blood: chikungunya virus (ChikV) and influenza virus A H5N1. **Methods:** The platelet ChikV study was performed using strain LR2006 OPY1, isolated in La Reunion in 2006, and the plasma study used ChikV strain 27, isolated in Tanganyika in 1953. Influenza studies were performed with the VNH5N1-PR8/CDC-RG strain. Platelet units consisted of 2.5 - 6.0e11 platelets suspended in ~300 mL of 35% plasma/65% PASIII, and plasma units were ~600 mL. The inoculated platelets

and plasma were treated with 150 uM amotosalen and 3.0 J/cm sq UVA. ChikV titers were determined in vero cells and influenza titers in modified MDCK cells. **Results:**Complete inactivation of influenza H5N1 was achieved in all experiments (>3.3 ±0.5 logs in platelets and >3.4 ±0 logs in plasma), and complete inactivation of ChikV was observed in platelets (>6.4 ±0.6 logs). The very high ChikV titer achieved in plasma resulted in one or two residual plaques in 2 of 4 replicate experiments (greater than or equal to 7.2 ±0.9 logs inactivated). The dynamic range for influenza is small due to the growth characteristics of the virus, which preclude truly high titer input or evaluation of a large sample post UVA. Influenza studies are in progress and data is preliminary. **Conclusions:** Both chikungunya virus and influenza H5N1 were effectively inactivated in platelets and plasma by treatment with the INTERCEPT Blood System.

Chagas Disease in Mississippi: Investigation of Suspected Autochthonous Infections in the United States

P.T. Cantey[1], S. Hand[2], M. Currier[2], P. Jett[3], S. Montgomery[1];

[1]DPD/NCZVED/CDC, Atlanta, GA, [2]Mississippi State Department of Health, Jackson, MS, [3]Mississippi Blood Services, Jackson, MS.

Background: Infection with *Trypanosoma cruzi*, the parasite that causes Chagas disease, is rarely considered in the United States in non-immigrant populations because autochthonous transmission is presumed rare. Since 1955, six cases of autochthonous transmission have been reported in four states. Triatomine vectors and infected reservoir mammal hosts maintain the parasite in a sylvatic cycle throughout the southern United States. However, little is known about the risk of vector-borne and host reservoir-associated transmission of infection in this country. Recently initiated screening of the United States blood supply is identifying infected donors, without typical risk factors, who may have acquired the infection locally. **Methods:** Two cases of suspected autochthonous *T. cruzi* infection identified by blood donor serological screening were investigated in Mississippi. The donors were retested at blood bank laboratories and at CDC, which uses different tests. Family members, pets, and a triatomine insect found near the home were tested for *T. cruzi* infection at CDC. **Results:** Repeat tests of both donors were positive at blood bank laboratories. At CDC, donor A had borderline positive results; donor B had a negative and an equivocal result. Neither donor had traveled to endemic areas in Latin America, had received contaminated blood products or human tissue, or had risk factors for congenital disease acquisition. Both donors had potential exposures to animal reservoirs and sylvatic vectors. All family members tested negative for *T. cruzi* infection, as did donor A's hunting dogs. *Trypanosoma cruzi* was identified in the vector found on property adjacent to donor A's home. **Conclusions:** The differences in the results of blood bank and CDC testing highlight the complexities of the serological diagnosis of chronic *T. cruzi* infection in the absence of a 'gold standard' diagnostic test and in people who have not have exposure to the traditional risk factors found in Latin America. There is an urgent need for the investigation of potential autochthonous cases in order to further delineate risk factors for exposure to the sylvatic vector and refine testing methodology.

Preliminary Description of the Organ Transplant Infection Project (OTIP), a Multi-Year Cohort Study of Stem Cell and Lung Transplant Recipients

D. L. Wagner[1], S. Husain[2], D. L. Paterson[2], C. A. Kauffman[3], E. R. Dubberke[4], M. G. Schuster[5], P. G. Pappas[6], R. K. Avery[7], K. A. Wannemuehler[1], B. J. Park[1], T. M. Chiller[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]University of Pittsburgh Medical Center, Pittsburgh, PA, [3]University of Michigan and VA Medical Center, Ann Arbor, MI, [4]Washington University School of Medicine, St. Louis, MO, [5]Hospital of the University of Pennsylvania, Philadelphia, PA, [6]University of Alabama at Birmingham, Birmingham, AL, [7]Cleveland Clinic Foundation, Cleveland, OH.

Background: Infection remains one of the most important causes of morbidity and mortality in transplant recipients, although few estimates exist. In order to better define the epidemiology of infections in this group, we analyzed data from the Organ Transplant Infection Program (OTIP). **Methods**: OTIP is a prospective cohort study that began in 2006 in which stem cell (SCT) and lung transplant patients are followed for 18 months post-transplantation. Specimens and clinical data are collected at weekly clinical assessments, which are performed during the first 12 weeks and monthly thereafter. Clinical data include demographics, underlying disease, medications, diagnostic tests, and infections (bacterial, viral and fungal); specimens include blood, serum, and BAL. **Results**: As of November 1, 2007, 170 SCT and 159 lung transplant recipients have been enrolled. Median age is 54 years, 93% are Caucasian and 53% are male. Median follow-up time is 147 days for surviving patients and 108 days among those who died. Among all transplanted patients, 126 (74%) SCTs and 97 (61%) lung transplants have had at least one infection. Among SCT recipients, blood stream infections (BSI) were the most common, (45% of patients), followed by gastroenteritis (28%), and febrile neutropenia (28%). Among lung transplant recipients, pneumonia was the most common infection (35%), followed by lower respiratory tract infection (26%) and BSI (18%). To date, 45 different pathogens have caused infection. The most common bacterial pathogens were *Pseudomonas aeruginosa* (12% of pathogens), *Clostridium difficile* (11%), coagulase negative *Staphylococcus* (7%), and vancomycin-resistant *Enterococcus* (7%). Cytomegalovirus was the most frequently reported viral pathogen (7%), and *Candida* species (2%) and *Aspergillus fumigatus* (1%) were the predominant fungal pathogens. Among the 52 deaths in the cohort, 83% had at least one infection post transplant; the most common infection among the deaths was BSI (52%). **Conclusions**: In this preliminary analysis of infections, BSI and respiratory infection are common among high-risk organ transplants, and associated pathogens are diverse. Future analyses will include syndrome- or pathogen-specific incidences and factors associated with infection.

H4. Tropical Diseases

Tuesday, March 18
3:00 PM – 4:30 PM
Centennial IV

Paederus Dermatitis : an Outbreak in Thai Soldiers

P. Suwannahitatorn[1], A. Jatapai[2], R. Rangsin[1];

[1]Phramongkutklao College of Medicine, Bangkok, THAILAND, [2]Thammasart University, Bangkok, THAILAND.

Background: Paederus dermatitis is an irritant contact dermatitis occurred when beetles of the genus *Paederus* are crushed on the skin provokes the release of its coelomic fluid which contains a potent vesicant agent called pederin. These beetles are found in tropical and subtropical areas. **Methods:** A total of 249 Thai soldiers in supreme command signal battalion were interviewed and examined during April - May, 2007. **Results:** The peak time of presentation was in the end of May, about 1 week after continuous raining. Attack rate was 44.6% (111 cases).The most common clinical manifestations were blisters (30.8%) and burn - like erythematous rash (30.7%) to the skin. The most affected areas were arms (32 %), head and neck (31.2%). Pustules were seen in 19.0 % of cases while 15.8 % had classical "kissing lesion". Multiple lesions occurred in

47.7 % of cases. **Conclusions:** Paederus dermatitis is one of the causes of blistering dermatitis. The disease should be recognized as a differential diagnosis especially in tropical area. Awareness of the condition and its clinical features will prevent misdiagnosis.

A Coordinated Epidemiologic and Water Assessment to Investigate a Cholera Outbreak in a Temporary Shelter for Displaced Persons in Thailand

V.T. Nyunt[1], A. Henderson[2], J. Gindler[2], D. Lantagne[3], J. Mosser[1], P. Hemhongsa[4], H. Baggett[2], J. Painter[5], G. Armstrong[5], S. Thamthitiwat[2], S. Karuchit[2], P. Udomdejsup[2], S. Henchaichon[2], S. Sutthirattana[2], K. Sukamon[2], K. Noonsate[2], S. Maloney[2], M. Lynch[3];

[1]Aide Médicale Internationale, Mae Sot, Tak Province, THAILAND, [2]Thailand MOPH-US CDC Collaboration Office, Bangkok, THAILAND, [3]Enteric Diseases Epidemiology Branch, Centers for Disease Control and Prevention, Atlanta, GA, [4]Tak Provincial Health Office, Mae Sot, Tak Province, THAILAND, [5]Division of Global Migration and Quarantine, Centers for Disease Control and Prevention, Atlanta, GA.

Background: On June 26, 2007, a clinic in a temporary shelter (housing approximately 50,000 displaced persons from Burma) admitted a patient with acute, severe, watery diarrhea; laboratory culture confirmed *V. cholera* O1 Inaba. The medical non-governmental organization (NGO) in the shelter opened a cholera treatment center (CTC) and in collaboration with the Thai Ministry of Public Health (MOPH), the Tak Provincial Health Office, the Centers for Disease Control and Prevention (CDC), and the Thai MOPH-CDC Collaboration office investigated the outbreak. **Methods:** Community health workers investigated all suspected cholera cases (*i.e.*, ≥3 watery stools/24 hours with dehydration in a person >age 2) admitted to the CTC. Rectal swabs were obtained from each patient upon admission. All NGO piped taps and well water points were GPS-mapped, and evaluated for turbidity and residual chlorine levels; an assessment of household water quality and storage, and hygiene practices was conducted in a convenience sample of 31 households. A sex-, age-, and neighborhood-matched case-control study was conducted to investigate cholera risk factors. **Results:** Among 287 cases admitted to the CTC from June 26-November 9, 2007, 106 (37%) were laboratory confirmed. Chlorine residual was adequate in the NGO piped water system taps, but not in NGO wells. Among 56 cases and 112 controls, cholera was not associated with drinking tap water (OR=1.6, 95% CI =0.6, 4.9). Drinking well water (OR=3.8, 95% CI=1.1, 13.1), using well water for washing (OR=3.1, 95% CI=1.3, 8.4), and eating street-vended food (OR=3.2, 95% CI=1.1, 6.3) were associated with cholera. Drinking boiled water (OR=0.2, 95% CI=0.04, 0.9) and handwashing with soap before eating (OR=0.4, 95% CI=0.2, 0.9) were protective. **Conclusions:** The piped distribution system in the camp had adequate chlorine residual; however, using open shallow wells, eating street-vended food, and inadequate hygiene were associated with increased risk of cholera; Recommendations were made to improve access to piped water, provide education on handwashing and appropriate well water use, and develop hygiene education for food vendors.

First Reported Outbreak of Eosinophilic Meningitis Caused by *Angiostrongylus cantonensis* in Brazil

M. H. Garcia[1], C. Moraes[2], G. L. Almada[2], O. S. Carvalho[3], R. L. Caldeira[3], C. L. Mendonça[3], D. M. Zanon[2], F. A. Antunes[4], A. C. Santelli[1], S. Castro[2], M. T. Obara[5], A. K. Reis[5], W. N. de Araujo[1];

[1]Brazilian Field Epidemiology Training Program (EPISUS), Secretaria of Health Surveillance, Ministry of Health, Brasilia, BRAZIL, [2]State Secretariat of Health of Espírito Santo, Brasilia, BRAZIL, [3]Centro de Pesquisas René Rachou – FIOCRUZ/MG, Belo Horizonte, BRAZIL, [4]Universidade Federal do Espírito Santo, Brasilia, BRAZIL, [5]CGLAB, Secretariat of Health Surveillance, Ministry of Health, Brasilia, BRAZIL.

Background: Eosinophilic meningitis is usually caused by helminthic parasites, mostly *Angiostrongylus cantonensis*. The parasite develops in rats, intermediate hosts are snails/slugs, and humans accidentally acquire infection by consumption of or contact with contaminated mollusks. Cases present peripherial eosinophilia and eosinophilic pleocytosis. Detection of larvae in CSF is diagnostically definitive but rarely done. Following reports of two possible cases, we conducted an epidemiologic and environmental investigation. **Methods:** Suspect cases were those presenting meningitis with eosinophilic pleocytosis (≥10%) in CSF occurring between January 1st, 2006 and February 15th, 2007 in Espírito Santo State. Probable case was a suspect case with reactive serology for *Angiostrongylus sp* by ELISA. Confirmed case was a suspect case who ate snails/slugs, or had isolation of larvae in the CSF. Suspect cases were interviewed and medical records reviewed. Active surveillance in the state Children's Hospital and review of National Meningitis Surveillance System data were conducted. We collected snails/slugs and rat feces from suspect cases' households to identify parasite larvae using PCR-RFLP. Larvae were inoculated in rats. **Results:** Two suspect male cases aged 22 and 39 years were confirmed: each ate half of one raw snail (*Sarasinula marginata*) on December 31th, 2006, with onset of illness four days later. Signs and symptoms included: abdominal pain, severe headache, cervical pain, myalgia, arthralgia, neck rigidity, disorientation, dysarthria, and limb paralysis. CSF eosinophil counts were 20-45%. Active case-finding detected one probable case aged 1.5 years with onset of strabismus on January 2nd, 2007 and CSF eosinophilic pleocytosis (16%); no direct exposure was identified; snails and rat feces were detected around the household. All three cases had reactive IgG to *Angiostrongylus sp*. Larvae extracted from rat feces and 420 snails/slugs were consistent with *A. cantonensis* by PCR-RFLP. Experimentally infected rats had immature worms in meninges and brain. **Conclusions:** This first reported outbreak of eosinophilic meningitis caused by *Angiostrongylus cantonensis* in Brazil consisted of two confirmed and one probable case. The absence of other cases suggests that illness is rare in this region.

Clinical and Epidemiologic Characteristics of Patients with Orally-transmitted Acute Chagas Disease, Brazil - 2005-2006

E. Tatto, S. O. Santos, S. M. Oliveira, M. T. Obara, J. C. Silva, M. Flores;

Secretariat of Health Surveillance (SVS), Ministry of Health, Brasilia, BRAZIL.

Background: Acute Chagas Disease (ACD), caused by *Trypanosoma cruzi* infection, is responsible for at least 3 million chronic cases in Brazil (2006). Oral transmission of ACD from contaminated drink/food is an ongoing cause of outbreaks of ACD in Brazil. **Methods**: We report clinical, laboratory and entomological characteristics observed in five outbreaks of orally-transmitted ACD in 2005-2006. A confirmed case was defined as illness in a person with compatible clinical and epidemiologic findings and a positive direct parasitological blood exam, specific IgM or IgG anti-*T. cruzi* serology, or positive PCR. **Results**: A total of 65 confirmed ACD cases occurred in five outbreaks with a median of 15 cases (range 6 to 24) and 6 deaths (9%). Other forms of transmission but oral were discarded by epidemiological investigation. Diagnosis was confirmed by parasitological exam in 27 (41%) cases, IgM or IgG serology (n=25 and n=8 respectively), PCR (n=1), and epidemiologic criteria (n=4). Incubation period was 3-21 days; timeliness of diagnosis was 27-48 days (mean=34). Clinical manifestations included fever (80%), myalgia (78%), facial/lower limb edema (70%), elevated

transaminases (41%), rash (37%); epigastric pain (55%), vomit (52%), diarrhea and hepatomegaly (25%), hyperbilirubinemia (18%), GI bleeding (26%); pericardial effusion (29%), cardiomegaly (26%), pleural effusion (23%). The infection was associated with ingestion of sugar cane juice in 2 outbreaks, and bacaba, a type of palm tree fruit, in one. Entomological investigation, conducted in the probable area of contamination of foods, identified *Triatoma tibiamaculata, T. sordida, Panstrongylus lutzi, Rhodnius robustos, R. pictipes* and *P. lignarius* vectors, with *T. cruzi* infection rate ≥30%. Analysis of triatomine stools revealed that the sources of their blood meals were marsupials, rodents and avians. **Conclusions**: Oral transmission of *T. cruzi* is responsible for ongoing outbreaks of ACD. The lack of timely diagnosis may underlie the high mortality rate. Gastrointestinal manifestations are common, with atypical characteristics. Only 41% of cases were confirmed by parasitologic blood exam in these outbreaks. Safe food handling education has been implemented to help prevent contamination by *T. cruzi* during preparation.

Yellow Fever resurgence in Africa - Public Health measures to assess the risk of YF outbreaks

T. Nguyen[1], S. Briand[1], S. Yactayo[1], A. Beresniak[2], F. Avokey[3], A. Berthe[3], Y. Allarangar[4], W. Perea[1];

[1]World Health Organization - Epidemic and Pandemic Alert and Response department, Geneva, SWITZERLAND, [2]DataMining, Geneva, SWITZERLAND, [3]World Health Organization - Regional Office for Africa, Ouagadougou, BURKINA FASO, [4]World Health Organization - Regional Office for Africa, Brazzaville, CONGO, DEMOCRATIC REPUBLIC OF THE.

Background: Yellow fever (YF) is an acute viral haemorrhagic fever transmitted to humans by infected Aedes mosquitoes. Symptoms can vary in intensity, from a mild fever to a jaundice that is associated with widespread hemorrhage leading to death in 20-50% of cases. At present there is no specific treatment for the disease. The disease can be prevented through a single injection. YF nearly disappeared for 40 years after the mass vaccination campaigns carried out during the 19640-60's. Since the late 80's the deadly disease returned affecting most of West and Central Africa. Currently, the risk of devastating urban epidemics is the most feared. In 2006, WHO launched the YF Initiative which is supported by GAVI. It aims to reduce the risk of YF outbreaks in 12 endemic countries in Africa and will result in the vaccination of 48 million people until 2010. A risk assessment exercise (RA) is spearheading this initiative to identify the districts at highest risk of YF outbreaks in order to carry out preventive vaccination campaigns. **Methods**: A tool was developed for countries to conduct data collection on 6 risk factors. 5 risk factors associate to 'Exposure' to virus/vector and 1 to 'Susceptibility'. A Multiple Correspondence Analysis (MCA) aggregates data of the 5 variables of exposure into 1 synthetic indicator of exposure (SIE). Health districts are then projected on a 2-dimension plane with 'SIE' on horizontal and 'Susceptibility' on vertical axis to define vulnerable population. Districts are presented on risk maps for discussion and decision making. **Results**: The RA for 4 countries was performed from Dec 2006 to Aug 2007. Out of a total of 208 districts, 110 were identified as high risk districts. Final decision on priority districts was taken by the Ministries of Health (MoH) after discussion with public health agencies. Altogether, the four MoHs agreed to immunize 23 million people as part of catch up campaigns planed between Sep 2007 to July 2008. **Conclusion**: The RA has proven to be a useful evidence base tool for decision making. It facilitated the prioritization of at-risk districts for preventive immunization and the effective use of limited vaccine supply and resources. This approach has favored ownership of the tool by the MoH and allowed consensual public health decisions among key stakeholders.

Integration of Neglected Disease Programs in Togo: Evaluation of a Pilot Project

J. R. Verani[1], E. Mathieu[1], G. Anthony[2], P. Assih[3], E. Mathieu[4];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Direction Generale de la Sante, Lome, TOGO, [3]Directon Generale de la Sante, Lome, TOGO, [4]Mectizan Donation Program, Decatur, GA.

Background: The integration of neglected disease programs is considered essential for achieving an effective and sustainable public health impact. In Togo, a project integrating malaria, lymphatic filariasis, onchocerciasis, guinea worm, schistosomiasis, geohelminths, and trachoma programs was piloted in Binah district in May 2007. The project included nurse and village volunteer (VV) training, health education and mass drug administration (MDA) with albendazole (ALB)/ ivermectin (IVM), followed by praziquantel (PZQ) a week later. PZQ distribution (≥5 yr olds, 5-15 yr olds or no PZQ) depended on schistosomiasis prevalence. Annual ALB/IVM MDA for lymphatic filariasis and onchocerciasis began in 2000. **Methods:** We evaluated the integration project one week after integrated MDA, including a cluster sample MDA coverage survey, knowledge-attitude-practice (KAP) survey of randomly selected household members ≥14 yrs, VV survey (2 randomly selected per community), and semi-structured interviews with nurses. **Results:** The coverage survey (n=2184) showed that 82% of the total population took ALB/IVM; reported ALB/IVM coverage was 86% in 2004 and 85% in 2005. For PZQ, target population coverage was 95%; in areas where PZQ treatment targeted 5-15 yr olds, 43% of older persons were treated with PZQ. While 82% of the KAP survey respondents (n=298) heard of the MDA prior to distribution, most were unaware of the diseases treated. The VV survey (n=56) found high satisfaction with the health education materials and the dosing pole.While 75% felt the work load was greater in 2007 than in 2006, the mean time spent distributing was similar (7.9 and 6.8 days respectively). In interviews, nurses (n=8) recommended more local involvement in project planning, additional VV training, more health education prior to MDA, and greater compensation for VV and nurses. Nurses received many complaints of PZQ side effects. **Conclusions:** The pilot integration project was well accepted at all levels, ALB/IVM coverage was similar to pre-integration, and coverage was high for both distribution rounds (ALB/IVM and PZQ). Confusion regarding PZQ distribution was likely due to variable target groups. We recommend a more uniform PZQ distribution and that for multiple distribution rounds, the drug with fewest side effects be administered first.

H5. Late Breakers

Tuesday, March 18
3:00 PM – 4:30 PM
Regency VII

Vaccines & Vaccine-Preventable Diseases

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 219. Outbreak of Measles in Norway among Nomadic Travellers from England

Ø. Løvoll;

Norwegian Institute of Public Health, Oslo, NORWAY.

Background: WHO plan to eliminate measles from Europe by 2010. Norway has experienced only a few cases since the last indigenous case in 1999, all linked to importation. Children receive MMR vaccine at 15 months and 12 years of age; the coverage being 91 %. Measles is notifiable and is also subject to immediate 24/7 telephone warning to local health authority and the Norwegian Institute of Public Health (NIPH). We describe here an outbreak of measles among nomadic Irish Travellers from England staying at camping sites in Norway. **Methods:** A probable case was a Traveller in Norway with clinical measles and onset since April 2007. Confirmed cases had measles IgM or RNA in serum, saliva, urine or throat swabs. Cases were notified through the surveillance system from April to June. Municipal medical officers actively inquired about cases and possible epidemiological links. **Results:** As of July 2007 19 cases had been reported, with onsets from April 27 to June 24; sixteen confirmed and three probable cases. All but one patient belonged to families of Irish Travellers from England. The index case fell ill on the day of arrival in Norway from England. Seventeen of the cases were children aged between 2 months and 9 years (three less than one year, seven between 1 and 3 years, six between 4 and 5 years, and one aged 9 years). Sixteen cases were either reported as unvaccinated or assessed as most likely unvaccinated. Three cases were vaccinated during the early course of the outbreak, but developed measles. The virus strains from 13 patients have been sequenced and all shown to be a D4 strain closely matching the measles strain causing a simultaneous outbreak among Travellers in the UK. The very last case was a Norwegian child 14 months of age who neither had any link to other cases nor any link from abroad. This case was laboratory confirmed, but sequencing was unfortunately not possible. **Conclusions:** The outbreak in Norway confirms that nomadic peoples of Europe constitute a particular challenge in the measles elimination efforts because they seem to have low vaccination coverage and travel widely. These groups need to be targeted with MMR vaccine actively if the elimination efforts are to succeed. The high prevalence of immunity and limited contact with the Travellers seem to have protected the Norwegian population.

Board 220. Comparative Study of pertussis Dynamics in the pre- and post-vaccination Era in 30 Countries

H. Broutin[1], C. Viboud[1], B. T. Grenfell[2], M. M. Miller[1];

[1]Division of International Epidemiology and Population Studies, Fogarty International Center, National Institutes of Health, Bethesda, MD, [2]Center for Infectious Diseases Dynamics, Pennsylvania University, University Park, PA.

Background: Despite many years of vaccination, *Bordetella pertussis* infection causes recurrent epidemics worldwide of periodicity ranging from 2-5 years without well defined seasonality. Determinants of pertussis periodicity are poorly understood. We explored pertussis disease dynamics and seasonal patterns in relation with birth rate and vaccine coverage, using long-term time series from 30 countries over 5 continents. Understanding periodicity of epidemics would allow the derivation of novel vaccination strategies and optimization of the timing of booster doses. **Methods:** Reported pertussis incidence, vaccine coverage and demographic data were collected from national health ministries and UN databases. Annual pertussis data were obtained for 30 countries covering the pre- and post-vaccination periods (8 countries) or solely the post-vaccination era (22 countries). Nine countries also provided monthly data. We described trends in seasonal patterns as vaccine use increased, in countries with monthly data. We also quantified the relationship between birth rate, vaccination coverage and the mean inter-epidemic period, based on annual data. **Results:** Seasonal patterns were identified in all 9 countries in the pre- or post-vaccination period, or both. Globally, seasonality was more pronounced in high vaccine coverage countries, with peak activity occurring in summer months. Periodicity estimates ranged from 1.5 to 4 years, inverse to the rate of susceptible recruitment (birth rate*(1-vaccine coverage)) ($p<0.005$). Africa in recent years had pertussis periodicity similar to Europe and North America in the pre-vaccination period (range, 1.5-2.8 years). Mean incidence increased with the rate of susceptible recruitment ($p=0.003$). **Conclusions:** We found high heterogeneity in country-specific pertussis epidemic patterns, likely due to the diversity of vaccine strategies used and the particularly high susceptibility to noise of this disease. However, as theoretically predicted, pertussis dynamics were related to birth rate and vaccine coverage at a global scale. To help refine vaccination strategies, further studies could explore how the use of novel acellular vaccines and periodic boosters would affect pertussis periodicity.

Board 221. Nationwide Outbreak of Rubella Caused by a Single Viral Genotype during Rubella and Congenital Rubella Syndrome Elimination Phase – Brazil, 2007

F. R. Marques[1], C. V. Segatto[2], T. M. Lanzieri[1];

[1]Field Epidemiology Training Program, Secretariat of Health Surveillance, MoH, Brasilia, BRAZIL, [2]Secretariat of Health Surveillance, MoH, Brasilia, BRAZIL.

Introduction: Rubella is a mild viral disease that may cause the congenital rubella syndrome (CRS) of birth defects when infection occurs early in pregnancy. In Brazil, rubella and CRS became notifiable diseases in 1996. Childhood vaccination began in 1992 and national vaccination campaigns targeted at women aged 12-49 years and children <5 years were conducted in 2001-2002. In 2003, a goal of rubella and CRS elimination by 2010 was established. We describe a nationwide rubella outbreak in 2007. **Methods:** Descriptive study using data from the National Notifiable Disease Information System. A confirmed rubella case was defined as a suspected case (fever, rash and lymphadenopathy) with specific IgM antibodies or epidemiological link to a laboratory-confirmed case. **Results:** During January-September 2007, 4,178 rubella cases were confirmed in 17 of 27 states in Brazil, including 272 of 5,560 municipalities; genotype 2B was identified in six states and 3,969 (95%) cases were laboratory confirmed. Males accounted for 2,849 (68%) cases (incidence, 245/100,000) and had a 2.3 increased risk of infection compared to females (95%CI=2.2-2.5; $p<0.01$). Persons aged 20-29 years accounted for 2,273 (55%) cases, of which 1.796 (79%) were males. Investigation was initiated within 48hr of notification in 80% of cases, and 41% of cases had vaccination of contacts initiated within 72hr of rash onset. A total of 6,544,911 rubella vaccine doses was administered to persons aged >12 years; 1,700,777 doses during vaccination of contacts and the remaining in the course of outbreak control activities at crowded places such as large companies. **Conclusions:** Previous rubella vaccination campaigns may have reduced susceptibility among children and adolescents; however young adult males were not targeted and

remained an important susceptible group. Therefore, in addition to outbreak control measures, the Ministry of Health is planning a mass campaign of young adults for the year 2008 to assure rubella and CRS elimination by 2010.

Board 222. An Explosive Outbreak of Modified Measles Posing as a Rash Illness of Unknown Etiology in a High School, TaiYuan, Shanxi Province, China, 2007

P. Zhang[1], I. Ii[2], L. Zhou[2], R. Fontaine[3], L. Zhang[2], H. Ma[2], B. Zhao[4];

[1]Chinese Field Epidemiology Training Program, Beijing, CHINA, [2]Centers for Disease Prevention and Control of China, Beijing, CHINA, [3]Centers for Disease Control and Prevention, Atlanta, USA, Atlanta, GA, [4]Centers for Disease Control and Prevention of Taiyuan city,Shanxi prvience,China, taiyuan, CHINA.

Background: Extensive use of measles vaccine has led to the appearance of modified measles (MM) and can create confusion in initial diagnosis. In May 2007, an explosive outbreak of rash illness affected a high school. The initial investigation focused on emerging infections with high epidemic potential and included extensive laboratory testing for potential emerging infections. We continued this investigation to identify the causative agent and determine the method of exposure. **Methods:** We identified al students or teachers with fever >37.5C or rash with onset during May and June 2007. We collected serum for anti-measles IgG and IgM determinations and tracked the change in antibody titers on serial serum specimens. We defined typical measles (TM) fever >37.5 C and rash beginning from face and chest and extending to the extremities. We defined modified measles as fever >37.5 with sparse rash beginning on extremities or anti-measles IgM on acute serum of a 4-fold rise in anti-measles IgG. We interviewed case-patients about exposures using a standard questionnaire. **Results:** We found 17 TM and 60 MM among 3543 students. 13 TM and 43 MM had anti-measles IgM or a four-fold rise in anti-measles IgG on appropriately timed specimens and the remaining TM and MM had a high anti-measles IgG on a convalescent specimen. By 10 days after onset anti-measles IgG reached ≥1:12800 in 87% of MM and 53% of TM. All cases had onset within a 26 day period. The first case was in a student in the 12th grade who presented with TM. He attended class while he was sick and vomited three times in the classroom. All other MM and TM followed his onset of illness by 10 to 21 days. The attack rate in his classroom was 48%, compared to 2.5% in the rest of the 12th grade and 0.2% in the other grades. No written records of measles vaccination were available and 51% could not remember if they had or did not have MV **Conclusions:** This explosive outbreak a rash illness of unknown etiology was from MM that resulted from exposure to a single case of TM. Investigations of rash illnesses of unknown etiology need to consider MM and other variants of common diseases before launching extensive searches for emerging agents.

Antimicrobial Resistance

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 223. Impact of the New Clinical and Laboratory Standards Institute Nonmeningitis Penicillin Breakpoints on the Incidence of Penicillin Resistance among Invasive Pneumococcal Disease Isolates

M. Deutscher[1], J. Jorgensen[2], B. Beall[1], A. Glennen[3], M. R. Moore[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]University of Texas Health Science Center, San Antonio, TX, [3]Minnesota Public Health Laboratory, St. Paul, MN.

Background: In January 2008, the Clinical and Laboratory Standards Institute (CLSI) will publish new breakpoints for defining susceptibility of *Streptococcus pneumoniae* to penicillin (PEN). The old susceptible (S), intermediate (I), and resistant (R) breakpoints were, respectively, ≤0.06, 0.12-1, and ≥2 µg/ml. The new breakpoints for nonmeningitis isolates are ≤2, 4, and ≥8 µg/ml for intravenous PEN. All meningitis isolates will be considered S (≤0.06 µg/ml) or R (≥0.12 µg/ml). We determined the impact of these new breakpoints on the proportions of pneumococci identified as S, I, and R. **Methods**: Cases of invasive pneumococcal disease (IPD) were defined by isolation of pneumococcus from a normally sterile site in a resident of any of 10 Active Bacterial Core surveillance (ABCs) areas during 2005-2006. Isolates were tested for susceptibility by the CLSI broth microdilution method. **Results**: Of the 7834 cases of IPD identified during 2005-2006, isolates were available for 6800 (87%) of which 6383 (94%) were from nonmeningitis cases. Using the old PEN breakpoints, 4818 (75%), 920 (15%), and 645 (10%) of nonmeningitis isolates were S, I, and R, respectively. Using the new nonmeningitis PEN breakpoints, 5991 (94%), 326 (5%), and 66 (1%) of nonmeningitis isolates were S, I, and R, respectively. Among nonmeningitis isolates, 285 (4.5%) and 68 (1.1%) were cefotaxime intermediate and resistant, respectively, while 426 (6.7%) and 181 (2.8%) were ceftriaxone intermediate and resistant, respectively. By classifying all meningitis isolates as either PEN S or PEN R, 308 (74%) and 109 (26%) were S and R, respectively. **Conclusions**: The new breakpoints markedly reduce the number of reported PEN-resistant isolates. The change in PEN breakpoints could encourage use of PEN for treatment of susceptible nonmeningitis cases of IPD. Microbiologists and clinicians should be aware of the new breakpoints when reporting and using susceptibility results for clinical management.

Board 224. Antimicrobial Resistance in *Salmonella* Serotype I 4,[5],12:i:-, NARMS 1996-2005

S. A. Greene[1], F. Medalla[2], K. Joyce[1], A. Stuart[1], J. M. Whichard[2], E. J. Barzilay[2];

[1]Atlanta Research and Education Foundation, Decatur, GA, [2]Centers for Disease Control and Prevention, Atlanta, GA.

Background: Non-Typhi *Salmonella* (NTS) is estimated to cause 1.4 million infections in the U.S. yearly. Most are self-limited but antibiotic treatment is essential for invasive infections. The National *Salmonella* Surveillance System reported *Salmonella* I 4,[5],12:i:- as the 6th most common serotype in 2005. *Salmonella* I 4,[5],12:i:- is similar to *Salmonella* Typhimurium; it lacks a phase 2 flagellar antigen and may be misclassified as Typhimurium. This serotype has been linked to outbreaks, including a 1998 New York City and a 2007 multistate outbreak resulting in 31 and 65 hospitalizations, respectively. Antimicrobial resistant I 4,[5],12:i:- is of concern in Europe where resistance to at least ampicillin, chloramphenicol, streptomycin, sulfonamide, and tetracycline (ACSSuT) has been reported. **Methods:** From 1996-2005 sites submitted NTS isolates to the National Antimicrobial Resistance Monitoring System (NARMS) at CDC for susceptibility testing. Participation increased from 14 sites in 1996 to nationwide in 2003. Typhimurium lacking the second phase flagellar antigen was reported as serotype I 4,[5],12:i:-. Minimum inhibitory concentrations (MIC) were determined by broth microdilution and interpreted using CLSI criteria when available. **Results:** NARMS tested 16,107 NTS isolates: 181 (1%) were serotype I 4,[5],12:i:-, 3,463 (21%) were

Typhimurium. The proportion of I 4,[5],12:i:- among total NTS increased from 3/1,324 (<1%) in 1996 to 31/2,067 (2%) in 2005. The proportion of I 4,[5],12:i:- among Typhimurium and I 4,[5],12:i:- increased from 3/309 (1%) in 1996 to 31/416 (7%) in 2005. Of 181 I 4,[5],12:i:- isolates, resistance to ≥ 1 antimicrobial agent was found in 31 (17%); resistance to sulfonamides in 14 (8%), ampicillin in 13 (7%), streptomycin in 13 (7%), tetracycline in 10 (6%). Six (3%) were ceftiofur-resistant and also showed decreased susceptibility to cetriaxone (MIC ≥ 2 µg/mL); 1 was ceftriaxone-resistant. While 2 (1%) isolates were resistant to nalidixic acid, all were susceptible to ciprofloxacin. ACSSuT was shown in 4 (2%) isolates. **Conclusions:** *Salmonella* I 4,[5],12:i:- reporting in NARMS has increased since 1996. ACSSuT is rare among NARMS submissions. Differentiating I 4,[5],12:i:- from Typhimurium is important; accurate reporting is critical to monitor antimicrobial resistance.

Board 225. Longitudinal Study of Antimicrobial Resistance among *Escherichia coli* Isolated from Integrated Multi-site Cohorts of Humans and Swine

W. Alali[1], H. M. Scott[1], R. Harvey[2], B. Norby[1], B. Lawhorn[1], S. Pillai[1];

[1]Texas A&M University, College Station, TX, [2]USDA-ARS-SPARC, College Station, TX.

Background: Many studies have attempted to link antimicrobial use in food animal agriculture with an increased risk of antimicrobial-resistant (AR) bacterial levels in humans. **Methods:** We examined the relationship between the prevalence of AR *E. coli* isolated from human wastewater and swine fecal samples and the risk factors: (host species, production type (swine), vocation (human swine workers, non-workers, and slaughter-plant workers), and season) in a multi-site housing, vertically integrated swine and human population agri-food system. Human and swine *E. coli* (N = 4048 and 3485, respectively) isolated from wastewater and fecal samples were tested for antimicrobial susceptibility using the Sensititre™ broth microdilution system. **Results:** There were significant (P < 0.05) differences in AR isolates: 1) between host-species with swine at higher risk for tetracycline, kanamycin, ceftiofur, gentamicin, streptomycin, chloramphenicol, sulfisoxazole, and ampicillin, 2) swine production group was significantly associated with AR with purchased boars, nursery piglets, and breeding boars at a higher risk of resistance to streptomycin and tetracycline, and 3) human swine worker cohorts exhibited lowered sulfisoxazole and cefoxitin prevalence compared to non-workers, while slaughter-plant workers exhibited elevated cefoxitin prevalence compared to non-workers. High variability among seasonal samples over the 3-year period was observed. There were significant differences in multiple resistance isolates between host species, with swine at higher risk than humans of carrying multi-resistant strains, slaughter-plant workers at higher risk than swine non-workers; however, there were no significant differences in multiple resistance isolates within swine by production group. **Conclusions:** Occupational exposure to slaughter facilities appeared to be associated with an increased relative odds for the prevalence of cefoxitin resistance and multiple resistance compared to swine non-workers.

Board 226. Antibiotic Restriction Policy and Practice in Selected U.S. Hospitals: Results of a Regional Survey

R. P. Ferguson, J. Han;

Union Memorial Hospital, Baltimore, MD.

Background Few studies on hospital antibiotic restriction policies exist. We examined these policies at selected U.S. hospitals with a focus on the impact of concern about *Clostridium difficile* infection. **Methods** An electronic survey on antibiotic restriction policies was developed. Answers were 1-4 on a Leikert scale, yes/no, or a narrative. We identified 45 Maryland, Pennsylvania, and District of Columbia teaching hospitals in the Association of Program Directors of Internal Medicine. We obtained contact information for the infectious disease specialist or pharmacist or both at 39 of these institutions. We contacted one individual at each institution by e-mail and asked this contact to complete the survey. Follow-up e-mails were sent. **Results** Of the 35 respondents (a 90% survey response rate), 33 (94%) had antibacterial restriction policies. The infectious disease specialist alone or as part of a Pharmacy and Therapeutics Committee made the final decision on these policies 91% (29) of the time. The most frequently restricted antibacterials were linezolid (26) and daptomycin (23). Seventeen respondents said their institution restricted at least one cephalosporin, and 13 said at least one quinolone was restricted. *C. difficile* infection risk was identified as an important consideration for antibiotic restriction by 22 respondents (66%), but only 4 (13%) considered it extremely important. In contrast, bacterial antibiotic resistance risk was considered important by 93% (31), the majority of whom (24) considered it extremely important. Although 88% (29)of the respondents considered *C. difficile* infection risk to be a significant problem in their hospital, only 18% (6) reported having made restrictions based on this concern. The most frequently cited reason (22 of the 33 with policies) for not restricting was that *C. difficile* infection could follow use of many different agents. **Conclusions** Antibiotic restriction policies are ubiquitous but vary greatly in their specifics. Infectious disease recommendations and concerns over bacterial resistance patterns are important influences in policy making. Although most responders consider *C. difficile* infection a significant problem in their institution, this concern has made minimal impact on antibiotic restriction policies.

Board 227. *Staphylococcus aureus* and Methicillin Resistant *Staphylococcus aureus* on surfaces in a University and a Jail Setting

M. Felkner[1], K. Bartlett[2], K. Andrews[2], L. Field[2], J. Taylor[1], T. Baldwin[1], J. Presley[2], J. Duncan[2], S. Newsome[1];

[1]Texas Department of State Health Services, Austin, TX, [2]The University of Texas at Austin, Austin, TX.

Background: Longtime pathogen *Staphylococcus aureus* has become more threatening with its evolution of antibiotic resistance, particularly the emergence of methicillin resistance outside health care settings. Commonly touched surfaces may harbor methicillin resistant *S. aureus* (MRSA) and be possible reservoirs of organisms facilitating disease transmission in the community. This study provides information regarding the presence of MRSA on commonly touched objects in both a university and a jail setting. **Methods**: University surface samples were obtained from bathrooms, common use areas, and recreational and sports facilities. Samples were collected at the jail from bathrooms, cells, common use areas, the clinic, laundry, and vehicles. Samples were collected using sterile, cotton-tipped swabs. Specimens were screened for *S. aureus* and MRSA using standard media. Susceptibility was determined using the ETest strip. Percentages of contaminated surfaces were calculated and chi-square comparisons were made between university and jail settings. **Results**: Seventeen (7.0%) of 244 university samples and 10 (7.5%) of 132 jail samples grew *S. aureus*. MRSA was recovered from 3 (1.2%) university samples, constituting 17.6% of *S. aureus* samples. Eight (6.1%) jail samples were MRSA, comprising 80% of jail *S. aureus* samples. The proportion of MRSA-contaminated surfaces and the ratio of MRSA to methicillin susceptible *S. aureus* were significantly greater at the jail that at the university ($p<0.05$). **Conclusions**: Our results indicate that environmental contamination with MRSA may be positively correlated with the carriage rate within the population. Implementation of environmental sanitation should be of particular concern in populations with high MRSA nasal carriage rates.

Bioterrorism Preparedness

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 228. Clinical Experience, Infection Control Practices and Diagnostic Algorithms for Poxvirus Infections - an Emerging Infections Network Survey

C. Hughes[1], E. Lederman[1], M. Reynolds[1], I. Damon[1], S. Beekmann[2], P. Polgreen[2];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]University of Iowa, Iowa City, IA.

Background: The Emerging Infections Network (EIN) is a sentinel, provider-based network of infectious disease consultants. In February 2007, we conducted a survey of EIN members to determine their experience with human poxvirus infections, and their likely approaches to diagnosis and reporting of suspected cases. **Methods:** A poxvirus survey was distributed by e-mail or facsimile to EIN members. The survey consisted of two case scenarios (monkeypox and orf) and included questions regarding likely approaches to diagnostic testing, transmission precautions, and reporting mechanisms for each case. Respondents were also asked about the frequency of various poxvirus infections in their practices. **Results:** Of the 213 respondents who completed the questionnaire (20% of those surveyed), 89% of those responding to the monkeypox scenario reported that they would request diagnostic confirmation by PCR, through either a local/academic laboratory (29%) or a State or Federal laboratory (66%). Only 3% reported that they would likely rely on clinical diagnosis alone. In contrast, when presented with the orf scenario, 22% of respondents reported that they would rely on clinical diagnosis, though PCR testing is now available. The likely level of transmission precautions that would be employed during patient exam for either scenario varied greatly among respondents. When recalling suspected poxvirus cases in their practices, 97% of respondents had seen at least one case of molluscum contagiosum, 16% orf, and 9% vaccinia from contact of vacinees. **Conclusions:** There was considerable variability in responses to the survey. More respondents would order diagnostics and institute a higher level of transmission precautions for suspected cases of monkeypox than orf, but the results of this survey suggest a greater level of physician outreach is needed to reinforce optimal detection, management and reporting of suspected poxvirus infections.

Board 229. Societal Implications of Biodefense and Emerging Infectious Disease Research: Perspectives from the SERCEB Policy, Ethics and Law Core

A. T. Chamberlain[1], R. Cook-Deegan[1], R. Berkelman[2], L. Burnett[3], A. Eisen[2], P. Gulig[4], E. Heitman[3], N. M. King[5], R. McKinney[1], J. Thomas[6], S. Tilden[7], N. Vangsnes[1], E. M. Davidson[1];

[1]Duke University, Durham, NC, [2]Emory University, Atlanta, GA, [3]Vanderbilt University, Nashville, TN, [4]University of Florida, Gainesville, FL, [5]Wake Forest University, Winston-Salem, NC, [6]University of North Carolina, Chapel Hill, NC, [7]University of Alabama, Birmingham, AL. The Policy, Ethics and Law (PEL) Core has been a core program of the Southeastern Regional Center of Excellence for Biodefense (SERCEB) since the Center was created in 2003. The Core functions in an advisory capacity to the investigators within SERCEB labs; its mission is to identify and address the ethical and societal issues that arise in biodefense and infectious disease research. With at least one participant from each of SERCEB's six member universities, the PEL Core Advisory Committee members have expertise in areas ranging from microbiology to biosafety to bioethics and law. In addition to reviewing SERCEB research proposals for dual-use concerns, the PEL Core explores issues such as human subjects research oversight in studies of rapidly emerging infections, public health ethics and pandemic flu, and how the Biological and Toxins Weapons Convention impacts biodefense investigators. Beyond SERCEB, the PEL Core engages with government, non-government organizations, and other research institutions, commissioning papers on policy or law-related topics relevant to SERCEB and infectious disease investigators.

Board 230. Enhanced Public Health Surveillance Activities in Miami-Dade County for a Special Event

E. OConnell[1], G. Zhang[2], D. Rodriguez[2], R. Borroto-Ponce[2], F. Leguen[2];

[1]Florida Department of Health, Miami, FL, [2]Miami-Dade County Health Department, Miami, FL.

Background: A large event such as the Super Bowl that attracts over 120,000 visitors to an area within a short period of time has the potential to increase the risk of unusual public events. The MDCHD implemented the syndromic surveillance system with additional public health measures to ensure the health and safety during the event. **Methods:** The following systems were used: Biological Warning and Incident Characterization (BWIC) system to support the BioWatch program, the Electronic Surveillance System for the Early Notification of Community Based Epidemics (ESSENCE), the Miami-Dade Fire Rescue 911 Call and school absenteeism data. Urgent care hospitals were required to submit daily reports to MDCHD during the event. **Results:** BioWatch air samplers were negative. Daily ED visits progressively increased each of the 4 days after the Super Bowl to 2,584 from the average of 2,315 for the first two months of 2007. ESSENCE detected a significant increase of Respiratory Syndrome lasting for 8 days after event. Both ESSENCE and 911 call data detected a statistically significant increase of motor vehicle accidents on the day of and one day after the Super Bowl. Notably, 25% of 911 calls about general sickness on the day of the event were from Dolphin Stadium which included falls, injuries and general illness. 104 of the 392 public schools had above 8% absenteeism after the Super Bowl day, which is a 143% increase from the average level. **Conclusions:** Multiple sources are able to detect a broad range of unusual increases of health-related issues during special events.

Emerging Opportunistic Infections

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 231. Toxicity of Kingella kingae on Human Cells

N. V. Balashova, S. E. Quiles-Guzman, S. C. Kachlany;

UMDNJ, Newark, NJ.

Background. Kingella kingae is a fastidious gram-negative coccobacillus of the Nesseriaceae family and is a normal inhabitant of the human oropharyngeal flora. This bacterium belongs to HACEK group and can cause infective endocarditis. Recently, as the result of improved isolation and identification techniques, an increasing number on invasive K. kingae infections have been

reported throughout the world, suggesting that the organism is an important cause of bacterimia and septic arthritis in pediatric patients. Despite the emerging body of information on the clinical and diagnostic aspects of K.kingae infections, the virulence mechanisms of this pathogen remain largely unknown. **Methods**. A K.kingae nasal isolate and human cell lines were purchased from ATCC. Erythrocytes were obtained from fresh human blood. K. kingae was grown on Columbia agar with 5% sheep blood or in Columbia broth. The toxicity on human cells was determined by Trypan blue assay after incubation with K. kingae cells or supernatant for four hours. To estimate erythrocytes lysis, hemoglobin release was measured at 450 nm. Purification of hemolysin from K. kingae cell culture supernatant was done by ammonium sulfate precipitation followed by gel filtration chromatography. Proteins were identified by MALDI-TOF MS. **Results**. In attempt to identify virulence factors we tested K. kingae cells and cell culture supernatant toxicity on different human cells. The hemolytic activity was found in K. kingae cell culture supernatant. The hemolysin was purified and identified as an RTX toxin. K. kingae cells could not lyse erythrocytes and epithelial cells but was highly toxic to human white blood cells including monocytes, myeloblasts and megakaryoblasts. K. kingae cell fractionation revealed that the leukotoxic factor (Ktx) is membrane-associated. Protease and high temperature treatment abolished toxic activity of the K.kingae membrane fraction indicating that Ktx is proteinaceious. **Conclusions**: Our results suggest that K. kingae produces at least two different toxins: the RTX hemolysin that is secreted into cell culture supernatant and leukotoxic Ktx that is associated with cell membranes. This is the first evidence of a leukotoxin in K. kingae that may be an important virulence factor for evasion of the host immune response during infection.

Board 232. Estimating the Global Burden of Cryptococcal Meningitis

B. J. Park[1], K. Wannemuehler[1], B. J. Marston[1], P. G. Pappas[2], T. M. Chiller[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]University of Alabama at Birmingham, Birmingham, AL.

Background: Cryptococcal meningitis (CM) is one of the most important HIV-related opportunistic infections, especially in the developing world, where overall mortality may be greater than 50%. In order to help develop global strategies for prevention and treatment, it is important to estimate the burden of CM. **Methods:** We searched the English language literature for cohort studies published after 1996 that reported an estimate of CM burden among HIV-positive persons. This incidence rate was generalized to the other countries in the region, and multiplied by the 2005 UNAIDS HIV prevalence estimates to calculate a regional incidence and burden estimate. For regions with multiple studies, we used the mean of the reported incidence rates, and estimated the range based on the lowest and highest rates. If no studies were published from any countries in a given region, we assumed CM rates from regions with similar proportions of anti-retroviral coverage. To estimate deaths, we assumed a 10% 3-month case-fatality rate among high-income regions, and a 50% rate among low- and middle-income regions, based on randomized controlled trials published in these areas. **Results:** Overall, 18 studies were identified that met the search criteria. Published incidence ranged from 0.1%-12% per year among persons with HIV. Sub-Saharan Africa was the region with the highest yearly burden estimate (mean incidence 3.6%, 886,900 cases (range, 784,000 - 990,000)), followed by South/ Southeast Asia (mean incidence 5.3%, 401,280 cases (range, 129,200 - 912,000)). Estimated incidence was lowest in Western and Central Europe and Oceania (0.1% each). Globally, approximately 1.41 million cases (range, 1.03M - 2.03M) of CM occur each year, resulting in 700,000 deaths (range, 510,000 - 1.0M) by 3 months. **Conclusions:** This study, the first attempt to estimate the global burden of CM, finds the number of cases is likely to be very high, with most occurring in Sub-Saharan Africa and South/ Southeast Asia. Further work is needed to better define and track the epidemiology of this infection, in order to prioritize prevention, diagnosis, and treatment strategies.

Board 233. Changing Epidemiology of human pneumocystosis in India:

B. R. Mirdha, R. Gupta, R. Guleria, A. Mohan, L. Kumar, S. K. Kabra, S. K. Agarwal, K. Luthra;

All India Institute of Medical Sciences, New Delhi, INDIA.

Background: Overwhelming of infections due to tuberculosis, in resource limited countries has somewhat undermined the role for other opportunistic respiratory infections in population "at risk". *Pneumocystis jiroveci (P. jiroveci)*, cause of *Pneumocystis carinii* pneumonia (PCP) is said to be rare in India. Over twelve months period, we studied epidemiologic characteristics of *P. jiroveci* infection in our tertiary health care centre. **Methods:** We applied polymerase chain reaction (PCR) using three different genes i.e. Major Surface Glycoprotein (MSG),Mitochondrial large sub-unit ribosomal RNA (mtLSUrRNA) & Internal Transcribed Spacer (ITS) to detect *P. jiroveci* infection in different respiratory clinical samples. A total of 200 respiratory samples, obtained from 150 clinically suspected PCP patients were analysed. Another fifty (n=50) clinical specimens from patients with a clinical diagnosis other than PCP were included as control groups. Bronchoalveolar lavage (BAL), Induced sputum (IS), Expectorated sputum (ES), Tracheal Aspirate (TS) and Nasopharyngeal aspirate (NPA) constituted the specimens**. Results:** Direct demonstration of *P.jiroveci* was carried out using Grocott's Gomori Methenamine Silver (GMS) and Direct Immunofluorescence Assay (DFA). Microscopy was positive in only six (n=6) patients. Single (external) round MSG PCR could detect *P.jiroveci* DNA in 16 cases. However, mtLSU rRNA and ITS nested PCR assays detected seven (n= 7) additional cases of PCP .Amongst the 81 Bronchoalveolar Lavage (BAL) samples tested, 16 were positive by MSG PCR, while 20 were positive by both nested i.e, mt LSU rRNA and ITS PCR assays. Similarly, out of 50 sputum samples, only 3 were positive by MSG, 7 by mtLSU rRNA and 6 by ITS nested PCR assays. Based on PCR results, infection rate of 12% *P. jiroveci* infection could be observed. None of the clinical specimens in control group (n=50) were positive by any of the techniques. Individuals living with HIV/AIDS were the commonest risk population followed by patient with post-renal transplants. **Conclusions:** The finding that *P.jiroveci* is more frequently detected in seriously ill patients are similar to those in their counterparts from industrialized countries, has implications for improved diagnosis to understand the changing epidemiology of PCP in Indian sub-continent.

Board 234. *Acanthamoeba* spp. Cysts are Resistant to Desiccation for at Least 20 Years

R. Sriram[1], M. Shoff[2], G. Booton[2], P. Fuerst[2], G. S. Visvesvara[1];

[1]Centers for Disease Control & Prevention, Atlanta, GA, [2]Ohio State University, Columbus, OH.

Background: *Acanthamoeba* is a free-living ameba that occurs worldwide. It has been isolated from diverse habitats including soil, fresh water ponds, pools, lakes, brackish water, as well as contact lens paraphernalia, and human nostrils. *Acanthamoeba* is also an opportunistic pathogen and is known to cause diseases in humans including fatal granulomatous amebic encephalitis, cutaneous infection and *Acanthamoeba* keratitis (AK). *Acanthamoeba* has two stages, a trophozoite and a cyst, in its life cycle. The cyst stage is resistant to extreme physical and chemical conditions, including pH (2.0), freezing, and γ (250 rads) and UV (800 mj/cm^2) irradiation. Acanthamoebae are also known to be hosts for pathogenic microorganisms such as *Legionella*, *Burkholderia*, *Mycobacterium*. Further, *Legionella* and *Staphylococcus* have been found within *Acanthamoeba* cysts. **Methods:** As many as 20

isolates of *Acanthamoeba* from soil, water and human tissue were grown on bacteria-coated agar plates and after amebae encysted the plates were stored at room temperature for a period of 5 to 20 years. Agar plates that had dried to parchment consistency were rehydrated, scraped, centrifuged, and the sediment inoculated on to fresh agar plates coated with bacteria and incubated at 30ºC. The amebae were axenized using PYG medium and DNA extracted. PCR was used to amplify a partial *Rns* region (ASA.S1) that contains a diagnostic fragment using the primers JDP1 (5_-GGCCCAGATCGTTTACCGTGAA-3_) and JDP2 (5_-TCTCACAAGCTGCTAGGGGAGTCA-3_). The obtained sequences were aligned with other *Acanthamoeba* sequences in our database using the alignment program XESEE. **Results:** All 20 plates were positive for trophozoites of *Acanthamoeba* within a week and were found to belong to Group II. The results from *Rns* sequencing demonstrated that the 20 isolates belonged to three *Acanthamoeba* genotypes. Eighteen isolates were categorized as genotype T4, one as T7 and one as T10. **Conclusions:** We conclude that *Acanthamoeba* cysts have the ability to survivedesiccation and that they belonged to the most commonly observed genotype and the genotype (T4) predominantly associated with AK infections.. Since the cysts may harbor and protect pathogenic bacteria they have great public health significance.

Board 235. Trends in Hospital Admissions for Skin and Soft Tissue Infections (SSTIs) Among Medicare Enrollees, 2001-2005

C. Taneja[1], M. J. Zervos[2], J. S. Edelsberg[1], N. Z. Haque[2], J. Spalding[3], G. Oster[1];

[1]Policy Analysis Inc, Brookline, MA, [2]Henry Ford Health System, Detroit, MI, [3]Astellas Pharma US, Inc., Deerfield, IL.

Background. While methicillin-resistant *Staphylococcus aureus* (MRSA) skin and soft tissue infections (SSTIs) have been a common cause of morbidity among hospitalized patients, community-acquired (CA) MRSA SSTIs were uncommon until recently. Of late, however, reports of such infections have been increasing rapidly. It is unknown whether this phenomenon is reflected in trends in aggregate data on US hospital admissions for SSTIs. **Methods**. Using the Medicare Provider Analysis and Review (MEDPAR) Limited Data Set (LDS)-Hospital (National) for 2001-2005, we identified all persons aged ≥65 years who were admitted to hospital with a principal diagnosis of SSTI. For purposes of comparison (i.e., to ascertain if changes in SSTI admissions reflect general trends in hospitalization for infection), we also identified all admissions for infectious pneumonia (IP). We then examined changes in admission rates on an overall basis over this five-year period, as well as stratified by selected patient and hospital characteristics. **Results**. Total SSTI admissions to US hospitals among Medicare enrollees increased by 17% between 2001 and 2005 (from 216,449 to 253,212); over the same period, Medicare admissions for IP increased by only 9% (from 589,751 to 643,675). The increase in SSTI admissions was greatest among Medicare enrollees aged 65-74 years versus older (26% and 11% respectively), and for urban versus rural hospitals (16% increase vs 12% decline respectively). **Conclusions**. The number of admissions to US hospitals for SSTIs among Medicare beneficiaries has increased disproportionately in recent years. While not necessarily attributable exclusively to MRSA, our findings are consistent with increasing numbers of serious infections due to CA-MRSA.

Foodborne & Waterborne Infections

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 236. Description of Shiga-toxin Producing *E. coli* Infections in Georgia

M. Tobin-D'Angelo, S. M. Thomas, T. Hayes;

Georgia Division of Public Health, Atlanta, GA.

Background: Shiga-toxin producing *E. coli* (STEC) infections cause bloody diarrhea, and, especially in children, hemolytic uremic syndrome (HUS). STEC patients often have had exposures to ground beef, produce, or livestock. *E. coli* O157:H7 is the best described STEC serotype, but other types (non-O157) have been reported. An increase in total STEC cases in Georgia occurred in 2006 (82 cases) compared to 2005 (49 cases). We analyzed our data to determine the cause of the increase and characterize STEC cases. **Methods:** We analyzed exposure, clinical and demographic data of O157 and non-O157 STEC reported during 2000-2006, and compared characteristics of STEC cases in 2005 and 2006. We also reviewed outbreak data to determine if any common-source outbreaks explain the increasing numbers of STEC cases and performed a preliminary analysis on the FoodNet STEC laboratory survey. **Results:** While a higher proportion of non-O157 cases were identified in 2006 (30%) than in 2005 (22%), the difference was not significant. Higher numbers of both O157 (42 vs.31) and non-O157 STEC (18 vs. 9)occurred in 2006. Over the entire time period, STEC non-O157 cases had significantly lower proportions of HUS (3% vs. 11%, $p=0.02$) and hospitalizations (11% vs. 51%, $p<0.01$) than O157 cases. Non-O157 cases were more likely to have traveled outside of their community (53% vs. 29%, $p<0.01$) than O157 cases. A significantly higher proportion of 2006 STEC cases were white compared to 2005 cases (85% vs. 63%, $p<0.01$). **Conclusions:** Non-O157 STEC reports are increasing in Georgia, contributing to the overall increase in total STEC in 2006, but not fully explaining it. Although it results in less severe disease, it is still necessary to provide public health follow-up for non-0157 STEC cases. Further examination of sources of STEC infections is needed. The racial differences in STEC cases between 2005 and 2006 warrants evaluation. Continued evaluation of the impact of changing laboratory practices on STEC epidemiology is necessary.

Board 237. *Vibrio vulnificus* Infections in Georgia

S. Thomas[1], M. Tobin-D'Angelo[1], S. Shepherd[2], T. Stivers[3];

[1]Geogia Division of Public Health, Atlanta, GA, [2]Georgia Department of Agriculture - Consumer Protection Division, Savannah, GA, [3]University of Georgia Marine Extension Service, Peachtree City, GA.

Background: While *Vibrio vulnificus* (*V.v*) is a rare foodborne disease, it can result in high rates of hospitalization and death. *V.v* infection and these negative outcomes are more common in individuals with underlying conditions. Georgia continues to annually report *V.v* cases, so it is important to know the population affected and the sources of the infection for both educational and regulatory purposes. **Methods:** Georgia data were analyzed with SAS to characterize *V.v* cases and potential exposures. Cases were identified through FoodNet Active Surveillance. Data were collected on a standard CDC form. Trace back information was acquired from Georgia and other states' Departments of Agriculture. **Results:** Between 2001-2006, Georgia reported 36 *V.v* cases. Most were in the 20 counties of Metro Atlanta (47%) and the six coastal counties

of Georgia (28%). The majority of cases were adults (94%), males (75%) and whites (69%). *V.v* infections were severe with 92% of cases hospitalized and 39% case fatality rate. More than 80% of cases had documented underlying conditions; the most common were liver disease (42%), diabetes (31%), and alcoholism (28%). Most (92%) *V.v* cases ate or touched seafood or had direct contact with salt or brackish water. Eating seafood was the most common exposure (75%), and oysters were the most common type eaten (61%). Twenty-two percent of cases were exposed to salt or brackish water. Since 2004, six *V.v* cases had confirmed association with Georgia waters or indigenous seafood. Two of these cases involved exposure to seafood (shrimp and crab). Prior 2004, exposure to Georgia harvested seafood or water had not been documented in any *V.v* cases. **Conclusions:** The epidemiology of *V.v* in Georgia, similar to the U.S. in general, is characterized by infections in people with underlying conditions and severe outcomes. Therefore, it is important to target specific populations for education efforts. The University of Georgia Marine Extension Service has created the SafeOysters.org website as a resource for healthcare, seafood industry, and the public. The low numbers of *V.v* cases associated with indigenous Georgia seafood can partially be explained by the low seafood production in Georgia and the types of seafood harvested. Additionally, practices by the Georgia seafood industry and regulators could contribute.

Board 238. Outbreaks in Australia from Imported Foods, 2001-2007

M. D. Kirk[1], K. Fullerton[1], J. Gregory[2], J. Musto[3];

[1]OzFoodNet, Canberra, AUSTRALIA, [2]OzFoodNet, Department Human Services, Victoria, AUSTRALIA, [3]New South Wales Health Department, Sydney, AUSTRALIA.

Background: Each year in Australia, approximately 100 outbreaks of foodborne disease are reported. The nature of foodborne outbreaks has changed in recent years due to the increasingly complex distribution and processing of food. In particular, imported foods have caused a number of outbreaks. **Methods:** To examine outbreaks associated with foods imported into Australia we reviewed data from 2001 to 2007 from the OzFoodNet Outbreak Register. OzFoodNet Sites complete a summary form for all foodborne disease outbreaks and enter it into the Outbreak Register. All records from 2001 to 2007 were assessed to identify outbreaks implicating foods imported to Australia. **Results:** Between 2001 and 2007, fourteen outbreaks were reported from food imported into Australia. *Salmonella* was the agent in 28% (4/14) of outbreaks, viruses were either confirmed or suspected in 43% (6/14) of outbreaks and ciguatoxin sodium nitrate, *Vibrio cholerae* and *Shigella sonnei* biotype g were confirmed in four outbreaks. Pathogens that are rare in Australia_Salmonella Typhimurium 104 and *Vibrio cholerae*_ were responsible for two outbreaks. Imported seafood was the most common food implicated (8/14, 57%) and imported sesame seed products caused three outbreaks in both Australia and overseas. **Conclusions:** Globalisation of the food supply may result in the introduction of novel pathogens in exotic foods. Despite this, the total number of outbreaks associated with imported food is low. Seafood caused the majority for outbreaks implicating imported food in Australia. Efforts should be made to improve international cooperation and standardise outbreak investigations across country borders.

Board 239. Antimicrobial Resistant *Salmonella* from Retail Chicken in Pennsylvania 2006-2007

S. C. Rankin[1], N. M. Mikanatha[2], D. Tewari[3], A. Russo[3], R. Localio[1], S. Altekruse[4], C. Sandt[5], E. Lautenbach[1], J. Tait[2], M. Hydock[3], S. Reynolds[5], N. G. Warren[5], T. M. Chiller[6], D. G. White[7];

[1]University of Pennsylvania, Philadelphia, PA, [2]Pennsylvania Department of Health, Harrisburg, PA, [3]Pennsylvania Department of Agriculture, Harrisburg, PA, [4]National Institutes of Health, Bethesda, MD, [5]Pennsylvania Department of Health, Lionville, PA, [6]Centers for Disease Control and Prevention, Atlanta, GA, [7]Food and Drug Administration, Laurel, MD.

Background: Infections caused by antibiotic-resistant *Salmonella* strains are associated with more severe illnesse, and higher mortality than those due to susceptible strains. Consumption of chicken is a known risk factor for salmonellosis. However, the prevalence of resistant *Salmonella* in poultry meat and their relationship to human *Salmonella* isolates has not been well-characterized. **Methods:** Chicken was purchased from a stratified random sample of retail outlets in a three county region of Central Pennsylvania for 12 months during 2006-2007. Each month 30 samples were purchased from retail outlets. The samples included prepackaged and open display poultry. Information was obtained on USDA establishment numbers and organic/antibiotic-free status from package labels, where available. Isolates were characterized by serotyping, antibiotic susceptibility testing and pulsed-field gel electrophoresis (PFGE). Antibiotic resistant strains were analyzed for the presence of resistance genes by PCR. PFGE profiles of antibiotic resistant isolates were compared with human *Salmonella* isolates from the state public health laboratory during the study period. **Results:** *Salmonella* was isolated from 84 (22%) of 378 samples. The most common serotypes were Typhimurium 28 (33%), Kentucky 24 (29%), and Enteritidis 22 (26%). 45 isolates showed resistance to one or more drugs; 40% demonstrated resistance to at least five drugs. 8/45 (18%) resistant isolates had a bla_{CMY} ß-lactamase gene. The packaged chicken originated from 20 different establishments. *Salmonella* isolation was associated with poultry from particular establishments (p=0.007, chi sq=37.6, df=19). In one establishment that processed only organic poultry, 10 (53%) of 19 samples were positive. PFGE patterns of Typhimurium and Kentucky isolates from chicken matched patterns in the human database. **Conclusion:** The occurrence of drug-resistant *Salmonella* in retail chicken is a public health concern. This study identified strains with reduced susceptibility to expanded-spectrum cephalosporins and isolates from humans and chickens with the same PFGE profiles. The study also identified an association of *Salmonella* contamination with poultry from specific establishments. These results indicate the need for enhanced inter-agency surveillance.

Board 240. Rotavirus Diarrhea in Children in Cambodia

L. Bodhidatta[1], O. Sethabutr[1], C. Y. Meng[2], S. Silapong[1], T. Singhsilarak[1], B. L. Smith[1], C. J. Mason[1];

[1]Armed Forces Research Institute of Medical Sciences, Bangkok, THAILAND, [2]National Pediatric Hospital, Phnom Penh, CAMBODIA.

Background: Rotavirus, genotypes G1-G4 and G9, causes significant morbidity and mortality among children worldwide. Several effective vaccines will soon become available and can reduce the disease burden and health care costs of rotavirus-specific diarrhea. We conducted a hospital based surveillance of rotavirus diarrhea in the National Pediatric Hospital in Phnom Penh, Cambodia in 2004-2006 to describe the epidemiology of the disease and the genotypic distribution of rotavirus which are important for decision-makers on a future vaccine testing and implementation. **Methods:** Stool samples collected from children under 5 years of age with acute diarrhea and non diarrhea controls were examined for rotavirus by a real-time reverse transcriptase polymerase chain reaction (RT-PCR) using primers and probes targeted on VP6 gene. Samples positive for Rotavirus were genotyped using primers targeted on VP7 gene to identify 5 genotypes (G1-G4 and G9) by a conventional PCR. **Results:** Rotavirus was detected in 161/536 (30%) of children with diarrhea and none of 287 non-diarrhea controls. All except 3 cases were children less than 2 years of age.

G1 was the predominating type (57%), followed by G9 (12%), G2 (10%), G4 (3%) and G3 (0.6%). Approximately 18% of samples that cannot be characterized by our system are being analyzed by sequencing and compared with sequence database. **Conclusions:** Rotavirus is a significant cause of acute pediatric diarrhea in Cambodia. The most common genotype was G1, G9 and G2. Results of the sequence analysis will be reported to describe the emergence of unusual serotypes which will be necessary information for future polyvalent vaccine development to control rotavirus diarrhea.

Board 241. First Report of Spontaneous Clinical Recovery in the Presence of Circulating Botulinum Toxin Type F in an Adult

J. Sobel[1], T. Dill[2], C. L. Kirkpatrick[2], L. Riek[3], P. Luedtke[4], T. Damrow[5];

[1]CDC, Atlanta, GA, [2]St. Peter's Hospital, Helena, MT, [3]Lewis & Clark City-County Health Department, Helena, MT, [4]Utah Department of Health, Salt Lake City, UT, [5]Montana Department of Health and Human Services, Helena, MT.

Background: Botulism is characterized by cranial nerve (CN) palsies and flaccid paralysis. Botulism type F causes 1% of US cases; illness is more precipitous and recovery is more rapid than with other toxin types. **Methods:** Case report, culture and standard mouse toxin bioassay at two Public Health laboratories. **Results:** A 56 year-old woman with abdominal pain, CN III-VII palsies and partial symmetric limb paralysis had respiratory arrest. Brain imaging and CSF studies were normal. Anti-ABE antitoxins were administered within 24 hours of presentation; paralysis progressed and within 48 hours the patient had no voluntary muscle function or distal tendon reflexes. Improvement began on day eight, when she moved eyebrow and head, gripped, and plantarflexed/dorsiflexed her feet. Heptavalent (anti-ABCDEFG) antitoxin was not administered but because of clinical improvement, it was surmised that no toxin remained in circulation. Gradual improvement followed: cranial nerve function recovered by day 12; distal tendon reflexes appeared on day 17; mechanical ventilation was stopped on day 35. Gasroparesis necessitated total parenteral nutrition for 23 days. She was discharged on hospital day 47. Complications included aspiration pneumonia, fungemia, heart failure, and otitis media. Following discharge the patient required help getting out of bed and washing for a month; help dressing for two months, and help rising from a chair for over seven months. She attained pre-illness health 10 months after discharge. Botulinum toxin type F was identified in serum drawn on hospital days one and eight; estimated minimum toxin serum concentration was 1 MIPLD50/ml on hospital day eight, the day she demonstrated unequivocal signs of recovery from total quadriplegia. No cross reactivity with type E toxin was present. Stool tested negative for toxin but yielded toxin type F-producing *Clostridium baratii*. No suspect food was identified. Hospital charges were ~$230,000.**Conclusion**: This is the first reported case of a patient with lethal levels of botulinum toxin in circulation even as she demonstrated clinical improvement and recovery from paralysis. This finding, together with previously documented clinical course of illness for this toxin type, suggest the action of botulinum toxin type F differs from that of other botulinum toxins.

Board 242. Serotypes, antimicrobial susceptibility and molecular characterization of Salmonella from infections in humans in Henan province, China

S. Xia[1], R. S. Hendriksen[2], W. Guo[1], B. Xu[1], R. Lu[3], F. M. Aarestrup[2];

[1]Branch for Enteric Disease Control and Prevention, Institue for Infectious Disease Control and Prevention, Henan Center for Disease Control and Prevention, Zhengzhou, CHINA, [2]WHO Collaborating Centre for Antimicrobial Resistance in Food borne Pathogens and EU Community Reference Laboratory for Antimicrobial Resistance, National Food Institute, Technical University of Denmark, Bülowsvej 27, DK-1790, Copenhagen V, DENMARK, [3]Branch for Enteric Disease Control and Prevention, Office for Disease Control and Emergency Response, Chinese Center for Disease Control and Prevention, Beijing, CHINA.

Background *Salmonella enterica* is a common cause of human gastroenteritis and bacteremia worldwide and a wide variety of animals, particularly food animals, have been identified as reservoirs for nontyphoidal *Salmonella*. Shifts in prevalence of specific strain types and serovars can reflect the influence of international travel and trade of animals and food products, and can therefore serve as useful epidemiological markers. There is only limited information on the occurrence of serotypes and their antimicrobial resistance in China. This study was conducted to determine the occurrence of different salmonella serovars and their antimicrobial susceptibility among isolates obtained from infections in humans in Henan province in China. In addition, the molecular types of the most common serovars were determined. **Methods** A total of 214 *Salmonella enterica* isolates from infections in humans from the Henan province in China during 2006-2007 were serotyped according to the Kauffmann-White scheme and tested for antimicrobial susceptibility using MIC determinations. **Results** The most common serovars were S. Typhimurium (26%), S. Enteritidis (16%), S. Derby (11%), S. Indiana (6%) and S. Litchfield (6%). A high frequency of resistance (109 isolates; 51%) was observed to nalidixic acid. Of these isolates 52 isolates were high-level resistant to ciprofloxacin (MIC > 2 mg/L), whereas the remaining isolates had MIC from 0.125 to 2. Five isolates were low-level ciprofloxacin resistant, but susceptible to nalidixic acid. None of the five isolates harboured a qnr gene. Five (2%) of the isolates were resistant to ceftiofur and harboured a bla_{CTX} gene. **Conclusions** This study showed that S. Typhimurium and S. Enteritidis are the most common serovars causing human salmonellosis in henan province in China, but also show that other serovars are of importance. The study document a very high frequency of quinolone resistance, but still a low frequency of resistance to cephalosporins.

Board 243. Evidence that Fresh Chicken is the Main Source of New Zealand's Sustained Campylobacteriosis Epidemic

M. G. Baker, N. Wilson, K. Venugopal;

University of Otago, Wellington, Wellington, NEW ZEALAND.

Background: New Zealand (NZ) has the highest documented national incidence rate of campylobacteriosis in the developed world. Here we provide an update of the epidemiology of this epidemic and review evidence that fresh chicken meat is the dominant source. **Methods**: We examined national campylobacteriosis notification data (1980-2006) and hospitalisation data (1995-2006). We correlated these notification rates with data on production of fresh chicken meat (1982-2006). Virtually all chicken produced in NZ is consumed within the country and this food is not imported. An updated literature search was undertaken to identify relevant laboratory and pidemiological studies. **Results**: *Campylobacter* infections reached a new peak in 2006 with 15,873 notifications and 969 hospitalizations, the highest totals ever reported in NZ. The notification rate of 383 / 100,000 in 2006 is the highest national rate reported in the literature. Trends in annual notification and hospitalisation rates were highly correlated over the 1996 to 2006 period (Spearman's rho 0.900, $p<0.01$) and both were increasing suggesting that this rise in incidence is unlikely to be a surveillance artefact. We conservatively estimate the total annual burden of community infections to be 120,000 cases with a cost to the economy of $NZ 75 million per annum. The rise in campylobacteriosis notification rates was highly correlated with the

increase in fresh poultry consumption per person (Spearman's rho 0.952, p<0.01). The literature review also provided strong evidence for the dominant importance of chicken meat as the source of human infection in NZ (based on epidemiological, laboratory, intervention, and ecological evidence). Contaminated water supplies and overseas travel appear to play a minor role. **Conclusions**: The health impact of the campylobacteriosis epidemic in NZ now places it amongst this country's most important infectious disease problems. The focus for public health authorities, food safety regulators and researchers should now be on interventions to reduce population exposure to highly contaminated fresh poultry meat. One option that has been proposed is mandatory freezing of poultry to reduce contamination levels.

Board 244. Global Survey by the World Health Organization (WHO) to Assess Public Health Surveillance Systems for *Salmonella*; WHO Global Salm-Surv, 2006

S. M. DeLong[1], T. N. Maxwell[1], V. P. Carlson[2], D. Lo Fo Wong[3], F. J. Angulo[2], and WHO Global Salm-Surv;

[1]Centers for Disease Control and Prevention and United States Veterans Administration, Atlanta, GA, [2]Centers for Disease Control and Prevention, Atlanta, GA, [3]World Health Organization, Geneva, SWITZERLAND.

Background: In 2000, the World Health Organization (WHO) conducted a global survey and determined that although the majority of countries reported having a public health surveillance system for *Salmonella*, there was a need to enhance capacity for laboratory-based surveillance and outbreak detection and response. To address this need, WHO Global Salm-Surv, which conducts several capacity building activities including international training courses, was launched. To determine the impact of WHO Global Salm-Surv, WHO repeated the global survey in 2006. **Methods:** A questionnaire was developed by members of the WHO Global Salm-Surv Steering Committee and was distributed by WHO, through the WHO Regional Offices, to WHO Country Representatives. WHO Country Representatives and existing laboratories responsible for national *Salmonella* surveillance completed and returned the questionnaires to the participating WHO Collaborating Center at CDC for data entry and analysis. **Results:** Completed surveys were received for 76 countries; 61 (80%) reported a national public health system for *Salmonella* surveillance. Fifty-eight nations (76%) reported a designated laboratory responsible for national *Salmonella* surveillance. *Salmonella* case reporting was mandatory in 48 (84%) countries. The most frequently isolated serotypes in 2005 were *Salmonella* Enteritidis, *S.* Typhimurium, and *S.* Typhi. **Conclusions:** Results from this global survey suggest an increase in the proportion of countries with national public health systems for *Salmonella* surveillance in 2006 compared to 2000. This increase suggests that additional resources are being invested to fight foodborne diseases globally. More research should be conducted to explain the reasons for these changes. Advocacy for additional funds and skills for the surveillance systems may be generated from educational efforts such as those provided by WHO Global Salm-Surv. *Salmonella* Enteriditis remained the most frequently reported serotype in 2005.

Healthcare Worker Safety

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 245. Investigations of Close Contacts of Patients with Laboratory-confirmed H5N1 Virus Infection in Indonesia

S. Isfandari;

National Intitute of Health Research Development, MOH, Indonesia, DKI Jakarta, INDONESIA.

Background: Since 2005, 112 patients with H5N1 influenza virus infection have been identified in Indonesia including 91 (81%) who have died. Investigation of patient contacts and prevention of H5N1virus transmission within the health care setting is a high priority for the Ministry of Health. The objectives of this study were to measure the frequency of H5N1 infection among close contact of patients with laboratory-confirmed H5N1 infection and monitor compliance with MOH guideline of using PPE and recommendations for antiviral prophylaxis for contacts of H5N1 patients. **Methods**: Trained teams investigated family members, neighbors, and health care workers who had close contact to H5N1 patients during the course of clinical illness. Interviews were conducted to characterize exposure to the index patient as well as community exposures to sick poultry. Throat swabs from contacts with influenza-like illness were tested by polymerase chain reaction for evidence of H5N1 infection. Acute and convalescent serum samples were tested for antibody to H5N1 virus by heamaglutination inhibition assays. **Results**: Overall, 257 contacts were investigated including 130 HCWs, 90 family members, and 34 neighborhood contacts; 201 (78%) of interviews were conducted within 2 weeks of the last contact with the index case. One contact (a family member) tested positive for H5N1 infection. This contact also reported exposure to sick poultry. Fifty four contacts (21%) reported ILI in the post exposure time period; 7 (13%) of these contacts were treated with tamiflu according to MOH guidelines. HCWs with post-exposure ILI were more likely to take tamiflu prophylaxis than other contacts. Only 10 (4%) HCWs reported using PPE according to MOH guidelines when taking care of H5N1 patients. No contacts had antibody to H5N1 virus. **Conclusions**: We found no evidence of H5N1 virus infection among close contacts of patients laboratory-confirmed H5N1 infection. More efforts are needed to ensure compliance with MOH recommendations on antiviral prophylaxis and use of PPE.

Board 246. Evaluation of Effectiveness of Commercial Sanitizers / Disinfectants to Inactivate Human Norovirus using two Surrogate Model Strains (Feline Calicivirus and Murine Norovirus)

G. Park, L. Barclay, J. Vinjé;

Centers for Disease and Prevention, Atlanta, GA.

Background: Human noroviruses (NoVs) are the leading cause of nonbacterial gastroenteritis worldwide responsible for 80-90 % of the reported outbreaks. Fecally contaminated hands or inanimate surfaces can act as a source of continuing infection in outbreaks of NoVs. The use of sanitizers is an effective way to interrupt the hand- or surface mediated virus spread. However, little is known on the effectiveness of sanitizers against NoVs because no easy cell culture system is currently available. In this study we evaluated the effectiveness of commercial sanitizers on feline calicivirus (FCV) and murine norovirus (MNV) by viral plaque assay and realtime RT-PCR. **Methods**: We tested 11 commercial sanitizers containing at least one of key active ingredients such as

ethanol, triclosan, phenylphenol, quaternary ammonium compounds (QACs), or hydrogen peroxide and compared their effectiveness after exposure for 1, 2 and 5 minutes with FCV or MNV. Samples were then neutralized with either DE broth, fetal bovine serum or and assayed for remaining virus titers by plaque assay or for viral RNA by realtime RT-PCR for each virus. **Results**: phenol-, QAC-, triclosan- and hydrogen peroxide-based products did not inactivate MNV after 5 minutes of exposure. However, most of these products did inactivate FCV by more than 4 $\log_{10}$ PFU/ml. Ethanol based products did not inactivate FCV with 0.5 $\log_{10}$ reduction of infectivity after 5 minutes. Interestingly, MNV was inactivated by ethanol-based products by more than 3 $\log_{10}$ PFU/ml. Most infectivity results were confirmed by the realtime RT-PCR data. **Conclusions**: Phenol, QAC, and hydrogen peroxide based products were very effective in inactivating FCV, but not MNV. Ethanol based products inactivate MNV more easily than FCV. Overall, the two currently available cultivable surrogate viruses for human norovirus demonstrated different levels of susceptibility against a panel of commercially available sanitizers. These different inactivation patterns could lead to overestimation of the virucidal effectiveness of certain commercial sanitizers. Building a database on the effectiveness of active ingredients used in commercial sanitizers against two surrogate viruses may lead to a more scientific approach in recommending products that may be effective to control norovirus outbreaks.

Influenza

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 247. Protective Effect of Maritime Quarantine in South Pacific Islands During the 1918-1919 Influenza Pandemic

M. G. Baker[1], M. McLeod[1], H. Kelly[2], N. Wilson[1], F. Alvarado-Ramy[3], CDC funded NZ Pandemic Influenza Research Team;

[1]University of Otago, Wellington, Wellington, NEW ZEALAND, [2]Victorian Infectious Diseases Reference Laboratory, Melbourne, AUSTRALIA, [3]Centers for Disease Control and Prevention, San Juan, PR.

Background: Current theoretical modeling suggests a fairly limited role for border control in preventing spread of pandemic influenza, but no models have focused on islands. Given the inclusion of border control measures in the pandemic preparedness plans of many island nations, we reviewed the available evidence for the success of border control, employed by Pacific Island nations in the 1918-19 pandemic. **Methods:** Published historical data were retrieved through a systematic search of Medline, Embase, the Australasian Medical Index (AMI) and Web of Science. Archival searches were undertaken in New Zealand and Australia. Other source material was accessed from the WHO office in Fiji and the Secretariat of the Pacific Community. **Results:** The literature search identified 35 articles and documents that included information on the use of border control in 11 of 25 South Pacific Island jurisdictions including Australia, Tasmania and New Zealand. A further 21 archival documents were reviewed. We identified 4 jurisdictions that successfully employed strict maritime quarantine to protect against the 1918-19 influenza pandemic. Continental Australia, the state of Tasmania, and American Samoa all delayed the arrival of the pandemic by employing strict maritime quarantine for periods ranging from 3 months to 3 years in American Samoa. New Caledonia was protected by the home port quarantine of departing Australian vessels. Limited data also suggest that Australian quarantine of departing vessels also provided protection to the islands of Kiribati, Tuvalu, Vanuatu, Norfolk Island and the Solomon Islands. The experience of the Pacific islands is supported by evidence of successful quarantine in 6 islands in other parts of the world. These Pacific Island jurisdictions using strict quarantine also experienced lower mortality rates attributed to pandemic influenza when it subsequently arrived, compared to islands where late, inadequate or no border control measures were implemented. **Conclusions:** Strict maritime quarantine appeared to be successful in delaying the entry of pandemic influenza into a number of Pacific Islands from 1918-21. The development of an island specific theoretical model is required to investigate the potential of border control in a world with a larger population and modern transport patterns.

Board 248. Impact of Respiratory Syncytial Virus on Seasonal Influenza Surveillance - New York, 2005-2007

P. Duncan, C. L. Waters, G. S. Johnson, J. K. Schaffzin;

New York State Department of Health, Albany, NY.

Background: New York State Department of Health seasonal influenza surveillance consists of numerous components, including voluntary Sentinel Provider Influenza Surveillance Network (SPISN) and National Respiratory and Enteric Virus Surveillance System (NREVSS). SPISN tracks the weekly proportion of influenza-like illness (ILI) among patients of community providers. NREVSS reports on the weekly proportion of positive laboratory tests for influenza and other viruses. For the past two influenza seasons (between October and May), ILI has peaked in the absence of NREVSS influenza activity. **Methods:** For the 2005-06 and 2006-07 influenza seasons, the weekly percentage of ILI reported by SPISN was compared to the weekly percentage of laboratory tests positive for influenza, respiratory syncytial virus (RSV), parainfluenza (PIV), and adenovirus (ADV) reported by NREVSS. For comparison, data was normalized to the maximum in each season; ILI was adjusted by a factor of 10. **Results:** For both seasons, the percentage of patients seen with ILI showed a bi-modal distribution with peaks occurring in weeks 52 and 12 during 2005-06, and weeks 52 and 11 during 2006-07. For each season, influenza activity peaked late in the season, at weeks 8 and 11, respectively. RSV activity peaked early, at weeks 52 and 1, respectively. PIV and ADV activity both peaked outside of the influenza season. **Conclusions:** During the past two seasons, influenza activity correlated with the late peak of ILI activity; RSV correlated with the early peak. RSV disease is a possible explanation for increased ILI activity in the absence of influenza activity. Further study is needed to determine the true impact of RSV disease on ILI-related morbidity and to design and implement RSV prevention efforts.

Board 249. Knowledge, Attitudes, and Practices About Influenza Control Practices Among Hispanics in San Diego County, California – 2006

J. Bethel[1], S. Waterman[1], M. Ginsberg[2];

[1]Centers for Disease Control and Prevention, San Diego, CA, [2]San Diego County Health and Human Services Agency, Community Epidemiology Branch, San Diego, CA.

Background: Each year, more than 200,000 people are hospitalized and roughly 36,000 people die from complications of influenza infection. According to the Advisory Committee on Immunization Practices, an influenza vaccination is the most effective method to avoid influenza virus infection and its potential serious complications. However, the 2003 National Health Interview Survey (NHIS) reported that significantly fewer Hispanics aged ≥65 years (45.4%; 95% CI ±5.2) received an influenza vaccination in the preceding 12 months than non-Hispanic whites in the same age group (68.7%; 95% CI ±1.5). **Methods**: We assessed knowledge,

attitudes, and practices (KAP) about influenza control practices among Hispanics in San Diego County (SDC), California. We used a multistage cluster sampling scheme to administer an in-person KAP survey to 226 Hispanics over 18 years of age in three regions of SDC.**Results**: Nearly 80% of the respondents were foreign-born, and, of these, 85.5% had lived in the United States for more than 5 years. Nearly 89% of the study population was aware of the influenza vaccine, with women having a greater awareness than men (96.0% versus 75.3%, p=0.003). Among the respondents who had heard of the influenza vaccine, 42.0% received an influenza vaccination in their lifetime, and, of these, 21.5% received an influenza vaccination in the preceding 12 months. Influenza vaccination rates in the preceding 12 months varied by age and gender. Specifically, 51.6% of Hispanics over 65 years of age received an influenza vaccination in the preceding 12 months compared with 23.1%, 10.1%, and 18.8% of respondents in the 18-29, 30-44, and 45-64 year age groups (p=0.002), respectively. Overall, 26.5% of Hispanic men and 11.8% of Hispanic women (p=0.034) received an influenza vaccination in the preceding 12 months.**Conclusions**: Influenza vaccination rates among Hispanics in the current survey were similar to rates among Hispanics reported in the 2003 NHIS and lower than the national average. Our survey found that over 85% of the respondents preferred the survey in Spanish and, therefore, educational and outreach efforts to the Hispanic community about influenza control practices need to be culturally competent and should also address the differences in influenza awareness and practices between gender and age groups.

Board 250. Sentinel Surveillance for Influenza in Kenya

M. A. Katz[1], P. Muthoka[2], R. Kalani[2], J. Musembi[1], L. Mayieka[1], G. Kikwai[1], D. Kinyanjui[1], N. Charles[2], W. Ochieng[3], W. Bulimo[4], K. Njenga[1], R. F. Breiman[1];

[1]International Emerging Infections Program, Centers for Disease Control and Prevention - Kenya, Nairobi, KENYA, [2]Division of Disease Surveillance and Response, Ministry of Health, Kenya, Nairobi, KENYA, [3]National Influenza Center, Kenya Medical Research Institute, Nairobi, KENYA, [4]United States Army Medical Research Unit-Kenya, Nairobi, KENYA.

Background: In resource-poor Sub-Saharan Africa, little surveillance for influenza exists, making the region ill-prepared to detect new influenza strains or clusters of human cases that could herald a pandemic. To address these gaps, the Kenya Ministry of Health (KMoH) and collaborators developed a national sentinel surveillance system for influenza. **Methods:** We targeted 11 sentinel sites in Kenya: 8 provincial hospitals, 2 refugee camp health facilities, and one private hospital. Health workers at each site were trained on case definitions for Influenza-Like Illness (ILI), Severe Acute Respiratory Illness (SARI), and Suspected AI. For each patient meeting the case definition for SARI, and for the first 3 patients daily with ILI, a questionnaire was administered and nasopharyngeal and oropharyngeal specimens were taken and sent to the National Influenza Center in Nairobi for testing by real time RT-PCR. **Results:** From October 5, 2006 through September 15, 2007, 2,804 samples from 10 sites were tested at the NIC; influenza was detected in 336 (12.0%) specimens, including 114 (4.1%) with influenza A and 222 (7.9%) with influenza B. A total of 1599 (57.0% of total) patients with SARI and 1104 (39.4%) patients with ILI were identified. No distinction was made between ILI and SARI for 101 patients (3.6%). Of all patients identified, 1,488 (53.1%) were <2 years old, and 2,377 (84.8%) were <5 years old. In all, 86.8% of Influenza A positive samples came from patients <5 years old. Two patients with SARI reported exposures to sick or dead birds; identification of these patients triggered joint KMoH/Ministry of Livestock investigations, and samples from both patients tested negative for influenza. **Conclusions:** A sentinel surveillance system for influenza in Kenya identified patients with SARI, ILI and suspected AI. In Africa, national sentinel surveillance systems can be implemented to assess influenza seasonality and disease burden, identify circulating influenza strains, and detect clusters of human cases of SARI that could signal the start of a pandemic.

Board 251. A Cross-Sectional Study on Risk Behaviors for Avian Influenza Human Infection - China, 2007

Y. Shi[1], H. Yu[2], L. Zhou[2], Q. Liao[2], L. Li[2], Z. Peng[2], H. Zhou[2], M. Ye[2];

[1]Chinese field epidemiology training program, Beijing, CHINA, [2]Chinese Center for Disease Control and Prevention, China, Beijing, CHINA.

Background: The current H5N1 avian influenza (AI) virus could trigger a pandemic if the virus should acquire the capability for human-to-human transmission. Most of the Chinese cases had no known history of direct contact with sick poultry. The objective of this study was to evaluate exposures and factors known to increase the risk for AI human infection in urban and rural areas, to help the government develop strategies for AI control and prevention. **Methods:** A cross-sectional study using a standardized questionnaire collected information on demographic characteristics, poultry exposure, and risky behaviors in an urban and a rural area where AI human infections had previously occurred. A two stage, probability-proportional-to-size (PPS) sampling scheme was used in this study. **Results:** In total, 4950 residences (2058 urban and 2892 rural) were interviewed (response rate: 98%). In the urban area, 34% of the population had visited a wet market during the past year. For those who had visited a wet market, 80% of women had bought freshly slaughtered poultry, compared with 65% of men ($p<0.001$). Of those who had purchased freshly slaughtered poultry, 15% reportedly had frequent, direct contact with a live poultry. After touching a live poultry, 15% reported that they would touch their eyes or mouth "frequently" or "sometimes". In the rural area, 50% of the families raised poultry in their backyards, mostly small (median=7 birds) and free ranging (77%); 48% of the birds had been vaccinated with a poultry vaccine. On average, 24% the families had had 5 poultry deaths during the past year; however, only 1% of the families who had had a poultry death reported those deaths to local authorities. When asked how the dead poultry were disposed of, 5% of those interviewed said they would eat them, 44% would sell them or give them to others; 39% would burn or bury them. **Conclusions:** Visiting wet markets in urban areas and raising backyard poultry in rural areas are common. Many rural and urban residents are engaged in risky behaviors that could expose potentially them to the avian influenza virus.

Board 252. Preventing the Spread of Seasonal Flu: Measuring the Impact of a Voluntary Program on Influenza Immunization Coverage among Long Term Care Facility Residents and Employees

C. Person[1], J. Nadeau[2], J. Nicholas[1], C. Waters[1], B. Debra[1], L. Pollock[1], G. Johnson[1], L. McNutt[2], B. Wallace[1];

[1]New York State Department of Health, Albany, NY, [2]SUNY-University at Albany, School of Public Health, Rensselaer, NY.

Background: Annually, between 5-20% of the US population is infected with influenza. Over 200,000 individuals are hospitalized, a disproportionate number are over 65 and more likely to reside in long-term care facilities (LTCFs). On April 1, 2000, New York State enacted the Long-Term Care Resident and Employee Immunization Act for LTCFs, including nursing homes, adult day care facilities, and adult day health care programs. This law requires LTCFs to provide optional influenza vaccines to all residents and employees. In addition, LTCFs are required to report immunizations and immunization refusals to the New York State Department of

Health (NYSDOH) annually by May 1st of each influenza season. Without a mandate for immunization of healthcare workers and residents, there is a need to monitor trends in vaccination coverage rates and to determine whether the current law is sufficient to improve immunization coverage. **Methods**: Annual immunization report data from 2000-2006 was analyzed to identify trends in immunization coverage for employees and residents of NYS LTCFs. Site visits were made to LTCFs to provide educational resources on adult immunizations and methods for immunization coverage and reporting improvement. A facility's influenza vaccination coverage was defined as the proportion of eligible residents/employees of the facility who received influenza vaccination. **Results**: Immunization coverage levels for NYS LTCFs residents have neared the Healthy People 2010 objective of 90% for residents of chronic care facilities. The mean influenza vaccination coverage for residents reported in NYS LTCFs during 2000-2006 was 81.0% (Range: 67.8 - 87.7%). Immunization levels for employees fall far below that of residents. The mean LTCF influenza vaccination coverage for employees during 2000-2006 was only 37.4% (Range: 37.07 - 48.74%). Despite efforts to improve immunization coverage, there have been no major increases in immunization levels since 2000. **Conclusions**: Continued low influenza immunization coverage of LTCF employees is evidence that optional immunization programs have not been effective and that residents are continually put at risk. The results of this analysis will contribute objective data to assess the need for an influenza vaccine mandate for healthcare workers in LTCFs and other settings.

Board 253. Predominant Circulating Seasonal Influenza Strain May Predict Nosocomial Influenza Outbreak Severity - New York State, 2002-2007

C. L. Waters, P. Duncan, G. S. Johnson, J. K. Schaffzin;

New York State Department of Health, Albany, NY.

Background: Seasonal influenza severity and predominating viral subtype vary annually. The New York State Department of Health (NYSDOH) seasonal influenza surveillance system includes mandated nosocomial reporting that involves hospitals and long-term care facilities (LTCFs) reporting any single confirmed case of influenza. We compared the volume and severity of nosocomial reports with predominant viral subtype data to assess the consistency between the two. **Methods:** Official NYSDOH seasonal reports were used to identify predominant viral subtype. Nosocomial influenza reports for each of five seasons during 2002-2007 were analyzed for number of reports received, and per report number of patient/resident illnesses, hospitalizations, and deaths. Results were subjected to Student's t-test. **Results:** Influenza A(H1) predominated during the 2002-03 and 2006-07 seasons, Influenza A(H3N2) predominated during the 2003-04, 2004-05, and 2005-06 seasons. During 2002-03 and 2006-07, a mean 47 (range 24-71) nosocomial outbreaks were reported. Per report, there was an average of 11 patient/resident illnesses, 0.89 patient/resident hospitalizations, and 0.2 patient/resident deaths. During 2003-04, 2004-05, and 2005-06, a mean 287 (range 199-456) nosocomial outbreaks were reported. Per report, there was an average of 17 patient/resident illnesses, 1.4 patient/resident hospitalizations, and 0.3 patient/resident deaths. The differences of each measure between the influenza A(H1) and influenza A(H3N2) seasons were statistically significant ($p<0.001$). **Conclusions:** Seasonal variation in nosocomial reports correlates with viral subtype predominance. Nosocomial outbreak severity increased during seasons where influenza A(H3N2) predominated and decreased during seasons where influenza A(H1) predominated. Seasonal viral subtype predominance may predict volume and severity of nosocomial disease.

Laboratory Proficiency Testing/ Quality Assurance

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 254. Biological Enrichment of Low-Level Mycoplasma Contaminants Using Co-Cultivation with Permissive Cell Cultures

D. V. Volokhov, H. Kong, J. George, D. Chandler, C. Anderson, V. E. Chizhikov;

Center for Biologics Evaluation and Research, Food and Drug Administration, Rockville, MD.

Background: Mycoplasmas are reported to be frequent bacterial contaminants of primary and continuous cell lines. These contaminants have the potential to cause iatrogenic bacterial infections in immunocompromised as well as pediatric and geriatric patients. The current detection methods recommended by US FDA for *Mycoplasma* are tedious and time-consuming (28-30 days). Consequently, the development of new rapid mycoplasma testing methods is an important issue in human and veterinary vaccinology and medical biotechnology. **Methods:** Nine different mycoplasma species known to be common cell line contaminants and used in the study were obtained from ATCC. 80-95% confluent cell monolayers of MDBK, MDCK, Vero, HEK-293, HepG2, R9ab, EBTr, and WI-38 cells obtained from ATCC and High Five (*Trichoplusia ni*) insect cells from Invitrogen were infected with the mycoplasma species at concentrations ranging from 0.05 to 1 cfu/ml. The mycoplasma growth in cultured cells was monitored for up to 7 days post infection and detected using PCR to the 16S-23S ITS region and *rpoB* gene as well as MycoAlert® Mycoplasma Detection Kit (Lonza). **Results:** The results showed that among the tested mammalian cell lines, the MDCK cells provided most efficient enrichment of all nine *Mycoplasma* species used in the study. This cell line allowed for earliest detection of mycoplasma-specific products using PCR or MycoAlert detection assays. Moreover, seven day co-cultivation of any *Mycoplasma* species used in the study with MDCK cells followed by PCR or MycoAlert mycoplasma assays resulted in reliable detection of mycoplasma contamination at levels as low as 0.05-0.5 cfu/ml. The insect cells (High Five) were also tested and found to be able to support growth of most mycoplasma species with the exception of *M. hyorhinis* DBS1050. However, *Mycoplasma* growth in these cells was found to be temperature dependent and observed at temperature range from 35 to 37°C. **Conclusion:** Biological enrichment is a universal, simple and efficient way for to improve detection of low levels of mycoplasma contamination using PCR and biochemically-based methods.

Modeling

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 255. A SEIR Model for Assessing the Effects of School Dismissal during a Severe Seasonal Influenza Outbreak

M. Haber[1], X. Jin[2], D. Shay[2], P. Edelson[2], D. Fishbein[2], W. Thompson[2];

[1]Emory University, Atlanta, GA, [2]Centers for Disease Control and Prevention, Atlanta, GA.

Background: Previous modeling studies of school dismissal during an influenza pandemic have shown that school dismissals can reduce influenza-associated illnesses, hospitalizations and deaths. We modeled the effects of school dismissals during a severe seasonal influenza A(H3N2) epidemic on these outcomes. **Methods:** We adjusted the transmission rates of a recently published pandemic simulation model so that the resulting illness rates were similar to those observed during a severe influenza A(H3N2) epidemic in the U.S. For the unmitigated epidemic scenario, the rates of illness, hospitalizations, and deaths were 26%, 0.1%, and 0.02% respectively. The model assumes that individuals mix in households, day care centers, schools, nursing homes and in the community. In the model, when students are dismissed, students increase their contacts in their household and in the community. Unlike the previous model, we assumed day-care centers would remain open. There were no additional social distancing measures implemented in the model. **Results:** When the incidence of influenza in one school exceeded 3% and school dismissal was implemented for one week, influenza-associated illnesses, hospitalizations and deaths were reduced by 11%, 9% and 12% respectively. If schools dismissal was implemented for 2 weeks, the rates of influenza-associated illnesses, hospitalizations and deaths were reduced by 18%, 12% and 11%, respectively. When the incidence of influenza in one school exceeded 5%, the results were similar; illnesses, hospitalizations and deaths were reduced by 9%, 8% and 10% respectively. If students were dismissed for 2 weeks, influenza-associated illnesses, hospitalizations and deaths were reduced by 17%, 11% and 12%, respectively.**Conclusions:** These results suggest that in the absence of effective measures for social distancing, school dismissals during a severe seasonal epidemic would modestly reduce influenza-associated illnesses, hospitalizations and deaths.

Board 256. A Prediction Market for H5N1 Influenza

P. M. Polgreen[1], L. Madoff[2], G. Neumann[1], F. Nelson[1];

[1]University of Iowa, Iowa City, IA, [2]ProMED-mail, ISID, Harvard Medical School, Boston, MA.

Background: The pandemic potential of H5N1 influenza may be increasing, but the likelihood of that event, the timing and geographic route of spread are all unknown. Information about H5N1 does exist but it is disparate, geographically dispersed and often subjective, limiting the usefulness of traditional methods in the collection and interpretation of these data. Prediction markets have been successfully used to forecast future events with similar uncertainties in other fields. Here we adapt this new method to provide estimates of the likelihood of H5N1 influenza related events. **Methods:** Participants are given educational grants of approximately $100 with which to trade financial contracts. The future values of these contracts depend on the outcome of selected avian influenza watershed events regarding policy as well as numbers and locations of human and animal H5N1 cases. For example, one contract will be worth $1.00 if Phase 4 of the WHO-defined Pandemic Alert Period is declared by 7/1/08. After 7/1/08, it will cease trading and be replaced by a similar contract with a 1/1/09 target. Traders buy and sell contracts with one another at prices that depend on their beliefs about the likelihood of the underlying event. These prices can be interpreted as the consensus probabilities of event occurrence. **Results:** As of November 19, 2007, 260 ProMED-mail subscribers from more than 36 countries were trading in the market. Real time prices are displayed on our web site, http://fluprediction.uiowa.edu/fluhome/AvianFlu_Graphical.cfm. A sampling of predictions arising from the market as of November 19 includes: a 2% probability of a WHO Phase 4 announcement, an 81% probability of 350 or more human cases of H5N1 worldwide, a 19% probability of a human case in Hong Kong, a 12% probability of a human case in Singapore, and a 7% probability of a non-captive bird being infected in the Americas, all by January 1, 2008. The market predicts a 7% probability of a WHO Phase 4 announcement by July 2008. **Conclusions:** The probabilities generated by the market may help public health officials and health policy makers plan for the future and coordinate resources. While prediction markets will not replace existing avian influenza surveillance systems, we propose their use as a supplement to aggregate expert opinions quickly based on existing information.

Board 257. Using Geographic Information System (GIS) for Malaria Surveillance in a Township in the Brazilian Amazon Region, 2006

E. Macario, G. S. Dimech;

Field Epidemiology Training Program (EPISUS), Secretariat of Health Surveillance (SVS), Ministry of Health, Brasilia, BRAZIL.

Background: Malaria risk affects 40% of the population of over 100 countries. In Brazil in 2006, 545,415 cases of malaria were reported, 99.5% of them in the Amazon region. National surveillance is conducted by the Malaria Epidemiologic Surveillance Information System. We present a pilot of combining Geographic Information System and epidemiologic surveillance data for disease mapping, risk assessment, planning and outbreak detection. In this pilot we constructed a digital map of one town in the Amazon region with street plan with superimposition of spatial distribution of the principal epidemiologic indicators of malaria for 2003-2006. **Methods**: The study area was the township of Mâncio Lima, which has ecological, geographic and socioeconomic conditions similar to those of other Amazonian towns. It experienced a malaria outbreak at the time of the pilot study. We updated the cartographic base of existing roads using trail mapping in real time techniques with GPS Garmin 12XL, designed polygons of localities with software ArcView 3.2, and conducted spatial analysis of malaria cases reported between 2003 and 2006 using Terraview 3.1.4 software. **Results**: The updating of roads was carried out based on field sights and the design of localities was in accordance with local determination. The course of the malaria outbreak was observed in the township beginning in 2005 with its spatial distribution in localities. The importance of residential units in determining the risk of illness was demonstrated by means of analysis of autochthonous cases by location, and movement within the township, by means of flow mapping. **Conclusions**: The analysis of spatial epidemiologic indicators, using location as the smallest unit of aggregation of data allowed for spatial visualization of the area of greatest levels of autochthonous transmission. This helps control measures in an outbreak setting.

Board 258. A Modified Agent-Based Model for Assessing Effectiveness of Disease Surveillance for Detection of Acute Respiratory Outbreaks in Resource-Limited Settings

H. Burkom[1], J. Coberly[1], L. Ramac-Thomas[1], T. Philip[2], S. Happel Lewis[1], J. Chretien[2];

[1]JHU/APL, Laurel, MD, [2]Walter Reed Army Institute for Research, Global Emerging Infection System, Silver Spring, MD.

Background: This modeling effort will provide guidance for policy and planning decisions in the event of an epidemic of acute respiratory illness (ARI), particularly an outbreak with pandemic potential. A U.S. Department of Defense program is underway to investigate health surveillance in resource-poor settings and to evaluate the Early Warning Outbreak Reporting System (EWORS). This program has included several information-gathering trips, including a trip to Lao PDR in September, 2006. **Methods:** We are building a modified agent-based model to measure the spread of ARI in resource-poor countries. The initial implementation uses health and census data collected during the 2006 Lao visit and incorporates features of recently published agent-based modeling approaches. The model purposely includes only infected individuals and contacts, not the entire population. Model runs will be limited to outbreak stages before population behavior changes due to mass fear and emergency policy decisions. Modular software architecture was adopted for portability to similar settings. The final application is intended to be a stand-alone tool for examining the effectiveness of large-scale policy decisions such as travel restrictions or the installation of additional networked surveillance capability. **Results:** Parameters for the distributions of demographic characteristics for the population model were inferred from Lao census data. The resulting simulated populations are statistically similar to census table figures from 2006. Preliminary epidemic curves, before inclusion of the surveillance model, are plausible, and validation is underway. **Conclusions:** This effort is designed to help public health officials examine the effect of various interventions on the early course of an ARI outbreak and to inform a cost-benefit analysis of combinations of interventions that include surveillance capability, which has been lacking in similar models, and policy decisions. Information gathered by the EWORS International Working Group strongly indicates that realistic modeling of surveillance capability is essential for informative simulation of large-scale outbreak progression and for assessing effectiveness of countermeasures.

Board 259. Geographic Information System for the detection, risk stratification, and targeting of *Triatoma dimidiata* control in Guatemala

R. J. King[1], C. Cordon-Rosales[2], J. Cox[3], S. Brooker[3], E. M. Dotson[1], R. A. Wirtz[1], C. R. Davies[3];

[1]CDC/NCZVED/DPD, Atlanta, GA, [2]CDC-CAP/UVG, Guatemala City, GUATEMALA, [3]LSHTM, London, UNITED KINGDOM.

Background: Control of Chagas disease depends on the elimination and reduction of vector populations. The Central American Initiative was launched in 1997 and aims to interrupt Chagas transmission by 2010, reducing household infestations of *Triatoma dimidiata* to 5% and eliminating household infestations of *Rhodnius prolixus* through targeted surveillance and control. Here we present results for the prediction of *T. dimidiata* infestation in Guatemala prior to residual insecticide treatment. **Methods:** From 2000 - 2003, georeferenced *T. dimidiata* village infestation indices were measured pre-spray in 3,620 villages in 101 municipalities within nine departments. Outcome data were overlaid with candidate environmental and socioeconomic predictor variables in a GIS. The data were extracted and analyzed. Univariate logistic regression models for each explanatory variable were fitted and compared. Significant covariates were used to construct a multivariate logistic regression model to predict risk of *T. dimidiata* infestation in Guatemala. Validation of the multivariate model was performed by randomly selecting half the data set to construct the model and half the data set to test the model. Measures directly related to control decisions were derived and risk maps were generated. **Results:** *T. dimidiata* was present in all departments surveyed. Dispersion ranged from 25.61% to 69.30%, and infestation ranged from 3.81% to 13.06%. Twenty-four explanatory variables were selected by univariate analysis for inclusion in the multivariate model. Agreement between observed and predicted data sets was good. Diagnostic statistics of model accuracy were calculated and indicate that the multivariate model predictions are significantly better than chance. Predictions from the multivariate model were used to construct a risk map of *T. dimidiata* infestation in Guatemala. **Conclusions:** Analyses of preliminary data indicate that *T. dimidiata* control at the 5% threshold is possible with sustained vigilance. The targeting of control and surveillance activities to high risk areas and regions of reinfestation are needed. The GIS based predictive model presented here will aid in the targeting *T. dimidiata* control in Guatemala.

Board 260. Accessing and Utilizing Remote Sensing Data for Vectorborne Infectious Diseases Surveillance and Modeling

R. Kiang, F. Adimi, S. Kempler;

NASA Goddard Space Flight Center, Greenbelt, MD.

Background: The transmission of vectorborne infectious diseases is often influenced by environmental, meteorological and climatic parameters, because the vector life cycle depends on these factors. For example, the geophysical parameters relevant to malaria transmission include precipitation, surface temperature, humidity, elevation, and vegetation type. Because these parameters are routinely measured by satellites, remote sensing is an important technologic tool for predicting, preventing, and containing a number of vectorborne infectious diseases, such as malaria, dengue, West Nile virus, etc. **Methods:** A variety of NASA remote sensing data can be used for modeling vectorborne infectious disease transmission. We will discuss both the well known and less known remote sensing data, including Landsat, AVHRR (Advanced Very High Resolution Radiometer), MODIS (Moderate Resolution Imaging Spectroradiometer), TRMM (Tropical Rainfall Measuring Mission), ASTER (Advanced Spaceborne Thermal Emission and Reflection Radiometer), EO-1 (Earth Observing One) ALI (Advanced Land Imager), and SIESIP (Seasonal to Interannual Earth Science Information Partner) dataset. Giovanni is a Web-based application developed by the NASA Goddard Earth Sciences Data and Information Services Center. It provides a simple and intuitive way to visualize, analyze, and access vast amounts of Earth science remote sensing data. After remote sensing data is obtained, a variety of techniques, including generalized linear models and artificial intelligence oriented methods, can be used to model the dependency of disease transmission on these parameters. **Results:** The processes of accessing, visualizing and utilizing precipitation data using Giovanni, and acquiring other data at additional websites are illustrated. Malaria incidence time series for some parts of Thailand and Indonesia are used to demonstrate that malaria incidences are reasonably well modeled with generalized linear models and artificial intelligence based techniques. **Conclusions:** Remote sensing data relevant to the transmission of vectorborne infectious diseases can be conveniently accessed at NASA and some other websites. These data are useful for vectorborne infectious disease surveillance and modeling.

Board 261. Detection of Influenza Positive Cases Using Laboratory Databases in the Military Health Care Setting.

K. Otero-Fisher, G. Kubiak, A. Riegodedios, T. Hines;

Navy Environmental Health Center, Portsmouth, VA.

Background: EpiData Center pursued the development of a Department of Defense (DOD) Pandemic Influenza surveillance model based on Health Level 7 (HL7) laboratory results. The military population is susceptible to respiratory illnesses due to close living quarters and exposures during operations. Influenza outbreaks may significantly impact military force readiness. Application of HL7 data to surveillance is unprecedented in DOD. The benefit of using laboratory data versus clinical encounter data is the ability to identify cases where virus was isolated/detected. **Methods**: Text fields in the HL7 Chemistry and Microbiology data from the Military Health System, which include patient and clinic information, were queried for Orthomyxo influenza. Data were validated for content and structure. Influenza tests and results were coded in SPSS syntax. Results were stratified by test method, region, and military status. Graphs were created to describe the patterns in testing and positive test results. The methods were developed using Department of the Navy (DON) data for influenza seasons 2004-2005 and 2005-2006. Methods were validated and refined using DOD data for the 2006-2007 season. **Results**: The structure of HL7 allowed for accurate identification of positive laboratory results, including minimal changes in laboratory reporting methods over time. Rapid and Polymerase Chain Reaction testing results showed an added value due to the timeliness of the procedures, as opposed to culture results. The positive case distribution during each influenza season had characteristics of a typical influenza season and related well to nationwide weekly reports of sentinel influenza surveillance (CDC). **Conclusions**: Laboratory positive influenza results enhance surveillance by using timely data from existing processes. Finalized methods are currently applied to active surveillance of the military population. Deviations from the expected distribution are identified in a timely matter, and provide an opportunity for intervention. Methods and results can be used to supplement encounter data, as well as pharmacy and radiology records, for Pandemic Influenza surveillance to provide a comprehensive disease model.

Board 262. Stochastic model of HPAI spread among commercial poultry operations in Georgia

F. C. Dorea[1], A. R. Vieira[2], C. Hofacre[1], D. J. Cole[3];

[1]University of Georgia, Athens, GA, [2]National Food Institute, Søborg, DENMARK, [3]Division of Public Health, Atlanta, GA.

Background: Outbreaks of avian influenza in the commercial poultry industry are associated with mass culling of birds and significant economic losses. Rapid detection of infected flocks is critical to limiting the financial impact of avian influenza outbreaks, but poor knowledge of the most likely mechanism of inter-farm spread limits the success of surveillance efforts early in the outbreak. In 2005 a survey of poultry growers in two Georgia counties assessed the number and type of farm visitors in the previous 7 days, and the probability of bird contact of each visitor. The results of this survey were used to model the risk of farm infection with avian influenza associated with human movement between farms. **Methods:** A compartmental epidemic (SEIR) model was used to estimate the time to grower detection of infection following the introduction of a highly pathogenic avian influenza (HPAI) virus. Using the results of the on farm epidemic model, off farm spread of disease was stochastically modeled for the time period between disease introduction and the estimated day of grower detection of infection. Off farm spread of influenza was based upon the probability distributions of the following: the daily likelihood of each farm visitor, the risk that the visit was associated infectious material contact, and the daily number of farms visited by each visitor. **Results:** The results of the on farm model estimated that the introduction of HPAI virus strains into commercial poultry will likely be detected by the grower within 5 days. The off-farm disease spread model estimated the number of farms potentially infected by the index farm in the days prior to grower detection ranged from 0-5, depending upon the density of susceptible farms in the county. **Conclusions:** According to this stochastic model of HPAI spread, a sudden introduction of HPAI virus may take up to 5 days to be detected by the poultry grower. During this time the movement of people between farms plays a major role in the off-farm spread. The number of exposed farms was most influenced by the relative frequencies of different farm visitors and the probability of contact with infectious materials while on the farm. The likelihood that the exposed (contact) farms become infected is highly dependent upon the attention to biosecurity.

Nosocomial Infections

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 263. Endophthalmitis Outbreak Due To *Pseudomonas Aeruginosa* Infection After Ophthalmic Surgery - Roraima State, Brazil, 2006

J. R. Melo, Sr.[1], R. Benevides[1], D. Santos[2], V. Machado[1], W. Araujo, Sr.[3], S. Gomes[1], M. Pereira[4], C. Meneses[5], L. Daufenbach[6];

[1]National Agency for Sanitary Surveillance (ANVISA), Ministry of Health, Brasília, BRAZIL, [2]Ministry of Health, Brasília, BRAZIL, [3]Ministry of Health - FETP Brazil, Brasília, BRAZIL, [4]State Health Secretariat, Brazil, Roraima, BRAZIL, [5]State Health Secretariat, Roraima, BRAZIL, [6]Health Surveillance Secretariat (SVS), Ministry of Health -Brazil, Brasília, BRAZIL.

Background: Endophthalmitis an infection of the ocular cavity and its adjacent structures, may cause vision loss. In July 2006, an outbreak of endophthalmitis following ophthalmic surgery occurred at one clinic in Roraima State, Brazil. We conducted an investigation to identify risk factors and initiate control measures **Methods**: A retrospective cohort study was conducted in the clinic to identify persons with endophthalmitis (at least one or more of these following symptoms: eye discharge, redness, blurred vision, pain and worsening vision after ophthalmic surgery) during June 1st-July 24th, 2006. Products and medications used during surgeries and biological samples from professionals and patients were tested to identify bacterial contamination **Results**: We reviewed 91 (82%) charts of 115 ophthalmic surgery patients during the study period. Six (7%) had endophthalmitis 14 to 48 hours after cataract (n=5) or glaucoma surgery (n=1), and needed vitrectomy (n=6). The median age of case-patients was 61 (range: 54-77) years; 50% were male. Individuals who had surgery on July 19th or July 24th had higher risk of endophthalmitis compared to individuals who had surgery on other days, with respective relative risk (95% confidence intervals) of 21.7(6.0-76.0) and 29.0(10.0-89.0). Endophthalmitis was not associated with any medication or medical staff. *Pseudomonas aeruginosa* was identified in all case-patients and in one staff member who administered the eyedrops before surgery. Numerous sanitary violations were observed in the clinic.**Conclusions**: Following suspension of ophthalmic surgeries in the clinic and education the outbreak subsided. Although the primary source of infection was not identified, failure to follow infection control practices probably contributed to the outbreak. We recommended using universal precautions, monitoring infections after surgery

routinely and enacting standard guidelines for hospital infection prevention and control.

Board 264. 30-Day and 180-Day Case Fatality Rates among Invasive Methicillin-Resistant *Staphylococcus aureus* Patients (Tennessee, 2004-2007)

K. R. Glenn, M. A. Kainer;

Tennessee Department of Health, Nashville, TN.

Background: Tennessee had the second highest incidence of invasive MRSA (I-MRSA) of 10 EIP study sites in 2005, with an incidence of 53 per 100,000. The national in-hospital case-fatality was 17.8%. U.S. in-hospital mortality rate from I-MRSA was 6.3 per 100,000. We wanted to assess the 30-day and 180-day crude case-fatality (CFR) and mortality rates of I-MRSA and determine factors associated with death. **Methods:** Vital statistics data was available up to Oct. 31, 2007. We used data from the Active Bacterial Core (ABC) surveillance component of the Emerging Infections Program in Davidson County. Cases from Oct. 2004-Jul. 2007 were included for 30-day CFR/mortality rates. Cases from Oct. 2004-Apr. 2007 were included to determine 180-day CFR/mortality rates. We reviewed Tennessee vital statistic data to determine patient outcomes; we matched by name and birthdate. We calculated the number of days between the initial MRSA-positive culture and date of death recorded on death certificates for each matched case to determine the numerator for the 30- and 180-day CFR/mortality rates. **Results:** I-MRSA rates for 2004-2007 were 59.1 per 100,000. The 30-day I-MRSA mortality rate was 7.3; 180-day I-MRSA mortality rate was 9.9 per 100,000. Fifty-four of 192 deaths (28%) were identified from vital statistic records alone (i.e., occurred following discharge). The overall 30- and 180-day CFRs were 13.2% and 19.1%, respectively. Blood stream infections (BSI) accounted for 85% of I-MRSA. Patients with MRSA BSI had higher 30- and 180-day crude CFRs compared to patients with non-BSI I-MRSA (14.7% vs. 4.5% [relative risk {RR}= 3.3, 95% CI: 1.5-7.3] and 21.4% vs. 5.7%, [RR= 3.8, 95% CI: 1.8-7.9], respectively). 30-day CFRs were not statistically significant among Blacks and Whites (12.6% vs. 14.3%, respectively). Healthcare-associated I-MRSA had a higher 30- and 180-day CFR compared to community-associated MRSA (14.4% vs. 9% [RR= 1.7, 95% CI: 1.0-2.9] and 21.0% vs. 12.7%, [RR= 1.7, 95% CI: 1.1- 2.8] respectively). **Conclusions:** MRSA BSI is associated with much higher CFR than other I-MRSA. Policy and practices aimed toward the reduction of I-MRSA rates in Tennessee are necessary to decrease the number of deaths annually associated with I-MRSA.

Board 265. A Pilot Surveillance Strategy for Hospital Acquired Respiratory Illness in Bangladesh

E. S. Gurley[1], R. u. Zaman[1], R. Sultana[1], M. Bell[2], A. Fry[2], A. Srinivasan[2], J. Jernigan[2], M. Hossain[1], M. Rahman[3], S. P. Luby[1];

[1]ICDDR,B, Dhaka, BANGLADESH, [2]CDC, Atlanta, GA, [3]IEDCR, Bangladesh Ministry of Health and Family Welfare, Dhaka, BANGLADESH.

Background: Poor infection control in developing country hospitals could accelerate the spread of emerging respiratory pathogens such as pandemic influenza. To better understand nosocomial transmission of respiratory illness in Bangladesh, we piloted a low-cost surveillance system for hospital acquired respiratory illness in three public tertiary care facilities. **Methods:** Surveillance was conducted in one adult male and one pediatric medicine ward from each hospital. One physician from each hospital collected data on the number of patients hospitalized >72 hours who experienced new onset of fever, cough, rhinorhea, difficult breathing, or diarrhea prior to discharge. A patient with new onset of any respiratory symptom after 72 hours of hospitalization was defined as a case of hospital acquired respiratory infection. Structured observations were also conducted on each ward to describe sanitary conditions and patient-caregiver interactions. Surveys to document antimicrobial use and caregiver to patient ratios were conducted. **Results:** Between March and September 2007 a total of 171 nosocomial infections (new onset of any symptom) were identified from 22,462 patient days of observation from patients admitted >72 hours for a rate of 8 infections per 1000 patient days; ward rates varied from 3-13 per 1000. Fifteen percent of these infections (26/171) presented with at least one respiratory symptom. Bed occupation rates were frequently >100% and the majority of patient care was provided by non-hospital staff; patient visitors and attendants averaged 1.4 per patient per day. Approximately 100% of patients were prescribed antibiotics and handwashing was rarely observed. **Conclusions:** Patients hospitalized in these wards frequently suffered from hospital acquired respiratory infections; however, the rates of infection were lower than expected considering the crowding and poor hygienic conditions. Limited interaction between staff and patients might contribute to lower rates, but risk factors for wider spread of disease exist. Our surveillance strategy produced estimated rates of nosocomial respiratory infections using existing hospital staff and resources.

Outbreak Investigation: Lab & Epi Response

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 266. Seven Years of Field Epidemiology Training in Brazil: A National Strategy to Strengthen National Surveillance and Outbreak Response

T. M. Lanzieri[1], E. D. dos Santos[1], W. N. Araújo[1], L. de Knegt[1], D. L. Hatch[2], J. Sobel[3];

[1]Field Epidemiology Training Program, Secretariat of Health Surveillance, MoH, Brasilia, BRAZIL, [2]independent, Atlanta, GA, [3]Division of Global Public Health Capacity Development, Coordinating Office for Global Health,Centers for Disease Control and Prevention, Atlanta, GA.

Background: Brazil, is the fifth largest country in the world with an estimated 2007 population of 189 million. To improve detection and response to disease outbreaks and other serious health events, the Ministry of Health established EPISUS, the Brazilian Field Epidemiology Training Program (FETP) in 2000. We describe main outcomes of the program during 2000-2007. **Methods**: We reviewed EPISUS records of outbreak investigations, surveillance system evaluations, research projects, and current professional status of graduates. **Results**: EPISUS, based on CDC's Epidemic Intelligence Service (EIS) model, is a two-year applied epidemiology training program with CDC technical assistance. Since August 2000, six classes were enrolled; 45 health professionals have graduated, and 23 are first- or second-year trainees. Of graduates, 15 (33%) are nurses, 12 (27%) veterinarians, 11 (24%) physicians and 7 (15%) pharmacists and biologists; all continue to work in public health. Trainees led investigations of 145 outbreaks in all regions of Brazil, caused by water and foodborne diseases (30%), vectorborne and zoonotic (22%), respiratory and vaccine-preventable (12%), adverse reactions to vaccines or pharmaceuticals (9%), hospital infections (7%), intoxications (7%) and others (13%). The average annual number of outbreak investigations was 13 during 2000-2002 and 21 during 2003-2007. A total of 70 evaluations of surveillance

systems were conducted with recommendations that led to important changes in the national surveillance practices. To date, one state-level epidemiology training program modeled on EPISUS has been established in Brazil, and three others are in development. **Conclusions**: EPISUS provided the Brazilian Ministry of Health and State Health Departments with unique workforce possessing skills and practical field experience for outbreak investigation and control. It has made important contributions to surveillance system improvements s and to increased application of analytical epidemiology in public health practice. The emerging network of state-level epidemiology training programs led by EPISUS will require extensive commitment of program graduates. Institutional support and adequate laboratory support for fieldwork are critical sustainability issues.

Board 267. Mumps Outbreak Among Military Populations in Lima and Ayacucho, Peru – 2007

M. Ramos[1], C. Mundaca[1], J. Ruiz[2], R. Cruz[3], C. Hickman[4], P. Rota[4], W. Bellini[4], M. Huaman[1], G. Soto[1], J. Quispe[1], A. Huaman[1], D. L. Blazes[1], J. M. Montgomery[1];

[1]US Naval Medical Research Center Detachment, Lima, PERU, [2]Direccion General de Epidemiologia del Ministerio de Salud, Peru, Lima, PERU, [3]Direccion de Salud del Ejercito (DISALE), Lima, PERU, [4]US Centers for Disease Control and Prevention, Atlanta, GA.

Background Rates of mumps virus infection have steadily declined over the years in developed countries, likely due to successful vaccination campaigns. In 2003, Peru introduced mumps vaccine into their ongoing measles-rubella vaccination strategy for children 12 months of age. Although it is generally believed that natural infection provides long-term immunity, antibodies to mumps may wane in adulthood. We detected two outbreaks of mumps among military personnel in two separate facilities in Peru, occurring between September 2006 and October 2007. Investigations were conducted to determine potential source and scope of the outbreaks, and determine risk factors for infection. **Methods** We conducted outbreak investigations and contact tracing within two separate Peruvian military settings. The first investigation consisted of both military and community contacts while the second was exclusively military personnel. Demographic, clinical and risk factor data were obtained from each case and contact. Each participant was also tested for evidence of IgM/G mumps specific antibodies by ELISA. RT-PCR and viral isolation was performed on symptomatic persons. **Results** Twenty-two cases and 154 contacts were identified from the first outbreak (Lima) and 8 cases and 106 contacts from the second (Ayacucho). Most frequent symptoms were fever, malaise, parotid swelling and temporary hearing loss. Mean age of cases and controls was 21 and 29 in Lima and Ayacucho, respectively. We observed clinical attack rates of 12.5% and 5.4% in Lima and Ayacuho, respectively. An average of 52% of the cases and only 0.65% of the contacts from both outbreaks were IgM positive, while >90% of the cases and 74% of contacts were IgG positive. To date, RT-PCR and viral isolation results have been negative. All cases and contacts from the first outbreak were born along the coast near to Lima, while 67% of cases and 40% of the contacts from the second outbreak were born in isolated jungle regions. **Conclusions** Our data suggest that young adults in Lima and surrounding areas of Peru are at high risk of infection with mumps, specifically within military populations. This may reflect either waning protective antibodies in adulthood, an influx of naïve individuals into these populations or both. Vaccination strategies should be evaluated among these populations.

Board 268. Dissemination of Community-Associated Methicillin-Resistant Staphylococcus aureus CMRSA7 (USA400) in Northern Saskatchewan, Canada

J. Irvine[1], B. Quinn[1], D. Stockdale[1], S. Woods[2], M. Nsugngu[2], P. Levett[3], R. McDonald[3], G. Golding[4], G. Horsman[3], M. Mulvey[4], the Northern Antibiotic Resistance Partnership;

[1]Population Health Unit, LaRonge, SK, CANADA, [2]Northern Inter-tribal Health Authority, Prince Albert, SK, CANADA, [3]Saskatchewan Disease Control Laboratory, Regina, SK, CANADA, [4]National Microbiology Laboratory, Winnipeg, MB, CANADA.

Background: Although the USA300 (CMRSA10) strain of community-associated methicillin-resistance (CA-MRSA) is rapidly disseminating across North America, some reports have described the emergence of CA-MRSA in northern Canadian communities. This study examines the incidence and molecular epidemiology of CA-MRSA in three of the most northerly Saskatchewan health regions. **Methods:** Surveillance was conducted over six years beginning in 2001 in three of the most northerly Saskatchewan health regions for all communities (on and off-reserve). Specimens from clinical indications were collected from remote community health centers and small rural hospitals (<35 beds) and MRSA positive cases were reported to the respective health authorities. Cases with asymptomatic carriage were excluded. In order to calculate total CA-MRSA rates of recurrence, cases occurring more than 2 months of the preceding episode and / or at a different site, were considered a recurrent episode. Pulsed-field gel electrophoresis (PFGE) of SmaI digested genomic DNA and RT-PCR for the mecA, nuc, and PVL-encoding genes was used to characterize a subset of the isolates. **Results:** A total of 1,927 MRSA events in 1,409 individuals were reported over the study period with 99% being community-associated. Fifty-six percent (N=783) of the individuals were < 20 years of age, while the majority of their cases (80.8%) were skin and soft tissue infections. The annual rate of CA-MRSA distinct individuals reported in these health regions increased from 9 per 10,000 population in 2001 (range to 4-10 per 10,000) to 169 per 10,000 in 2006 (range 43-233 per 10,000). An annual periodicity was observed with the highest number of cases being reported during the third quarter (July-September). Of the CA-MRSA cases, 15.1% of the individuals had at least one recurrent episode after 2 months. A subset of strains (N=192) were typed and 97.4% (N=187) were found to be Canadian PFGE epidemic type CMRSA7 (USA400) with 3 strains being CMRSA2 (USA100/800) and 2 strains being CMRSA10 (USA300). **Conclusions:** This report describes the rapid emergence of CA-MRSA in Northern Saskatchewan. The molecular epidemiology appears to be different from urban centers in southern Canada with the majority of cases being caused by CMRSA7 (USA400).

Surveillance: International and New Strategies

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 269. Health Seeking Patterns in a Population-Based Surveillance System Offering Free Health Care in Western Kenya

G. Bigogo[1], A. Audi[1], B. Aura[1], R. Breiman[2], D. Feikin[3];

[1]KEMRI/CDC, Kisumu, KENYA, [2]CDC, Nairobi, KENYA, [3]CDC, Kisumu, KENYA.

Background We are conducting population-based surveillance for pneumonia, diarrhea, febrile illness and jaundice in rural western Kenya. Information on health-seeking patterns of the population is needed to extrapolate our case detection data to more precisely define disease burden. **Methods** Between September 2006 and August 2007 data were collected during biweekly household visits, as well as clinic visits. At household visits, a structured questionnaire enquiring about illnesses in the last 2 weeks was administered using PDAs. Participants reporting illness were asked if and where they sought care. Care was free to participants at the study's referral health facility, Lwak Hospital, within 5 km of all participants' homes. For clinic visits, standardized sick-patient visit forms were filled by clinic staff, enquiring about health-care seeking and medications taken prior to coming to the referral clinic. **Results** At the household visits, 75% of participants reporting fever, 62% reporting cough/difficulty breathing and 72% reporting diarrhea, sought care outside the home. Only 17%, 16% and 18% of the respective proportions above sought care at Lwak. The most common sites for care seeking were drug-sellers/chemists (35%), clinics other than Lwak (21%) and shops (16%). Children were more likely than adults to visit Lwak or other health clinics when ill (OR=2.3, 95% CI, 1.25-4.27). Reasons that participants cited for not going to Lwak for care were that the distance was too far (65%), some diseases not treated at Lwak (11.2%), and dissatisfaction with care at Lwak (7%). Based on Lwak clinic data, 43% of both children and adults making sick visits sought prior care. Forty-four percent took medication before visiting Lwak, most often from a chemist/drug seller - 14% took an antimalarial and 20% took an antibiotic. **Conclusions**: Despite care being free at Lwak, a considerable proportion of sick participants did not seek care outside the home or sought care at other sites before visiting the designated referral facility. Other factors besides cost influence care seeking. Defining the burden of infectious diseases in this rural African setting might require extending surveillance beyond health facilities, or making extrapolations based on health utilization data.

Board 270. Can Current Disease Reporting Systems Capture All Animal Bites?

E. OConnell, G. Zhang, D. Rodriguez, A. Torrecilla, F. Leguen, M. Etienne, A. Llau;

Miami-Dade County Health Department, Miami, FL.

Background: The American Veterinary Medical Association estimates there are over 4.7 million animal bites annually from dogs alone. Miami-Dade County Health Department (MDCHD) uses several systems to monitor animal bites and this is the first study to compare them to ensure accuracy. **Methods**: The 2006 information used in this study came from four systems: 1) Miami-Dade Fire Rescue 911 Center, 2) emergency department (ED) chief complaints in the Electronic Surveillance System for the Early Notification of Community Based Epidemics (ESSENCE), 3) Post-exposure prophylaxis (PEP) recommendations in the Florida Department of Health surveillance system, Merlin and 4) MDCHD Animal Bite database which receives reports from hospitals, Animal Services, clinics and residents. **Results**: There were 452 calls to the 911 Center, 1,824 ED visits in ESSENCE and 1,345 reports to the MDCHD. Among 1,824 ED visits, 529 (29.0%) were children 0 - 14 years and 975 (53.5%) were Hispanic. The majority (85.3%) of bites were from dogs. Among 1,345 reports, 331 (24.6%) were among children 0 - 14 years and 1,108 (82.6%) were from dogs. Most (70.7%) were not from stray animals. 816 (60.7%) of them visited hospitals, 552 (41.0%) of 816 were reported by hospitals initially. In addition, 43 (3.2%) were recommended to take PEP; 14 (32.6%) of 43 cases were in Merlin. **Conclusions**: There were 1,272 hospital visits reported in ESSENCE but not reported to MDCHD and 29 cases in which PEP was recommended in the Animal Bite database but not in Merlin. Systematic quality control measures and an educational campaign among providers should be implemented to improve accuracy and timeliness of current animal bite surveillance.

Board 271. Global ID Surveillance and Diplomacy: Case Study in Strategic Local Investment

J. J. Sueker;

DoD Global Emerging Infections Surveillance and Response System, Silver Spring, MD.

Background: The U.S. Dept. of Defense (DoD) Global Emerging Infections System (GEIS) leverages the DoD's five overseas medical research labs (OSL) as platforms for global EID surveillance. Long-term local investment has built trust and transcended fluctuations in U.S.-Host Country relations, ensuring programmatic sustainability. Treated as a case study, what lessons these OSLs can offer the global ID surveillance community as funding and mandates for global surveillance increase? **Methods:** Research comprised three phases: 1) A literature review of OSL history, using published and internal documents; 2) In-depth, 1-2 hour personal interviews with OSL staff to identify factors critical to the long-term success of research and surveillance in Host Nations; 3) A literature review of the role of health in foreign policy, focused on the United States, Canada, and Australia. **Results:** DoD OSLs have consistently allocated resources for surveillance projects that only indirectly contribute to their mission by reducing global disease, increasing Host Nation response capacity and augmenting regional stability. By directly benefiting Host Nations - through training personnel in epidemiology and laboratory techniques, developing locally relevant surveillance systems and supporting outbreak responses - they build trust and enable the core research and surveillance missions. Literature research suggests that the foreign policy benefits of medicine are well-recognized, but efforts have prioritized infrastructure and clinical care projects, not surveillance or human capacity. **Conclusions:** The DoD OSL case study suggests that overseas investment in ID surveillance and human capacity can reap diplomatic benefits equal to, if not greater than, highly visible, short-term "medical diplomacy". This approach is sustainable, advancing global surveillance priorities in tandem with local capacity. Moreover, long-term surveillance investment may appear more sincere to Host Nation officials than conventional medical diplomacy. Recent publications assist in illustrating this point. By recognizing and emphasizing the foreign policy benefits of global EID surveillance, sponsor-nations can "earn their keep" while increasing their reach and effectiveness.

Board 272. WHO Global Salm-Surv: Worldwide *Salmonella* Distribution, 1995 – 2006

A. R. Vieira[1], S. M. Pires[1], H. C. Wegener[1], S. Karlsmose[1], D. M. Lo Fo Wong[2], WHO-GSS Members;

[1]National Food Institute, Technical University of Denmark, Mørkhøj, DENMARK, [2]Department of Food Safety, Zoonoses and Foodborne Diseases, World Health Organization, Geneva, SWITZERLAND.

Background: National foodborne disease surveillance programs can determine the magnitude of the public health problem posed by foodborne agents. Salmonellae are among the most common bacterial foodborne pathogens and several countries have well established programs for their monitoring and control. WHO Global Salm-Surv builds global capacity to conduct integrated, laboratory based surveillance, detection and respond to outbreaks of foodborne and other infectious enteric diseases through a number of activities and facilities. One such facility is the WHO GSS Country Databank (CDB). The CDB is a web-based databank where national reference laboratories report data on *Salmonella* serovars isolated from human and non-human sources. **Methods:** The 15 most commonly isolated serovars are annually reported by member institutions and analysis of this data provides a better understanding of the *Salmonella* worldwide distribution. Descriptive analysis of human and non-human data between 1995 and 2006, as available by November 2007, was performed and the top 15 human and non-human serovars from each continent was calculated. **Results:** Data from 76 countries comprising a total of 1,397,283 human and 173,889 non-human isolates were included in the analysis. Although 239 different serovars were reported, *S.* Enteritidis and *S.* Thyphimurium accounted for 78.8% of the all human isolates globally reported (40.4% of the non-human isolates). Other serovars, such as *S.* Colindale (Africa), *S.* Birkehead (Oceania) and *S.* Rubislaw (Americas) were reported in only one continent over the studied period. Associations between the top human and non-human reported serovars were observed in every region. **Conclusions:** This databank allows countries to follow trends of specific serovars both regionally and worldwide. The information contained in the databank is free and readily available for consultation both for members and the scientific community in general and provides an enhanced understanding of the global distribution of the most common serovars.

Board 273. *Campylobacter* Serology is Consistent with High Infection Pressure

P. Teunis[1], W. Ang[2], W. van Pelt[1], Y. van Duynhoven[1], J. Simonsen[3], J. van Eijkeren[1];

[1]RIVM, Bilthoven, THE NETHERLANDS, [2]VUMC, Amsterdam, THE NETHERLANDS, [3]SSI, Copenhagen, DENMARK.

Background: In cross--sectional serum samples from the general population in the Netherlands most sera appear positive for a recent or past Campylobacter infection, with high antibody levels in all but the youngest subjects. These high antibody titers can be interpreted as an indication of recent infection in many of the sampled subjects. A longitudinal study of antibody responses in patients with symptomatic Campylobacter infection shows a rapid increase to peak levels followed by a slow decline with a geometric mean halftime of approximately 1 year for IgG and IgM, and 1 month for IgA. Antibody peak levels and decay rates are highly variable among subjects, suggesting individual variation in immune response. **Methods:** Given the quantitative description of the longitudinal serological response, any observed cross-sectional antibody titer can be attributed a time from infection and, hence, be used to estimate incidence. This includes asymptomatic infections. Here a simplified model of the serological response is used to construct a marginal distribution of antibody titres that can be fitted to a cross--sectional population sample. This allows direct estimation of incidences, as well as simple tests for homogeneity across age, sex or regional categories, using likelihood ratios. Also, consistency of estimates from different antibody classes (IgG, IgM, IgA) can be tested. **Results:** The results show that Campylobacter infection is a frequent event, occurring possibly as often as once every month, in the Netherlands. Incidence estimates from the three antibody classes are consistent. **Conclusions:** High serum antibody levels, combined with rapid antibody decay can only indicate high incidence of infection. In adults, the majority of these infections is asymptomatic: hence most exposure-infection events of Campylobacter in the Netherlands remain undetected in standard epidemiological studies and laboratory surveillance.

Board 274. Assessing the Public Health Impact of the First Six Years of WHO Global Salm-Surv

K. Naik[1], A. J. Deokar[1], S. M. DeLong[2], L. Ran[3], T. Chalermchaikit[4], L. Kaftyreva[5], M. C. Fonkoua[6], M. Elmi[7], N. Binsztein[8], D. Lo Fo Wong[9], F. J. Angulo[1], and WHO Global Salm-Surv;

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Centers for Disease Control and Prevention and United States Veterans Administration, Atlanta, GA, [3]China Centers for Disease Control and Prevention, Beijing, CHINA, [4]Chulalongkorn University, Bangkok, THAILAND, [5]Pasteur Institute, St. Petersburg, RUSSIAN FEDERATION, [6]Centre Pasteur, Yaounde', CAMEROON, [7]World Health Organization Regional Office for the Eastern Mediterranean (EMRO), Cairo, EGYPT, [8]Instituto Nacional de Enfermedades Infecciosas-ANLIS "Carlos G Malbran", Buenos Aires, ARGENTINA, [9]World Health Organization, Geneva, SWITZERLAND.

Background: WHO Global Salm-Surv (WHO GSS) promotes integrated, laboratory-based foodborne disease surveillance and response and fosters inter-sectoral collaboration among human health, veterinary, and food-related disciplines through international training courses and activities. Thirty-one international training courses were conducted at eleven training sites from June 2000-August 2005. **Methods:** To assess the public health impact of WHO GSS Training Courses, nine training sites distributed a questionnaire in Chinese, English, French, Russian, or Spanish to participants who had attended courses prior to August 2005. Completed questionnaires were returned to the sites, who forwarded them to the WHO Collaborating Center for Surveillance, Epidemiology, and Control of *Salmonella* and Other Foodborne Diseases at the Centers for Disease Control and Prevention (CDC). Data were analyzed at CDC using Excel, SAS 9.1 and JMP 6 (SAS). **Results:** Surveys were returned by 238 course participants. Of 172 microbiologists who responded to the survey, 93 (54%) spent more than 50% of their time working on foodborne disease-related issues. One hundred and forty three (83%) reported that attending WHO GSS Training contributed to improved identification and isolation of *Salmonella* in their laboratories, 139 (81%) reported improved serotyping, and 128 (74%) reported improved antimicrobial susceptibility testing of *Salmonella*. Of 66 epidemiologists or environmental health officers who responded, 26 (39%) spent more than 25% of their time working on foodborne disease-related issues, 57 (86%) stated that attending WHO GSS Training contributed to improved foodborne disease surveillance, and 60 (91%) reported improved outbreak detection and investigation. **Conclusions:** WHO GSS is making a positive impact on National and Regional Laboratories and Ministries of Health, Agriculture, and the Environment through its training courses. The majority of WHO GSS Training Course Participants reported using the skills they acquired after the course. Additional assessments will be conducted to evaluate impact and to determine areas of growth for the future.

Board 275. Optimizing Influenza Sentinel Surveillance at the State Level

P. M. Polgreen[1], Z. Chen, Zunqiu[1], A. M. Segre[1], M. A. Pentella[2], G. Rushton[1];

[1]University of Iowa, Iowa City, IA, [2]The University Hygenic Laboratory, University of Iowa, Iowa City, IA.

Background: Influenza-like illness (ILI) data is collected in the US via an Influenza Sentinel Provider Surveillance Network. Members represent individual healthcare providers, group practices, emergency departments, and student-health clinics. In Iowa, members are recruited by the Iowa Department of Public Health (IDPH). Because participation is voluntary, locations of sentinel providers may not reflect optimal geographic placement. Location-allocation modeling has been used to find optimal locations for banks and retail stores. The purpose of this study was to use this approach to find the optimal location for sentinel providers in Iowa. **Methods:** The population in each zip code area (ZCTA) in Iowa was obtained from the 2000 US Census, the geographic location of hospitals in Iowa from the Natural Resources Geographic Information Systems Library, the location of existing sentinel members from IDPH for 2006-2007, and ZCTA to hospital distances were computed from their respective geocodes. Using a maximal coverage model (MCM), we maximized the number of persons in Iowa within 25 miles of N hospitals that were placed within a known population distribution. Starting with N=1, we found the optimal location for one sentinel provider. Holding each previously selected sentinel location, we increased N by 1 unit until we reached 148 (number of existing sites and possible new sites). This gave us the "best" possible locations for adding individual sentinels to a network of known size. Next we calculated the coverage derived from the existing 22 sentinel locations and then added additional sentinel locations using the MCM. **Results:** For the first optimal zip code location, the covered population was 17%, for two it was 29%, and additional locations provided more coverage but with diminishing marginal returns. Maximal coverage (99%) was achieved with 46 locations. The existing sentinel locations (22 sites) covered 66% of the population in Iowa. Using the MCM we could have achieved the same coverage with just 17 sites. Using 22 MCM sites would have covered over 81% of the population. **Conclusions:** The current system has sentinels in ZCTAs within 25 miles of 66% of the population in Iowa. Given scarce public-health resources in Iowa and other states, using a MCM can help optimally target recruitment efforts for new sentinel locations.

Baord 276. DoD Public Health Laboratory Services Internet-Accessible Databases

V. Kalasinsky[1], J. O. Tristan[1], S. L. Strausborger[1], L. M. Blubaugh[1], L. E. Burry[1], J. C. Gaydos[2], V. H. MacIntosh[2], D. S. Johnston[3], F. G. Mullick[1];

[1]Armed Forces Institute of Pathology, Washington, DC, [2]Global Emerging Infections Curveillance and Response System, Silver Spring, MD, [3]US Army Center for Health Promotion & Preventive Medicine, Aberdeen Proving Ground, MD.

Background: With continuing operations overseas, it is crucial for military personal to have immediate access to vital information regarding uncommon pathogenic and chemical agents. The Directory of Public Health Laboratory Services is a compendium of DoD laboratories that test for biological agents and infectious diseases. Developed by DoD Global Emerging Infections System (GEIS) in association with Armed Forces Institute of Pathology (AFIP), the database is a unique searching tool for locating DoD and other government laboratories worldwide to provide users with the ability to easily access laboratory testing information, such as testing availability, turn-around time, cost, and contact information. **Methods:** This online directory was written using Microsoft® SQL 2000 Database Server for the backend and the latest technologies for design of the web pages (ASP, Javascript, Visual Studio 2003). The system is currently migrating to Net Platform, Flash, and SQL Server 2005. Several levels of access exist, depending on the position of the registrant. **Results:** The Directory currently contains 179 biological agents, 45 international military laboratories, and 24 State Public Health Laboratories. Within the directory, each agent and disease has an information page providing details on symptoms, diagnoses, references, and participating laboratories that test for the specific agent or disease. A statistical breakdown of the agents and events searched has also been created to show the types of search inquiries, agents, diseases, and laboratories that are of greatest interest during any given month. Database usage is variable, but is often tied to concerns over reported outbreaks of infectious diseases. **Conclusions:** The directory serves a valuable function to the military and authorized federal agencies by providing rapid access to information on agents, diseases, and available laboratory tests. Its connection to the internet allows authorized users access from any location in the world. Based on our statistical breakdown of searches, we are currently investigating the potential of database utilization as a tool for epidemiologic surveillance. The Directory is also growing in collaboration with the State Public Health Laboratories as an avenue for influenza surveillance.

Board 277. Online News Monitoring for Global Infectious Disease Intelligence: Evaluation of the HealthMap System

J. S. Brownstein[1], C. C. Freifeld[2], B. Y. Reis[1], K. D. Mandl[3];

[1]Harvard Medical School, Boston, MA, [2]Children's Hosptial Boston, Boston, MA, [3]Harvard-MIT Division of Health Sciences and Technology, Boston, MA.

Background: While traditional means of surveillance by governments, multi-national agencies, and institutional networks assist in reporting and confirming infectious disease outbreaks, these formal sources of information are limited by their geographic coverage and timeliness of information flow. In contrast, Internet-based resources such as discussion sites and online news sources have become invaluable sources for a new wave of surveillance systems. For instance, the WHO relies on these data for the majority of their outbreak investigations. Despite widespread use of unstructured information, there has been little, if any, data evaluation. **Methods:** Our analysis is informed by evaluation of HealthMap.org, a freely accessible, automated system for real-time monitoring of online information about emerging diseases. In our evaluation, we used officially confirmed outbreaks obtained from WHO Outbreak News, available in the public domain, as a "gold standard" as well as ProMED mail reports. We measured detection characteristics of Google News reports for outbreaks over the 12-month period (October 1 2006-September 30 2007) in both English and Spanish. We apply standard evaluation metrics (volume, geography covered, diseases captured, timeliness, sensitivity and specificity). **Results:** HealthMap found 11,194 news reports of infectious disease outbreaks (a mean of 38.6 per day, 95% CI, 33.1 to 44.1) covering a 105 pathogens and 160 countries. Mean timeliness for news sources, defined as the time between detection by the surveillance source and report by the WHO, was 31 days. However, timeliness varied widely from 102 days earlier to 59 days after the WHO report. Sensitivity, defined as the proportion of WHO alerts detected by news data, was 88%. Compared to ProMED, news sources reported on outbreaks on average 6.5 days earlier but had a sensitivity of only 44%. Despite important biases, news sources are shown to be especially valuable for monitoring spatial and temporal patterns of larger scale epidemics, as well as seasonal or endemic diseases. **Conclusions:** Overall, we find that online news sources are a promising tool for surveillance, public health communication and intervention. Future work should be directed at modeling and data integration, including improving risk assessment.

Board 278. Use of oral rehydration solution among persons with diarrhea in rural Guatemala_2006

W. Arvelo[1], N. Padilla[1], O. Henao[2], L. Reyes[3], E. Mintz[2], K. Lindblade[2];

[1]Universidad del Valle, Guatemala City, GUATEMALA, [2]Centers for Disease Control and Prevention, Atlanta, GA, [3]Ministerio de Salud Publica y Asistencia Social, Guatemala City, GUATEMALA.

Background: Each year, approximately 4 billion cases of diarrhea and 1.9 million diarrhea-related deaths occur worldwide. Use of oral rehydration solution (ORS), introduced in the 1970's to decrease diarrheal morbidity and mortality, appears to be diminishing worldwide. In Guatemala, diarrhea is a leading cause of death, particularly among children. We conducted a community survey to determine use of ORS among persons with diarrhea in the Department of Santa Rosa, Guatemala, and describe behaviors related to treatment of diarrhea. **Methods:** We used a stratified, two-stage cluster sampling scheme with probability proportional to size to select 1,200 households from 60 populated areas. Household members were interviewed using a standardized questionnaire. An episode of diarrhea was defined as ≥3 loose stools in a 24-hour period reported during the 30 days before the interview; severe diarrhea included signs of dehydration. Odds ratios (OR) and 95% confidence intervals (CI) were calculated. **Results:** From October through December, 2006, we surveyed 5,356 persons from 1,116 households; 403 (8%) persons reported diarrhea during the previous month. Among these, 357 (89%) received or obtained treatment for their illness; 68 (19%) had an antibiotic and 49 (7%) had ORS. Sixteen (30%) children <5 years old with severe diarrhea were treated with ORS. When compared with person who did not seek health care in a government clinic (n=18, 19%), patients who visited a government clinic (n=31, 10%) were more likely to take ORS (OR 2.1; 95% CI 1.2 - 4.1). There was no significant association between ORS use and socioeconomic status or whether the patient lived in a rural or urban area. **Conclusions:** In Santa Rosa, less than a third of young children with severe diarrhea received ORS. Persons were more likely to be treated with ORS if they were evaluated at a government clinic. Prevention strategies to reduce future diarrheal morbidity and mortality may include educating families and other sources of care, such as pharmacies and shops, about the importance and proper use of ORS.

Vector-Borne Diseases

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 279. Insecticide Treated Mud as a Means of Malaria Control

B. Licitra[1], R. Beach[2], L. Quick[2], T. Burkot[2], J. Gimnig[2], J. Roberts[2];

[1]Association of Public Health Laboratories / Centers for Disease Control & Prevention, Atlanta, GA, [2]Centers for Disease Control & Prevention, Atlanta, GA.

Background: Malaria is transmitted in Africa by members of the *An. gambiae* and *An. funestus* complexes. These are efficient vectors as their ecological niche includes resting inside houses. Control of these vectors is by indoor residual spraying (IRS) and the use of insecticide treated bed nets. However, many people who live in mud dwellings re-plaster the walls of their homes by smearing them with a fresh layer of mud several times a year. This presents a problem in areas where IRS is the primary means of malaria/vector control since the insecticide is covered by a fresh layer of untreated mud. One potential solution to this problem is to treat the mud used to re-plaster the walls with insecticide. This study aimed to determine if insecticide treated mud for re-plastering or "smart mud" is a feasible means of vector/malaria control in communities where mud dwellings are common. **Methods:** Varying concentrations of cypermethrin treated clay were created: 1(0.03g/m^2) or 1 times (1X) the concentration of cypermethrin recommended by WHO for IRS, 2.5(0.03g/m^2) or 2.5X, and 5(0.03g/m^2) or 5X. Untreated clay served as a control. The WHO cone bioassay was used bi-weekly to assess the biological activity and persistence of the insecticide treatments through 1 hour knock down (KD) and 24 hour mortality measurements of susceptible *An. gambiae* females. **Results:** Initially, clay smeared with 5 times (5X) the amount of insecticide recommended for IRS yielded significantly higher KD (100% ± 0%) than untreated mud (33% ± 27%) or mud smeared with the level recommended for IRS (1X) (86% ± 11%). Similarly, a significantly higher mortality rate (100% ± 0%) was noted in the 5X group compared with the untreated (26% ± 18%) and 1X (36% ± 15%) group. High mortality in the 5X trial persisted for 0, 2, and 4 weeks post-treatment, while KD remained significantly greater in the 5X treatment group for weeks 0, 2, 4, and 6. **Conclusions:** Insecticide treated mud, or "smart mud" is capable of causing KD and mortality in susceptible mosquitoes. A more thorough study is needed to identify longer lasting insecticide formulations and to assess the concentration of insecticide needed to provide mosquito control for 3-6 months, the estimated length of time between re-plastering.

Board 280. "Dengue Fever with Complications," An Intermediate Reporting Category Between Dengue Fever and Dengue Hemorrhagic Fever Used in the Brazilian National Dengue Surveillance System: Case Characteristics and Classification issues

M. O. Mendes[1], A. C. Simplicio[1], G. E. Coelho[1], J. B. Siqueira, Jr.[2];

[1]MoH BRAZIL, Brasília, BRAZIL, [2]Federal University of Goiás State, Goiânia, BRAZIL.

Background: More than 3 million cases of Dengue Fever (DF) have been reported in Brazil in the last 20 years. The Brazilian Dengue Suveillance System (BDSS) adopts the World Health Organization (WHO) case definitions for DF and Dengue Hemorrhagic Fever (DHF). However, several severe cases do not fulfill the DHF case definition and an intermediate category denominated "DF with Complications" (DFC) is also currently adopted. **Methods:** We characterized reported cases of DFC using the surveillance system database from 2000 to 2006 and attempted to estimate the proportion of DFC cases that would fulfill DHF criteria. Analysis was performed using Epinfo 6.04d. **Results:** 12,585 cases of DFC were reported between 2000 and 2006, with 3,075 (31%) hospitalizations and 179 (1.4%) deaths. The highest number of cases (4,591) was reported in 2002, during the largest recorded epidemic in Brazil. The most frequent symptoms of DFC were: fever (96%), headache (91%), myalgia (85%) and retro-orbital pain (69%). Among warning or alert signs, 28% had abdominal pain, 0.5% had cardiopulmonary dysfunction, myocarditis, 2%; neurologic manifestation, 5%, painful hepatomegaly, and 11% had hypotension. During this time the average mortality rate was 5.3% for DHF and 1.4% for DFC. Among DFC cases, 79 (0.6%) met the DHF case-definition and were therefore misclassified. Additionally, reporting form fields were left blank in a subset of cases, making it impossible to determine whether cases fulfilled the criteria for DHF: 95 cases (0.8%) would have met DHF criteria but lacked data on a confirmatory test for dengue (serology or isolation); 53 (0.4%) cases would have met DHF criteria but lacked data on hemorrhagic manifestations; 58 (0.5%) cases would have met are all DHF criteria but lacked data on thrombocytopenia; 539 (4.3%) cases would have met all DHF criteria but lacked data on presence of plasma leakage.

Most (93.5%) cases had missing information for 2 criteria needed to meet the DHF case-definition. **Conclusions:** Important variables on the DF reporting for were left blank, making it impossible to determine if a subset of DFC cases were misclassified DHF cases. Strategies must be developed to assure that clinicians properly evaluate suspected DF, DFC and DHF patients and complete all fields on reporting forms.

Board 282. Emergence of Autochthonous Cutaneous Leishmaniasis in Northeast Texas and Oklahoma

K. K. Bradley[1], J. Glowicz[2], C. P. McHugh[3], C. Clarke[1], J. Wright[4];

[1]Oklahoma State Dept of Health, Oklahoma City, OK, [2]Collin County Health Care Services, McKinney, TX, [3]U.S. Air Force, Brooks City-Base, TX, [4]Texas Department of State Health Services, Tyler, TX.

Background: Leishmaniasis is a vectorborne parasitic disease that has widespread distribution in many parts of the world, but is very rare in the United States with only 30 cases recorded since 1903. At least 20 different species of *Leishmania* have been associated with human disease; cutaneous, mucocutaneous, and visceral leishmaniasis are the clinical disease forms. Autochthonous cutaneous leishmaniasis (ACL) caused by *L. mexicana* has previously been identified in south Texas. *Lutzomyia anthophora*, a species of sand fly, is considered the probable vector. Three species of *Neotoma* have been found naturally infected with *L. mexicana* in the U.S. and are likely reservoir hosts. In May 2006, the Texas Department of Health Services and the Oklahoma State Department of Health initiated a joint investigation to explore four recently recognized cases of ACL. Previously, cases of ACL had not been reported in north Texas or Oklahoma nor had collections of *Lu. anthophora* been reported beyond southern Texas or Arizona. **Methods:** Epidemiologic investigation of four cases of ACL included review of medical records, additional laboratory testing to ascertain diagnosis, and case interviews. A field investigation was conducted to assess the peridomestic environment of each case; trapping for rodents and insects was done to determine the presence of a reservoir and vector. Climatologic data from the National Weather Service was analyzed for each case county of residence. **Results:** Confirmation of leishmaniasis was made by histopathology, parasitic culture, and/or PCR testing. Vector trapping in Collin County, Texas and McCurtain County, Oklahoma yielded collections of *Lu. anthophora*. Above average temperatures and below average rainfall were observed for the six-month period prior to the onset of each case. **Conclusions:** Recent identification of four human cases of ACL and collections of *Lu. anthophora* in north Texas and southeastern Oklahoma extends the endemic range of *L. mexicana* northward by several hundred miles. Extensive urbanization in north Texas and/or climate change resulting in above average temperatures and extended periods of drought are likely factors contributing to the geographical extension of this vectorborne disease. Expanded regional surveillance and educational outreach to clinicians is warranted.

Board 283. Epidemiology of Malaria and Vector Distributions in the Republic of Korea

T. A. Klein[1], H. Kim[1], W. Lee[2], L. M. Rueda[3], J. Jacobs[4], S. Chong[1], W. Sames[1], R. Moore[4], J. Pike[1], D. Foley[3], R. Wilkerson[3];

[1]18th Medical Command, APO, AE, [2]Korea Center for Disease Control and Prevention, Seoul, REPUBLIC OF KOREA, [3]Walter Reed Biosystematics Unit, Silver Spring, MD, [4]US Army Center for Health Promotion and Prevention, APO, AE.

Background: *Plasmodium vivax* reemerged in 1993 and increased exponentially among ROK military and civilians through 1998. With the implementation of a chemoprophylaxis program by the ROK military in 1997, malaria stabilized and then decreased through 2004 as the use of chemoprophylaxis increased, but steadily increased in 2005 through 2007. **Methods:** The number of malaria cases were documented through reports and epidemiological investigations of patients at the 121st CSH, and reports from the Army Medical Surveillance Activity (AMSA) and the Korea Center for Disease Control and Prevention. Adult mosquito surveillance was conducted at selected US military installations and mosquitoes analyzed for malaria circumsporozoite antigen by ELISA. Larval collections were conducted throughout the Korean Peninsula and larvae identified by PCR to species. **Results:** The highest densities of malaria are reported in the two northern most provinces, with lower numbers reported in the central and southern provinces. Most of the cases reported in the central and southern provinces are from veteran Soldiers previously assigned to malaria high-risk areas near the DMZ. Extensive larval and adult surveillance demonstrated that *An. sinensis sensu strictu* is the most commonly collected anopheline throughout the ROK, followed by *An. kleini* and *An. pullus*. *An. kleini* and *An. pullus*, occur in highest densities (often >40%) near the DMZ in malaria high-risk areas, but account for <5% of anophelines collected south of Seoul. *An. belenrae* larvae were collected frequently in some areas, but were infrequently collected in adult traps (New Jersey light traps and Mosquito Magnets®). *An. lesteri*, a primary malaria vector in China, was infrequently collected in both larval and adult collections throughout Korea. Data suggests that *An. pullus* and *An. kleini* are the primary vectors of vivax malaria in malaria high-risk areas near the DMZ rather than *An. sinensis s.s.* **Conclusions:** Malaria case distributions are highest near the DMZ where the highest densities of *An. kleini* and *An. pullus* occur. While evidence shows that *An. sinensis sensu strictu* can become infected with malaria, it has only been found with low cs antigen levels of <50 sporozoites, indicating that it is a poor vector, while *An. pullus* and *An. kleini* are the primary vectors.

Viral Hepatitis

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 284. Epidemiologic Profile of Hepatitis C Cases in Brazil, 2002-2006

K. B. Campos, G. M. Figueiredo;

Secretariat of Health Surveillance, Ministry of Health, Brasilia, BRAZIL.

Background: Heptatitis C infection results in chronic carriage, cirrhosis, liver failure and death. The Pan American Health Organization estimates that 3 million infected persons live in Brazil at this time, corresponding to infection of about 1.5% of the population. The National Program for Viral Hepatitities was created in 2002 to promote early diagnosis and improve prevention and control strategies. **Methods:** We analyzed reports of Hepatitis C from two surveillance systems: The National Reportable Health Event Surveillance System, and the National Mortality Surveillance System, for 2002-2006. **Results:** From 2002 to 2006, 66,462 confirmed cases of Hepatitis C were reported in Brazil (population: 187,000,000). Of these, 9.4% occurred in 2002, 14.7% in 2003, 23.6 % in 2004, 26.0% in 2005 and 26.3% in 2006. During this period, 6,303 deaths from Hepatitis C were reported. The highest national mortality rate from Hepatitis C occurred in 2005: 8.31/1,000,000 inhabitants. The regions with highest prevalence were the South (14.4/100,000) and the Southeast (9.8/100,000). The median age of infected persons was 43 years (range, 1 - >80 years), 62% were male, 73% were white, and 37% reported 4-7 years of schooling. The principal reported modes of transmission were: blood transfusion

(29%) and injection drug use (29%); however, in 48.6% of cases, no mode of transmission was reported. **Conclusions:** Between 2002 and 2006, an increase in the number of reported cases of Hepatitis C occurred in Brazil. Adult white males with elementary education are the most affected. Reported exposure through blood transfusions and injection drug use is high, providing a clear target for control and prevention efforts and strategies. Improved surveillance data and analysis will also assist in optimizing prevention efforts.

Board 285. Use of Viral Hepatitis Surveillance to Detect a Cluster of Hepatitis C Virus Infection - New York, 2007

K. E. Mulhern[1], L. Leuchner[2], E. M. Rocchio[1], G. R. Burstein[2], H. Lindstrom[2], G. Johnson[1], J. Schaffzin[1];

[1]New York State Department of Health, Center for Community Health, Division of Epidemiology, Bureau of Communicable Disease Control, Albany, NY, [2]New York State Erie County Department of Health, Buffalo, NY.

Background: In 2004, the New York State Department of Health (NYSDOH) and Centers for Disease Control and Prevention initiated the Enhanced Acute Hepatitis Surveillance Project to develop viral hepatitis surveillance demonstration projects including development for priority patient follow-up. This includes positive hepatitis C virus (HCV) lab reports for persons <30 years. In March 2007, a cluster of HCV cases among young intravenous drug users (IVDUs) was detected. **Methods:** Lab reports were reviewed weekly for positive HCV results for individuals <30 years. Clinical and risk factor information was obtained from patient providers. Patient interviews were conducted using a standardized instrument for 11 new cases. Detection of a space-time cluster of new HCV infections among persons <30 years led to a collaborative investigation and comprehensive response by the Erie County DOH and NYSDOH. **Results:** During November 2004-April 2007, 20 newly HCV-infected individuals <30 years residing in one Buffalo, New York, suburb were identified. Of interviewed case-patients, median age was 19 years (range 17-28), all were Caucasian and 73% were male. IVDU was identified as a risk factor for 91% of cases, 50% of whom named at least one member of the cluster as a needle-sharing partner. The collaborative response included community education and informational campaigns. Academic detailing was conducted in pediatric and family medicine offices. An outreach program was developed to offer HCV, HIV and STI screening. **Conclusions:** This investigation demonstrated the effectiveness of enhanced surveillance in detecting new HCV cases. Targeted surveillance can enable real-time cluster detection. The identification of this cluster, which was likely due to needle sharing among IVDUs, resulted in community-based efforts and created public awareness of HCV risk factors and transmission, and improved screening. Ability to understand the true burden of HCV and detect future clusters underscores the need for improved and consistent national hepatitis surveillance. Once established, this can estimate disease burden, measure response, facilitate research, and measure the effect of prevention efforts.

Board 286. Characterization of perinatal hepatitis B cases in California, 2000-2005

K. Winter, K. Harriman;

California Department of Public Health, Richmond, CA.

Background: Hepatitis B virus (HBV) may be transmitted from infected mothers to their infants. To reduce perinatal transmission, ACIP recommends that all women be tested prenatally for HBV infection and all infants be given HBV vaccine within 12 hours of birth. Infants born to infected mothers should receive hepatitis B immune globulin, complete the vaccine series and be tested for immunity. **Methods:** We examined perinatal HBV case report data and case management data of infants enrolled in the California Perinatal Hepatitis B Prevention Program (CA PHPP) for infants born January 1, 2000 through December 31, 2005. **Results:** 198 of 8,639 (2.3%) infants born in California during the study period who had post-vaccination serologic testing (PVST) for HBV immunity were found to be HBV-infected. Most (86.0%) had been treated appropriately; 24 (12.1%) were administered a late dose of HBV vaccine, 3 (1.5%) were not administered HBIG, and 1 did not receive the 3rd dose of HBV vaccine. Exposed infants enrolled in the CA PHPP who had PVST were more likely to be infected with HBV if they were born to a mother who was Vietnamese (OR 2.9) or Hmong (OR 2.3) and less likely to be infected if born to a Chinese mother (OR 0.78). **Conclusions:** Appropriate clinical management prevents most but not all cases of perinatal HBV infection. Certain ethnic groups may be at higher risk for perinatal HBV transmission. It is unclear whether women in ethnic groups associated with an increased risk of transmission have higher viral load, viral mutations or other biological explanations for the failure of infant post-exposure prophylaxis. Prenatal antiviral treatment may be warranted in selected women.

Zoonotic & Animal Diseases

Tuesday, March 18
12:00 PM – 6:00 PM
(authors present 5:00 PM – 6:00 PM)
Exhibit Hall

Board 287. Time to Classify Zoonoses

S. D. Pitlik;

Rabin Medical Center, Petah Tikvah, ISRAEL.

Background: Microbes involved in emerging zoonoses are invariably originated in species of wild animals such as birds, primates, bats, or rodents. In order to better understand the routes of transmission and inter-species barrier crossing, a simple classification scheme of these infections is urgently needed. The current lack of systematization results not uncommonly in misunderstandings by the general public and even by persons involved in public health activities, on the specific threat posed by a specific emerging infection. **Methods:** The proposed organizational system is based on three major assumptions: 1) the primordial reservoir of emerging microbes is always a wild-animal species 2) crossing of the species barrier may occur directly to humans or alternatively, use domestic animal/s as intermediate amplifiers, and 3) humans may be a dead end in the chain of transmission or as an alternative, sustained human to human transmission may occur. **Results:** The basic principles of the proposed classification system are as follows: An emerging infection is defined as belonging to the "type 1" subgroup when transmission of the involved microorganism takes place directly from the wild animal reservoir to humans without the involvement of a domestic animal amplifier. No sustained occurs between humans occurs in this subgroup. The "type 1 plus" subgoup implicates the occurrence of subsequent long chains of transmission between humans. On the other hand, an emerging disease is classified as "type 2" when the causative microorganism originating in wildlife infects humans only after being "amplified" by a domestic animal interface, but without the occurrence of human to human transmission. Similarly, if sustained human to human chains of transmission occur, the disease will be categorized as "type 2 plus". **Conclusions:** The proposed classification facilitates the understanding of the epidemiology of emerging zoonoses.

Board 288. *Lagos bat virus* in Kenya

I. V. Kuzmin[1], M. Niezgoda[1], R. Franka[1], B. Agwanda[2], W. Markotter[3], J. C. Beagley[4], O. Urazova[1], R. F. Breiman[5], C. E. Rupprecht[1];

[1]CDC, Atlanta, GA, [2]National Museum of Natural History, Nairobi, KENYA, [3]Unoversity of Pretoria, Pretoria, SOUTH AFRICA, [4]University of Georgia, Athens, GA, [5]CDC, Nairobi, KENYA.

Background Lagos bat virus (LBV) is one of the most devergent species of *Lyssavirus* genus, known by several isolates from Africa. Principal hosts of LBV are fruit bats, but circulation patterns are unknown. Modern rabies biologicals do not protect against LBV. We conducted surveillance for emerging viral infections in bats of Kenya, and LBV was one of the key targets. **Material** A pilot study was done during July - August, 2006, in 17 locations across Kenya. Typically, 10-20 bats of each species were collected from each available roost or mist-netted in foraging areas. In total, 291 bats of at least 27 species were collected. Based on serologic results of the 2006 study, 5 bat species (*Rousettus aegyptiacus*, *Eidolon helvum*, *Miniopterus africanus*, *M. natalensis*, *M. minor*) were selected as targets for additional extensive sampling. During June - July 2007, 747 bats of these species from the desired locations were sampled, together with 184 bats of other species. Bat brains were tested for the presence of lyssavirus antigen and virus isolation , oral swabs were tested by RT-PCR, and blood sera for LBV-neutralizing antibododies **Results** One isolate of LBV was obtained from tissues of a dead *E.helvum*. Phylogenetic analysis demonstrated that the virus belongs to the most pathogenic lineage of LBV, previously known by two isolates from Senegal and from Togo or Egypt (occasionally translocated to France). Serologic assay demonstrated a seroprevalence of LBV-neutralizing antibodies in fruit bats *R. aegyptiacus*, sampled in 4 available locations (n= 339, seroprevalence 17-50%) and in *E. helvum* available from 2 roosts (n=102, seroprevalence 40-67%). All roosts were located within or in close proximity to human settlements and accounted thousands of bats. In other bat species LBV-neutralizing VNAs were not detected. **Conclusions** This is the first report of a lyssavirus isolate in Kenya. A high seroprevelance suggests LBV is broadly distributed among abundant fruit bats. Several large roosts were identified in densely human populated areas raising public health concerns for increased public awareness of bats and the potential for lyssavirus infection.

Board 289. The Prevalence of Q Fever in the United States:Data from NHANES 2003-2004

A. D. Anderson[1], D. Kruszon-Moran[2], A. D. Loftis[1], G. M. McQuillan[2], W. L. Nicholson[1], R. A. Priestley[1], A. J. Candee[1], N. E. Patterson[1], R. F. Massung[1];

[1]CDC, NCZVED, Atlanta, GA, [2]CDC, NHANES, Atlanta, GA.

Background: Q fever is a zoonotic disease caused by the organism *Coxiella burnetii.* Transmission to humans usually occurs by inhaling dust or aerosols from infected animals. On average, approximately 79 cases of Q fever are reported in the United States each year to the CDC. However, because the disease is not notifiable in many states and many human infections are inapparent, little is known regarding the current incidence or geographical distribution and the true prevalence of the disease is unknown in the U.S. as nationwide prevalence studies have never been done. **Methods:** This study analyzed data and sera from the National Health and Nutritional Examination Survey (NHANES) 2003-2004 to estimate seroprevalence of Q fever in the United States. Serologic testing of 4,437 specimens from persons aged twenty years or older was performed to identify those ever infected with Q fever. An enzyme-linked immunosorbent assay (ELISA) was used to screen for IgG Phase II antibody seropositivity and any samples positive by ELISA were then tested by immunofluorescence antibody assay (IFA) in order to obtain endpoint titers for IgG to phase I and phase II antigens to *Coxiella burnetii*. The NHANES 2003-2004 questionnaire completed by subject participants will also be analyzed to determine Q fever seroprevalence differences related to demographics and other epidemiologic factors. **Results:** All serologic testing has been completed. Full analysis of serology results and the NHANES questionnaire are pending. **Conclusions:** Study results will determine exposure to Q fever and thus provide evidence of acute infection in the U.S. population. The data will help us to better understand the distribution and determinants of disease and be better prepared to detect and respond to both natural and deliberate outbreaks of Q fever. Also state and local health departments will be able to estimate background prevalence which will be invaluable when determining appropriate investigational resources for naturally occurring outbreaks.

Board 290. Assessing the Risk for Introduction of Rabies and Other Zoonoses via Importation of Dogs to the United States

J. Sinclair[1], M. Stock[2], J. Atwell[3], G. Galland[1], N. Marano[1], T. Drew[1], S. Blumensaadt[1];

[1]CDC, Atlanta, GA, [2]University of Pennyslvania College of Veterinary Medicine, Philadelphia, PA, [3]Auburn College of Veterinary Medicine, Auburn, AL.

Background: In the United States (U.S.), rabies is a reportable disease. The U.S. is free of canine rabies. The Centers for Disease Control and Prevention regulates the importation of dogs to control rabies. Importers of unvaccinated dogs are required to sign an agreement to confine the dog until adequate rabies vaccination has been obtained, plus 30 days. In addition to rabies, dogs have the potential to transmit approximately 59 zoonotic diseases. Anecdotally, there has been an upward trend in the number of dogs entering the U.S. The objective of this project was to analyze the data from confinement agreements to better assess the dynamics of U.S. dog importation and the risk to public health. **Methods**: Confinement agreements issued during calendar year 2006-2007 were collected. An initial subset of the data was analyzed for dogs that entered through the Chicago and Miami Quarantine Stations during January through August 2007. The total number of confinement agreements, number of dogs, countries of origin, breeds, and estimated market values were determined. **Results**: A total of 744 confinement agreements were analyzed, with at least 3,911 dogs entering through the two Quarantine Stations. In Miami, 1-31 dogs were listed per confinement agreement; in Chicago that range was 1-16 dogs. The leading countries of origin were Mexico, Colombia, Germany, and Peru. Preliminary market value estimate of the 744 dogs was in the range of $78,445 to $15,165,000, with a median of $7,621,722. **Conclusions**: A high volume of dogs is being imported into the U.S. The risk of introducing or amplifying zoonotic diseases is a possibility, as dogs come from countries where a variety of zoonotic diseases are endemic. Dog importation may have a much larger economic impact than originally expected. Ongoing analysis will be essential for future review of the current regulations, balancing economic pursuits, and protecting public health.

Vaccines & Vaccine-Preventable Diseases

Wednesday, March 19
12:00 PM – 1:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 291. An outbreak of severe community-associated methicillin-resistant *Staphylococcus aureus* in children in Vietnam following vaccination: Implications for infection control in immunization programs

J. M. Simmerman[1], T. C. Trang[2], A. Bentsi-Enchill[3], R. Brown[3], M. Counahan[3], T. v. Le[3], C. V. Bac[2], D. S. To[4], T. D. Nguyen[5], H. T. Tran[4], H. T. Ngo[6], C. Schultsz[6];

[1]CDC/NCID/Emerging Infections Program, Bangkok, THAILAND, [2]Pediatric Hospital, Ho Chi Minh City, VIET NAM, [3]World Health Organization, Ho Chi Minh City, VIET NAM, [4]Hospital for Tropical Diseases, Ho Chi Minh City, VIET NAM, [5]Preventive Medicine Cente, Ho Chi Minh City, VIET NAM, [6]Oxford University Clinical Research Unit, Hospital for Tropical Diseases, Ho Chi Minh City, VIET NAM.

Background: Infections with community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) are emerging worldwide; however outbreaks in Vietnam have not been previously reported. In May 2006 a cluster of severe CA-MRSA infections was reported in young children following immunization in outpatient clinics in southern Vietnam **Methods**: A field investigation was conducted immediately after serious adverse events following immunization (AEFI) were reported in public outpatient clinics in southern Vietnam. Clinical and epidemiological data were collected and infection control practices were reviewed. Wound, nasal or throat swab specimens were collected from all cases and healthcare workers (HCW). **Results**: We identified nine children from 5 to 17 months of age who presented to hospital with AEFI. These adverse events included toxic shock syndrome (3), severe necrotizing soft tissue infection (1), purulent abscesses (4) or high grade fever with a rash (6). Despite aggressive treatment, one child died and another experienced profound neurological sequelae. All cases were previously healthy and had received a vaccination in a single district of Ho Chi Minh City, Vietnam within a 12 day period. Eight children had been vaccinated by the same health care worker. No deficiencies in vaccine quality or storage practices were identified. Infection control practices were found to be inadequate. CA-MRSA was cultured in four children and from nasal and throat swabs obtained from the HCW. All strains were indistinguishable and carried the Panton-Valentine leukocidine (PVL), and the gene encoding staphylococcal enterotoxin B. **Conclusions**: We describe an outbreak of severe CA-MRSA infections in children transmitted by an asymptomatic, colonized HCW during routine immunization practice. In light of the severity of this outbreak and the increasing incidence of CA-MRSA infections worldwide, infection control guidelines for vaccination programs should be reviewed.

Board 292. Acute Asthma Exacerbation following Immunization with Live Attenuated Influenza Vaccine among U.S. Service Members during 2006-2007 Influenza Season

Z. Wang, A. Eick, S. Tobler;

AMSA, Silver Spring, MD.

Background: Influenza vaccination is recommended for asthmatics, because influenza infection can trigger asthma exacerbations. Among asthmatics, the trivalent inactivated influenza vaccine has been shown to be safe for use; however, the safety of the live attenuated influenza vaccine (LAIV) has not been extensively studied and is not currently recommended for use in this population. This analysis was conducted to assess the association between LAIV and asthma exacerbation among U.S. military service members with asthma. **Methods**: For the 2006-2007 influenza season (September 1, 2006 - April 30, 2007), we identified healthcare encounters that resulted in a diagnosis (ICD-9-CM of 493.02, 493.12, 493.22, 493.92) consistent with an acute asthma exacerbation among active duty service members with a prior diagnosis of asthma (one asthma-related clinical encounter plus one asthma medication prescription). Among cases that received LAIV, we used a self-controlled case series method to determine the incidence rate ratio (IRR) for acute asthma exacerbation following vaccination with LAIV. The at-risk periods were 0-14 days and 15-42 days after vaccination. **Results**: We identified 138 asthmatics that had an asthma exacerbation during the influenza season and received LAIV. For both the 0-14 and 15-42 day periods, we saw elevated point estimates for the IRR, however the confidence intervals included 1.0 (IRR=1.22, 95% CI: 0.64-2.34 and IRR= 1.57, 95% [CI]: 1.00-2.45 for the 0-14 and 15-42 day periods, respectively).**Conclusions**: Although this study did not reach statistical significance, we found an elevated point estimate of risk of asthma exacerbation in the 15-42 day window after LAIV vaccination. The small sample size may be a factor in the confidence of this estimate and additional studies of larger size are needed to better investigate whether this is a true association.

Board 293. A Large Measles Outbreak in Dar es Salaam, Tanzania - Support for the Need for a Two-dose Measles Vaccination Strategy

J. L. Goodson[1], R. T. Perry[1], E. Wiesen[1], O. Mach[1], M. Kibona[2], D. Manyanga[3], E. Luman[1], L. K. Cairns[1];

[1]The Centers for Disease Control and Prevention, Atlanta, GA, [2]World Health Organization, Dar es Salaam, TANZANIA, UNITED REPUBLIC OF, [3]Ministry of Health and Social Welfare, Dar es Salaam, TANZANIA, UNITED REPUBLIC OF.

Background: The World Health Organization (WHO) recommends each child receive two doses of measles vaccine. In Tanzania the first dose is given at 9 months and reached an estimated 93% of eligible children in 2005; periodic supplemental immunization activities (SIAs) provide the second dose. In 2006, Dar es Salaam, Tanzania experienced a large measles outbreak. We conducted a case-control study of children aged 0-18 years to determine risk factors associated with contracting measles during the outbreak. **Methods**: All laboratory-confirmed measles cases identified between July 1 and October 15, 2006 were traced; all epidemiologically-linked cases were identified. Controls were randomly selected from households found by a random walk method within 5 to 25 houses away from case households. Case-patients and controls were interviewed between Oct 31 and Nov 18, 2006 using a household survey. An unmatched analysis was performed; variables were compared using odds ratios (OR) with chi-squared tests. Multivariate analysis was performed by backward stepwise selection for the regression model. Vaccine Effectiveness (VE) was calculated for children 9 - 59 months of age. **Results**: We interviewed 117 measles cases and 116 controls. Independent risk factors for measles included being unvaccinated (Adjusted Odds Ratio [aOR] =6.1, 95% Confidence Interval [CI] 2.6-14.3) or having received only one dose of measles vaccine compared to two doses (aOR=2.5, 95% CI 1.2 - 5.1). The number of case-patients that received 0, 1 or 2 doses was 21, 48 and 48 respectively. VE for one dose of measles vaccine was 88% compared to 96% for two doses. Other risk factors included being <9 months (aOR=13.3, 95% CI 2.9 - 61.8) or 9 - 59 months (aOR=4.4, 95% CI 1.1 - 17.1) compared to 15-18 years of age, having a caretaker with primary school education or less (aOR=2.3, 95% CI 1.3 - 4.4). Living in a highly

congested neighborhood was marginally significant (aOR=8.8, 95% CI 0.9 - 83.3). **Conclusions**: This investigation supports the need for providing two doses of measles vaccine to all children to reduce the risk of measles outbreaks. In addition, these findings indicate that special efforts are needed to reach children who are less than 5 years of age, have a caretaker with a low education level, or live in congested neighborhoods.

Antimicrobial Resistance

Wednesday, March 19
12:00 PM – 1:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 294. Daptomycin Resistance and hVISA Development in MRSA Endocarditis

M. Pastagia[1], N. Casau-Schulhof[1], S. G. Jenkins[2], J. Jao[2];

[1]Mount Sinai Hospital, New York, New York, NY, [2]Mount Sinai Medical Center, New York, NY.

Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) is a common etiology of endocarditis in hemodialysis patients. We present a patient without any prior hospitalizations or vancomycin usage within the past ten years who developed MRSA endocarditis with persistent bacteremia while on daptomycin therapy. She then became resistant to daptomycin while on therapy, and ultimately cleared her bacteremia only after valve replacement. We performed microbiological tests on her blood and valve isolates. **Methods:** We performed E-strip testing of the four blood isolates with MRSA bacteremia as well as the tissue heart valve after replacement with vancomycin, daptomycin, linezolid, and tigecycline E-strips to establish the MIC. These specimens were also tested for heterogeneously vancomycin intermediate *Staphylococcus aureus* (hVISA) via teicoplanin E-strips of 0.5 and 2 McFarland standards. **Results:** The initial positive blood culture with MRSA was shown to have a MIC to vancomycin of 6 and 3 for daptomycin. These numbers remained similar for the subsequent two positive blood cultures a few days later while she remained on daptomycin, renally dosed. The fourth positive blood culture nearly one week later while on daptomycin was found to have a vancomycin MIC of 6 and a daptomycin MIC of 4. The heart valve was subsequently replaced, and the MICs of the tissue valve to vancomycin was 3, and to daptomycin was 6. All of these isolates were then tested for hVISA via teicoplanin E-strip testing at 0.5 and 2 McFarland standards. This testing revealed MICs of 3 and 4 at 0.5 and 2 McFarland, respectively for the initial blood culture. The subsequent two blood cultures showed MICs of 6 and 8 respectively. By the fourth blood culture, the MICs were 12 and 8 respectively. Ultimately the tissue valve's MICs to teicoplanin were tested, and found to be 12 and 16, respectively. **Conclusions:** It is quite uncommon for patients who have not been on prior vancomycin therapy extensively to develop resistance to daptomycin so quickly. Here, we present such a case and were able to demonstrate that this isolate became a heterogeneously vancomyin intermediate *Staphylococcus aureus* after nearly one week of daptomycin therapy. This transformation from a non-hVISA to an hVISA strain may be predictive of antibiotic failure in this case.

Board 295. Laboratory Analysis of *Staphylococcus aureus* in Florida: January 1, 2003 to December 31, 2005 with an Emphasis on Methicillin Resistance

S. K. Kolar[1], R. Sanderson[2], A. Sanchez-Anguiano[1];

[1]University of South Florida, Tampa, FL, [2]Florida Department of Health, Tampa, FL.

Background: Methicillin resistance among *S. aureus* has been a concern in the healthcare setting. Recently, MRSA has emerged in the community setting. **Methods**: This cross-sectional study examines methicillin resistance among *S. aureus* laboratory isolates in an outpatient population in the state of Florida. The database included all *S. aureus* laboratory results from a large commercial laboratory from January 1, 2003 to December 31, 2005 provided to the Florida Department of Health. **Results**: There was a total of 61,596 isolates in the database with the number of isolates doubling each year. The percent of isolates that were methicillin resistant significantly increased each year from 35.1% in 2003 to 49.7% in 2005. Isolates from skin and soft tissue comprised 79.6% of the reported site of infections, of which 52.7% were methicillin resistant in 2005. Methicillin resistance varied by year, age group, gender, county, and region. There was little difference in methicillin resistance between males and females (49.0% and 50.2% in 2005). There was some variation between the age groups, the 21- 30 age group had the highest percentage of MRSA (51% in 2005) and the <1 age group the lowest (40.2% in 2005). Variation by region and county was noted with the western panhandle having the highest percentage of MRSA (62.5% in 2005) and the southwest region the lowest (41.7% in 2005). The percentage of MRSA isolates that were resistant to trimethoprim-sulfamethoxazole, gentamycin, and rifampin was less than three percent. **Discussion**: The percent of isolates that were methiclillin resistant significantly increased during the study period. The differences by age group and region of the state were larger and may be important to consider when evaluating a potential *S. aureus* infection. Resistance to non beta-lactam antibiotics remains low and these could be alternative for empiric antimicrobial therapy in the outpatient setting.

Board 296. Bactericidal Activity of Sphingosine on Coryneform (Diphtheroid) Species

D. Gadre, B Olson, A Villhauer, D Drake, P Wertz.;

Dows Research Institute,University of Iowa, Iowa City, IA.

Background: Sphingosine (SPH) is a natural antimicrobial lipid protecting skin and mucus membranes. It has broad spectrum membrane disrupting activity. The Diphtheroids are normal commensals of skin and mucosa. However they are emerging as important causative agents of Hospital Associated Infections particularly in immunocompromised, chronically ill patients. All these species are resistant to majority of the routine antimicrobials. The purpose of this study was to determine if diptheroids were susceptible to SPH. **Methods:** Sphingosine was obtained from Sigma, ST Louis MO. SPH dilutions of 15µg/ml; 30µg/ml and 60µg/ml in sterile distilled water were used,based on preliminary MIC data *Corynebacterium jeikeium*, *C. striatum* and *C. bovis* were inoculated in Brain Heart Infusion Broth (BHIB) with 0.1% Tween 80, incubated in 5%Co_2 incubator for 48 hours. Bacterial cells were harvested by centrifugation and resuspended in broth, to achieve an assay concentration. 50 µl of bacterial suspensions were added to the tubes containing different dilutions of SPH. Positive controls consisted of 0.1% Chlorhexidine (CHX) whereas negative control tubes received sterile distilled water. Aliquots were removed after 2 minutes, 5 minutes and 10 minutes and were diluted into Neutralizing broth (NB). Samples were spiral plated onto Brain Heart Infusion Agar (BHIA) supplemented with 0.1% Tween 80. Following incubation as above, numbers of cfu/ml were determined using standard spiral-plating methodology and analysis one-way ANOVA. **Results:** Exposure to 60µg/ml. SPH resulted into two orders of

magnitude decrease after 2 minutes, which decreased further with complete bactericidal activity in 10 minutes. This killing activity was equivalent to that of Positive Control 0.1% CHX and was statistically not different. There was bactericidal activity with 15µg/ml and 30µg/ml SPH with decreases of two orders of magnitude in 10 minutes and 5 minutes respectively, with no complete killing. No bactericidal activity was observed in negative controls.**Conclusions:** Complete killing activity of SPH against diphtheroids was achieved at 60µg/ml in 10 minutes which was comparable to 0.1% CHX. Thus Sphingosine shows promise as a natural antimicrobial agent against these emerging opportunistic pathogens.

Board 297. Antimicrobial Resistance Surveillance Tool for DoD Facilities

T. I. Nadal, MPH, C. Parker Rennix, CIH, ScD, A. Riegodedios, MSPH, J. Slosek, MS, Navy, Portsmouth, VA.

Background: Public health professionals must rapidly characterize emerging antibiotic resistant organisms to facilitate the development of treatment and control measures. Improving capabilities to enhance the detection and monitoring of antibiotic resistant organisms is essential to ensure medical readiness among U.S. military service members. Health Level (HL) 7 Laboratory Microbiology data from a military medical treatment facility were restructured and imported into WHONET© for early identification of antibiotic resistant organisms such as *Acinetobacter Baumannii* and Methicillin Resistant *Staphylococcus Aureus*.**Methods:** The HL7 Microbiology data from a military medical treatment facility were restructured using Standardized Query Language (SQL) and SAS programming and imported into WHONET using inherent standardization algorithms. Using WHONET, rapid analyses of pathogens and their drug resistance patterns can be performed to enhance management and surveillance of antibiotic resistant organisms. Reports can be generated quickly by medical facilities to address facility specific concerns and create alerts for organisms of importance to their facility. **Results:** 79 isolates were identified for *Acinetobacter baumannii* from blood or cerebrospinal fluid (CSF) specimens from a military hospital, from May 2004 to Dec 2006. For *Staphylococcus aureus*, 92 isolates were identified from blood or CSF specimens. **Conclusions:** Early identification of changes in antibiotic resistance patterns has a direct impact on medical readiness, health outcomes, and health care cost. Military medical treatment facilities can improve patient outcomes by utilizing restructured data as a surveillance tool. Identification of changes in organism specific resistance patterns can assist in ensuring that appropriate drug therapy is provided. This can lead to reduction of medications utilized, limiting transmission of pathogens to other patients, and decreasing length of illness, hospital stay, and treatment time, as well as reductions in secondary infections, amputations, cost, mortality, and patient risks. Rapid characterization of changes in antibiotic resistance patterns can be used in surveillance efforts to detect changes in disease trends in a way that hospital records or laboratory tests alone cannot.

Emerging Opportunistic Infections

Wednesday, March 19
12:00 PM – 1:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 298. Impact of Coccidioidomycosis (Valley Fever) in Arizona: Data from Enhanced Surveillance

R. H. Sunenshine[1], S. Chen[1], L. Erhart[2], S. Anderson[2], B. Casimir[2], B. Park[3], T. Chiller[3], K. K. Komatsu[2];

[1]Arizona Department of Health Services and CDC, Phoenix, AZ, [2]Arizona Department of Health Services, Phoenix, AZ, [3]Centers for Disease Control and Prevention, Atlanta, GA.

Background: Coccidioidomycosis (valley fever) is an emerging fungal disease endemic to the Southwestern US, Central and South America; 60% of reported US cases occur in Arizona, where physician and laboratory reporting is mandatory. Due to an increase in reported rates over the last five years, Arizona Department of Health Services (ADHS) initiated enhanced coccidioidomycosis surveillance to determine case characteristics, treatment, and disease impact to target public health interventions.**Methods:** Every tenth case of coccidioidomycosis reported to ADHS from January through August 2007 was telephoned and interviewed with a standardized questionnaire. If the case could not be reached after ≥3 attempts, the subsequent reported case was contacted. **Results:** Of 3268 cases reported, 262 were successfully interviewed (80% of targeted sample). Males comprised 49%, 76% were white, 5% African American, 4% Asian, and 11% were of Hispanic ethnicity. Median age was 54 years (range <1-95). Other characteristics included smoking history (55%), immunosuppressive therapy (18%), malignancy or transplant (18%), and living within one mile of construction (51%). Cases lived in Arizona a median of 16 years prior to diagnosis Of cases, 64% received antibacterial agents and 60% received antifungal treatment. Symptoms lasted a mean of 62 days and 40% required overnight hospitalization. Most (78%) cases reported interference with daily activities due to their illness (mean 94 days). Of 126 cases employed at diagnosis, 76% missed work due to illness (mean 32 days), and of 34 students, 50% missed school due to valley fever (mean 15 days). Two-thirds of cases (64%) had heard of valley fever prior to diagnosis, however only five heard of the disease from their healthcare provider. After their diagnosis, 20% did not know how valley fever is transmitted. **Conclusions:** The Arizona valley fever epidemic greatly impacts the public health and economy of Arizonans, supporting the delegation of additional resources toward education, prevention and treatment of this public health threat and select agent. Information learned from enhanced surveillance in Arizona could be used to develop education and public health interventions in other endemic states and countries.

Board 299. Identification of Novel Discistro-like Virus from Stool Samples of Children with Acute Flaccid Paralysis

J. G. Victoria[1], A. Kapoor[1], C. Wang[2], R. W. Shafer[2], A. Naeem[3], S. Sharif[3], S. Shaukat[3], M. Masroor[3], M. Angez[3], S. Z. Zaidi[3], E. L. Delwart[1];

[1]Department of Molecular Virology, Blood Systems Research Institute, San Francisco, CA, [2]Division of Infectious Diseases and Geographic Medicine, Stanford University School of Medicine, Stanford, CA, [3]Department of Virology, National Institute of Health, Islamabad, PAKISTAN.

Background: In 1988 the Global Polio Eradication Initiative was founded, facing over 350,000 worldwide infections

of poliovirus in children. Despite large strides in poliovirus eradication, four countries, India, Afghanistan, Nigeria and Pakistan are still endemic for polio. As part of the initiative stool samples are routinely collected from children with acute flaccid paralysis (AFP) and screened by serology and PCR for picornaviruses, including poliovirus. **Methods:** Poliovirus and enterovirus negative stool or stool-inoculated tissue culture supernatants from children presenting with AFP collected in Pakistan were used in these studies. We employed a shotgun metagenomics approach using sequence independent amplification of viral nucleic acids to detect new and divergent viruses. PCR products were cloned and sequenced by traditional Sanger sequencing or used directly for large scale 454 pyrosequencing. Sequences were assembled based on 95% identity over at least 35bp and characterized by nucleotide and protein BLAST similarities. A group of *dicistroviridae*-like viruses were identified, tentatively named Ervivirus. Conserved Ervivirus domains were used for consensus PCR primer design in prevalence and diversity studies. **Results:** Ervivirus exhibited only 22% amino acid identity to the closest dicisctrovirus family member, Israel acute paralysis virus of bees. Genomic arrangement of Ervivirus mirrored that of the dicistroviruses in which non-structural genes are 5' of structural genes, separated by a non-coding spacer region which was slightly larger in Ervivirus (250bp) when compared to dicistroviruses (170-200bp). Three genetic variants were identified in 14 samples tested exhibiting 80-85% amino acid identity to Ervivirus. Neighbor-joining and maximum likelihood phylogenetic reconstruction of conserved coding sequences indicate Ervivirus is a deeply rooted new genus within the *Dicistroviridae* family whose only reported host to date are invertebrates. **Conclusions:** We have identified novel dicistro-like virus isolated from children with AFP provisionally named Ervivirus. This is the first evidence of picorna-like viruses with a dicistronic genomic arrangement from mammalian samples. Ervivirus cellular tropism and prevalence are currently underway to determine linkage to AFP.

Board 300. Clinical and Epidemiological Characterization of *WU Polyomavirus* Infection in St. Louis, USA

B. Le, D. Hormozdi, L. M. Demertzis, G. Wu, R. Buller, R. J. Tibbetts, M. Q. Arens, A. M. Gaynor, G. A. Storch, D. Wang;

Washington University, Saint Louis, MO.

Background: WU virus is a recently described polyomavirus detected in respiratory secretions from patients with respiratory tract infections. **Methods:** To further define the clinical and epidemiologic characteristics of infections with WU polyomavirus, we tested 2637 pediatric respiratory samples collected July 2003 to June 2004 in St. Louis, Missouri using Taqman real time PCR assay. Positive samples were further screened for 17 other respiratory viruses using the Eragen MultiCode-Plx respiratory virus panel. Clinical data was collected on the WU positive samples. **Results:** Seventy out of 2637 (2.7%) samples were positive for WU polyomavirus. 71% of the samples positive for WU polyomavirus were co-infected with at least one other respiratory virus. The most frequent diagnoses observed were pneumonia and bronchiolitis. In two different immunocompromised patients, multiple specimens sampled over a 6-8 week period were continually positive for WU polyomavirus. WU polyomavirus was also observed in a one-day old infant. **Conclusions:** WU polyomavirus was detected in 2.7% of pediatric respiratory samples submitted over a 12 month period in St. Louis, Missouri, with a high percentage of co-infection. Notably, we reported the first observation of persistent human infection with WU polyomavirus in two immunocompromised patients, as well as the presence of the virus in a one-day old infant. These observations raise the question as to the modes of transmission of WU polyomavirus and the role of the immune system in viral eradication.

Board 301. *Staphylococcus aureus* Community-Acquired Pneumonia in Children During the 2006-07 Influenza Season

A. J. Kallen[1], C. Reed[1], M. Patton[1], K. E. Arnold[2], M. M. Farley[3], J. Hageman[1], L. Finelli[1];

[1]Centers for Disease Control, Atlanta, GA, [2]Georgia Department of Health, Atlanta, GA, [3]Emory University School of Medicine and VA Medical Center, Atlanta, GA.

Background: *Staphylococcus aureus* has increasingly been described as a cause of severe community-acquired pneumonia (CAP) during the influenza season. However, recent reports have described passively reported cases which may present a biased picture of this disorder. We conducted surveillance for *S. aureus* infection in the Atlanta area to systematically characterize *S. aureus* CAP in children during the influenza season. **Methods:** Charts from 249 patients who were admitted to one of the three Atlanta children's hospitals from October 1, 2006 to April 1, 2007 with *S. aureus* from a sterile site or respiratory specimen were reviewed to identify those who met a case definition for primary CAP (i.e., onset in the community and did not develop from another site of infection). Data was abstracted on exposures, past-history and outcome. **Results:** Fifty-three episodes of S. *aureus* CAP were identified; 48 episodes were primary CAP. Forty-six percent of all *S. aureus* isolated from primary CAP episodes were methicillin-resistant (MRSA). Episodes of primary *S. aureus* CAP involved patients with a median age of 8.5 years and 37 (77%) involved patients with prior medical diagnoses, including 18 with cystic fibrosis. In 22 (46%) of the episodes, patients with primary *S. aureus* CAP were seen as outpatients a median of 3.5 days prior to admission. In 3 of the 22, patients empirically received antibiotics as outpatients with activity against their *S. aureus*. At admission, 14 of the 22 (64%) episodes caused by MRSA were treated with linezolid or vancomycin. Twenty-seven (56%) episodes of primary *S. aureus* CAP were admitted to an intensive care unit and 23 (48%) required mechanical ventilation. Six persons (3 of whom had MRSA) died, with the median time from symptom onset to death of 13 days. **Conclusions:** Primary *S. aureus* CAP, particularly that caused by MRSA, appeared to be relatively common in this sample from the 2006-07 influenza season. Unlike recent case series, primary *S. aureus* CAP patients often had prior medical problems and lower mortality rates. Almost half were seen as outpatients prior to admission and few were treated empirically for their *S. aureus*. Coverage for methicillin-resistant *S. aureus* should be considered in children, particularly those with underlying medical conditions, admitted with CAP during the influenza season.

Board 302. *Nocardia mikamii* sp. nov., Isolated from Pulmonary Infections in the United States

D. P. Jannat-Khah, B. A. Lasker, A. G. Steigerwalt, J. M. Brown;

Bacterial Zoonoses Branch, Division of Foodborne, Bacterial, and Mycotic Diseases, National Center for Zoonotic, Vector-borne, and Enteric Diseases, Centers for Disease Control and Prevention, Atlanta, GA.

Background: Members of the genus *Nocardia* are an important source of cutaneous, pulmonary, and disseminated infections in both immunocompetent and immunocompromised persons. From 2001 to 2007, four clinical respiratory isolates, (W7467, W7811, W8061, and W9013), were obtained from patients in the United States. Standard phenotypic tests identified the isolates to the genus level and genetic tests indicated these isolates to be a novel species of *Nocardia*. **Methods:** Phenotypic studies performed included: microscopic examination, biochemical profiles, and antimicrobial susceptibility testing. Genetic studies included: 16S rRNA gene and DNA gyrase subunit B (*gyrB*) gene sequence determinations, which were obtained by cycle sequencing of PCR amplified fragments sequenced in both directions; and DNA-DNA relatedness, which

was determined using labeled DNA from isolate W8061.**Results:** Results of the phenotypic tests were consistent with the assignment of the isolates to the genus *Nocardia* but were not able to identify the isolates to the species level. Sequence analysis of a ≥1,440-bp fragment of the 16S rRNA gene showed the closest similarity to *Nocardia aobensis* (99.58%) and *Nocardia africana* (99.37%). Analysis of a 1,245-bp fragment of *gyrB* gene formed a clade separate from *N. aobensis* and other *Nocardia* species. The results of DNA-DNA hybridization studies of strain W8061 showed 67% and 12% relatedness to *N. aobensis* and *N. africana*, respectively. These values are below the 70% cut-off recommended for the delineation of genomic species. **Conclusions**: The combination of phenotypic, phylogenetic, and DNA-DNA hybridization studies suggested the clinical isolates represent a novel species of *Nocardia*, for which we propose the name *Nocardia mikamii* sp. nov. Phylogenetic analysis of the *gyrB* gene was more discriminatory than the 16S rRNA gene and was more consistent with the results of the DNA-DNA hybridization. Accurate identification of clinical *Nocardia* isolates may be useful for detecting species differences in pathogenicity, epidemiology, and predicting appropriate antimicrobial therapy. The characterization of this new species, *N. mikamii*, will enhance our understanding of the emergence of pathogenic nocardioforms.

Board 303. Characterization of a novel *Francisella* sp. isolated from human CSF and blood

K. J. Kugeler[1], P. S. Mead[1], K. L. McGowan[2], J. M. Burnham[2], M. D. Hogarty[2], K. Pollard[3], B. Husband[3], C. Gauthier[4], T. Kelesidis[5], J. E. Staples[1], L. Chalcraft[1], J. M. Petersen[1];

[1]Centers for Disease Control and Prevention, Fort Collins, CO, [2]Children's Hospital of Philadelphia and University of Pennsylvania, Philadelphia, PA, [3]Pennsylvania Department of Health, Bureau of Laboratories, Lionville, PA, [4]Bioterrorism Response Laboratory, Massachusetts Department of Public Health, Jamaica Plain, MA, [5]Caritas St. Elizabeth's Medical Center, Boston, MA.

Background: The *Francisellaceae* family is composed of *Francisella tularensis*, the etiologic agent of tularemia, and *Francisella philomiragia*, a rare cause of illness in immunocompromised hosts. Other *Francisellaceae* members have been identified in fish, soil, and as endosymbionts of ticks, though little is known about their potential to cause human illness. In 2005 and 2006, a *Francisella* sp. was cultured from two unrelated patients. One isolate, PA051188, grew from cerebrospinal fluid obtained from the shunt of a 15 month old immunocompromised female in Pennsylvania with fever, rash, vomiting and hydrocephalus. The other isolate, MA067296, grew from the blood of an 85 year old male in Massachusetts on hemodialysis with fever, cough, and a lung infiltrate. **Methods:** Isolate characterization was based on growth requirements, biochemical analysis, antimicrobial susceptibility, and reactivity with *F. tularensis*-specific tests (slide agglutination, direct fluorescence assay, and PCR). Polyclonal rabbit sera raised to PA051188 was used to evaluate agglutination. The 16S rRNA and *sdh*A genes were sequenced. The isolates were also subjected to pulsed-field gel electrophoresis (PFGE) with *Pme*I. **Results:** PA051188 and MA067296 required cysteine for growth, similar to *F. tularensis*, though *F. tularensis*-specific tests were negative. Biochemical profiles for these isolates differed from cultured *Francisella* spp. Antisera to PA051188 agglutinated itself and MA067296, but not other *Francisella* spp. 16S rRNA gene sequences of these two isolates showed 99.9% identity to each other, and only 97% identity to *F. philomiragia* and *F. tularensis*. The *sdh*A sequences of these isolates were indistinguishable, and displayed only 83% and 84% identity to *F. philomiragia* and *F. tularensis*, respectively. These isolates differed in PFGE patterns and susceptibility to cefepime. **Conclusions:** Our evaluation revealed that PA051188 and MA067296 likely represent a new *Francisella* sp. Differences between these isolates indicate they are not part of a point source event, such as contamination in manufacturing of hospital equipment or supplies. The testing methods described here can be used in the future to identify this *Francisella* sp. to provide insight regarding prevalence of this organism with respect to human illness.

Foodborne & Waterborne Infections

Wednesday, March 19
12:00 PM – 1:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 304. Clinical characteristics of O157 and non-O157 Shiga toxin-producing *Escherichia coli* (STEC) infections in Minnesota, 2000-2006

E. B. Hedican, C. Medus, J. M. Besser, B. A. Juni, B. Koziol, C. Taylor, K. E. Smith;

Minnesota Department of Health, St. Paul, MN.

Background: *E. coli* O157 (O157) is the serotype of STEC most frequently isolated and most often associated with hemolytic uremic syndrome (HUS) in the US. Non-O157 STEC serotypes can also cause serious illness and have been implicated in outbreaks. However, non-O157 STEC are not detected through standard stool culture methods available in clinical laboratories; therefore, their true impact as pathogens remains undefined. We compare here characteristics of non-O157 STEC and O157 infections in Minnesota (MN). **Methods:** Two sentinel sites participated in STEC surveillance: a large HMO laboratory serving the Minneapolis-St. Paul metropolitan area, and a hospital laboratory serving a small city and surrounding rural area. The MN Department of Health received SMAC plates from every stool culture done at both sites during 2000-2006. Colony sweeps were screened for gene sequences encoding STEC toxins Stx1 and Stx2 by PCR. *E. coli* identity, serotype, and presence of Stx1 and/or 2 were confirmed on individual isolates. **Results:** 206 STEC isolates were identified from the surveillance sites: 108 (52%) were non-O157 serotypes and 98 (48%) were O157. Serogroups O26, O103, O111, O145, and O45 accounted for 74% of non-O157 isolates. Of non-O157 cases, 98% had diarrhea (median duration, 7 days), 54% had bloody diarrhea, 39% had fever, and 8% were hospitalized. 40% of non-O157 isolates produced at least Stx2; these isolates were not more likely to cause severe illness than non-O157 isolates that produced only Stx1. 99% of O157 isolates produced at least Stx2. O157 cases were more likely than non-O157 cases to have bloody diarrhea (78% to 54%, $p<0.001$), be hospitalized (34% to 8%, $p<0.001$), and develop HUS (7% to 0%, $p=0.005$). When including only isolates that produced at least Stx2, O157 cases were still more likely to have bloody diarrhea (78% to 56%, $p=0.02$), and be hospitalized (33% to 12%, $p=0.01$) than non-O157 cases. **Discussion:** Non-O157 STEC were isolated as frequently as O157 from ill patients, and caused substantial morbidity. However, O157 cases were more likely to develop severe illness (bloody diarrhea, HUS, hospitalization). Differences in severity, either among non-O157 cases or in the O157/non-O157 comparison, could not be explained by production of Stx2, suggesting that additional factors are important in STEC virulence.

Board 305. Are There Gender Differences in Food Consumption? The FoodNet Population Survey, 2006-2007

B. Shiferaw[1], L. Verrill[2], H. Booth[1], S. Zansky[3], D. Norton[4], S. Crim[5], O. Henao[6];

[1]Oregon Department of Human Services, Portland, OR, [2]US Food and Drug Administration, College Park, MD, [3]EIP NY State Department of Health, Albany, NY, [4]CA EIP, Oakland, CA, [5]GA Division of Public Health, Atlanta, GA, [6]Centers for Disease Control and Prevention, Atlanta, GA.

Background: The Foodborne Diseases Active Surveillance Network (FoodNet) population survey has been used to describe food consumption patterns in the general population; these data have been useful for hypothesis generation during outbreak investigations. This analysis examined differences in consumption of various types of foods, including high- risk foods for foodborne illness, between men and women. **Methods:** The most recent population survey was conducted from May 2006 until April 2007, using a two-stage sampling design and random digit dialing. An algorithm that takes into account the number of males and females in the household is used to randomly select one participant per household. For analysis, food items were grouped into; dairy, meat and poultry, seafood, fresh vegetables, fruits, dried foods, and frozen foods. Six foods were considered to be high-risk; pink hamburger, raw oysters, unpasteurized milk, cheese made from unpasteurized milk, runny eggs, and alfalfa sprouts. Analysis was limited to those ≥ 18 years, and weighted to the FoodNet population. **Results:** A total of 14,660 persons ≥ 18 years of age were interviewed; 5,595 (38%) men and 9,065 (62%) women. Men were significantly more likely to eat meat and poultry items such as duck or game hen (1.5% vs 0.7%, p<0.0001), veal (2.3% vs 1.1%, p=0.004), and ham (21% vs 18%, p=0.004) than women. Women were more likely to eat vegetables, such as carrots (35% vs 29%, p<0.0001), and tomatoes (37% vs 32%, p<0.0001); fruits such as strawberries (24% vs 19%, p<0.0001), raspberries (5.7% vs 4.2%, p<0.0001), and dried foods such as almonds (16% vs 11%, p<0.0001), and walnuts (12% vs 8%, p<0.0001). Of the 6 high-risk foods, men had higher consumption of runny eggs (8.2% vs 5.7%, p-value <0.0001), and pink hamburger (12.4% vs 7.7%, p-value <0.0001). Women ate more alfalfa sprouts than men (1.9% vs 1.0%, p=0.01). No differences by gender were observed for the other high-risk foods. **Conclusions:** Food consumption patterns differed substantially between men and women. This information can be useful for the design of targeted interventions regarding consumption of high-risk foods. Moreover, in the investigation of outbreaks in which a preponderance of cases are among members of one sex, knowing the background rates of food consumption by sex can quickly suggest plausible vehicles.

Board 306. Prevalence of Multidrug *Salmonella* in Eggs from Poultry and Ducks in South India

M. Abdulla[1], H. Gopalakrishnan[2], S. Tiruppathi[3];

[1]Cochin University of Science and Technology, Cochin, INDIA, [2]Mahatma Gandhi University, Kottayam, INDIA, [3]Bharathiar University, Coimbtore, INDIA.

Background: The increasing evidence about the role of eggs as principal vehicle for food borne salmonellosis and a near pandemic spread of *Salmonella* Entertidis in eggs has prompted us to undertake a study on the prevalence of *Salmonella* in eggs from poultry and ducks which are popular and widely consumed in South India. Apart from that National Egg Co-ordination Committee (NECC) in India is promoting consumption of eggs though systematic studies about the risk associated with this food item and definite guidelines regarding preparation of egg based dishes are lacking. **Methods:** The prevalence of *Salmonella* on both the egg shell and in the egg contens were analysed as per USFDA's Bacteriological Analytical Manual (BAM). Briefly, the samples were pre-enriched in buffered peptone water, followed by selective enrichment in tetrathionate broth. After selective enrichment the samples were streaked on selective media such as xylose lysine deoxycholate agar (XLD), hektoen enteric agar (HEA) and MacConkey agar. Typical *Salmonella* like colonies were tested for primary and secondary biochemical reactions and were confirmed by slide agglutination test using polyvalent O serum (DIFCO). Serotyping of the isolates was done at National *Salmonella* and *Escherichia* Centre, Central Research Institute, Kasauli, India. All the *Salmonella* serotypes were then tested against 10 different antibiotics using disk diffusion assay to determine the antibiogram. **Results:** Of the 642 eggs from commercial layer hens about 15% of them were tested positive for *Salmonella* on egg shell, while it was only around 1% in the egg contents. Among the 150 eggs from non-commercial layer hens, the *Salmonella* contamination was 4% in the egg shell while all the egg contents were negative for *Salmonella*. Prevalence of Salmonella in duck eggs were 6% on the egg shell and 51% in the egg contents suggesting a transovarian route of contamination. *Salmonella* serotypes included *S.* Enteritidis, *S.* Molade, *S.* Mbandaka, *S.* Cerro, *S.* Dublin, *S.* Bareilley and *S.* Weltevreden. All the Salmonella serotypes were multidrug resistant. **Conclusions:** Prevalence of Salmonella in hens' egg and duck egg were significantly lower in South India, when compared to reports from other parts of the world. Drug resistance among the Salmonella strains from duck eggs was less frequent.

Board 307. Non-O157 Shiga toxin-producing *Escherichia coli* in Connecticut: Predominant Serogroups, Measures of Disease Severity and Risk Factors vs. O157, 2000-2007

Q. Phan[1], S. Hurd[2], P. Clogher[2], C. Welles[1], E. Sowers[3], J. Hadler[1];

[1]Connecticut Department of Public Health, Hartford, CT, [2]Yale University Emerging Infections Program, New Haven, CT, [3]Centers for Disease Control and Prevention, Atlanta, GA.

Background: The epidemiology of non-O157 Shiga-toxin (Stx) producing *Escherichia coli* (STEC) serotypes is not well understood. Standard culture methods for O157 do not detect non-O157. Since 1999, increasing numbers of laboratories in Connecticut have been using tests to detect Stx rather than culture for O157, providing an opportunity for identification of non-O157 STEC. We describe the clinical features, epidemiology and risk factors of leading non-O157 serogroups compared to O157. **Methods**: Since 2000, laboratories have been required to submit Stx-positive broths to the State Laboratory for isolation of STEC. Non-O157 isolates are forwarded to CDC for serotyping and testing for toxin type. Data from the past 8 years of surveillance and patient interviews for exposures during 2/1/00-1/31/03 and 4/1/04-9/30/07 were analyzed. **Results**: From 1/1/00 to 9/30/07, 544 STEC infections were reported, 306 (56%) detected by Stx testing. Among these, 61% were non-O157. The top 4 non-O157 serogroups were O111 (19%), O103 (19%), O26 (17%), and O45 (12%). As a group, non-O157 patients were less likely to be hospitalized (19% vs 30%), and develop hemolytic uremic syndrome (0.5% vs 6%), although hospitalization rates for O26 (23%) and O45 (29%) were similar to O157 (35%). Stx_2 production was much less likely among non-O157 (40/168) than O157 (43/43, $p<10^{-7}$). Comparing individual serogroups to O157, persons with each of the 4 leading types were equally or more likely to have eaten ground beef. There were no significant differences between the different serogroups and O157 in having visited farms/petting zoos, contact with animal manure or swam in a pond/lake/river. International travel was more frequent among O111 (30%) and O103 (14%) than O157 (3%). **Conclusions**: When using Stx testing, non-O157 STEC are found more often than O157. O157 is the most common single serogroup in CT, followed by O111, O103, O26, and O45. Differences in severity of disease between O157 and non-O157 may in part be due to relative

frequency of Stx_2 production. International travel is an important non-O157 risk factor, particularly for O111 and O103. Non-O157 STEC appear to have the same risk factors as O157, suggesting they share a common environmental reservoir. Ongoing surveillance for all STEC is needed to better understand the epidemiology of non-O157 STEC.

Board 308. Environmental Mycobacteriosis and Drinking Water: What are the Connections?

E. Hilborn, A. Ghio;

US Environmental Protection Agency, Research Triangle Park, NC.

Background: During the last 20 years, incidence rates of pulmonary environmental mycobacteriosis appear to be increasing in the US and other developed countries. Environmental mycobacteria have been detected in multiple media: soil, ground and surface waters, water aerosols and treated drinking water. The US Environmental Protection Agency regulates drinking water quality and has been directed to examine emerging contaminants for potential regulation under the Safe Drinking Water Act. The Agency has included *Mycobacterium avium* complex on the most recent Contaminant Candidate List of emerging drinking water contaminants. **Methods:** We systematically review the published peer-reviewed literature for reports of epidemiologic and/or molecular association between pulmonary environmental mycobacteriosis and drinking water among residents of developed countries.**Results:** We found multiple species of environmental mycobacteria implicated as the causative agent of human pulmonary disease and found in drinking water. Species associated with waterborne pulmonary mycobacteriosis vary by region and country of report but are most commonly slow-growing species such as *M. avium* and *M. kansasii*. **Conclusions:** There is clear evidence that drinking water is a source of pulmonary environmental mycobacteriosis; however the etiologic fraction of disease attributable to drinking water is unknown. Population-based studies including data collected at the individual level are needed to estimate the magnitude of risk associated with drinking water exposure. This is an abstract of a proposed presentation and does not necessarily reflect EPA policy.

Board 309. An Outbreak of Orally Transmitted Acute Chagas Disease in an Urban Area - Para State, Brazil, 2006

A. da Nobrega[1], M. H. Garcia[1], E. Tatto[2], E. Góes[3], J. Sobel[4], W. N. de Araújo[1];

[1]Field Epidemiology Training Program (EPI-SUS), Secretariat of Surveillance in Health (SVS), Ministry of Health, Brasilia, BRAZIL, [2]National Program of Chagas Disease Control (PNCDCh), SVS, Ministry of Health, Brasilia, BRAZIL, [3]State Secretariat of Health, Pará, Belem, BRAZIL, [4]Office of Global Health, Centers for Disease Control and Prevention (CDC), Atlanta, GA.

Background: In Latin America an estimated 20 million persons are chronically infected with *Trypanosoma cruzi*, the agent of Chagas' disease. Acute Chagas Disease (ACD) caused by oral transmission is an important emerging disease in Brazil. Most cases occur in the Amazon region. Contaminated açai juice has been suspected but never associated epidemiologically or confirmed by laboratory methods. We investigated an ACD cluster in Abaetetuba, Para state. **Methods:**We conducted a case-control study (1:3) matched for sex and age-group to evaluate disease-associated risk factors. A confirmed ACD case was defined as *T. cruzi* identified by microscopy of thick blood smears or serum reactive for Chagas-specific IgM by indirect immunofluorescence in a symptomatic patient. **Results:** We identified 11 confirmed case-patients in Abaetetuba between September 22 and October 5 2006. They were members of six families residing in three neighborhoods; two families resided on the same street. Two deaths occurred (mortality=18%). Median age of case-patients was 48 years (range, 26-72); 64% were male and all lived in an urban area. Principal symptoms included fever (100%), headache (100%), myalgia (100%), vomit (82%), weakness (82%), facial edema (73%), diarrhea (64%), epigastric pain (64%), abdominal pain (64%), jaundice (64%), and peripheral edema (64%). Drinking fresh açaí (palm tree fruit) juice was associated with ACD (mOR=6.8; CI: 1.2-43.4; p=0.02). Triatomine bites, blood transfusion, organ transplant, and sleeping in a rural or forested area were not associated with illness. **Conclusions:**This ACD outbreak was caused by oral transmission of *T. cruzi* and the likely exposure was consumption of unpasteurized açaí juice. Although açaí has long been suspected as the source of transmission of most outbreaks of orally transmitted ACD, this is one of the only reported outbreaks in which açaí juice was statistically implicated. The juice may have been contaminated by the parasite before production, although the specific mechanism of contamination was not identified.

Board 310. The Global Burden of *Salmonella*

J. Musto, Global Burden of Salmonella Working Group;

NSW Health, North Sydney, AUSTRALIA.

Background: Diarrheal illnesses are a significant cause of morbidity and mortality worldwide. The importance of *Salmonella* as a diarrheal agent in developing countries remains largely unknown. In 2004, the World Health Organization (WHO) and the Centers of Disease Control and Prevention (CDC) established the International Collaboration for Burden of Illness (BOI) Studies Group. This group aims to contribute to global foodborne disease estimates to assist public health policy makers. We aim to estimate the global burden of disease caused by Salmonella. **Methods:** We analysed three sources of data:

1. Incidence of salmonellosis from countries that have conducted population based burden of illness studies
2. Disease notification data adjusted for under-reporting using evidence based multipliers
3. Estimates of incidence of salmonellosis in Swedish travellers returning from specific countries or regions.

Where no country specific data were available, data were extrapolated across countries and regions.**Results:** There were 4 regions with burden of illness studies. Surveillance data was available in a further 4 regions. Travellers' data and extrapolation were used for the remaining 13 regions. We estimate that *Salmonella* caused 250 million illnesses and 1.5 million deaths. The resource poor regions of Africa and Asia have the highest incidence (>2,000/100,000 cases/year). Resources rich regions such as Europe, North America and Oceania have low incidence (<500/100,000 cases/year).**Conclusions:** *Salmonella* infections cause considerable burden globally. These data may be useful to contribute to global foodborne disease estimates for priority setting in specific regions. There were no systematically collected notification data available from countries with large populations such as China and India. Given the population of these two countries represents 60% of the global population, the estimated incidence of salmonellosis in these countries significantly influences the final estimate. To improve global burden estimates and inform priority setting, work to assess the true burden of Salmonella must been prioritised in these countries.

Board 311. *Shigella* from humans in Thailand during 1993 to 2006: spatial-time trends in species and serotype distribution

F. M. Aarestrup[1], A. R. Vieira[1], D. M. Lo Fo Wong[1], S. Pornreongwong[2], C. Pulsrikarn[2], P. Sawanpanyalert[2], R. S. Hendriksen[1], A. Bangtrakulnonth[2];

[1]WHO Collaborating Centre for Antimicrobial Resistance in Food borne Pathogens and EU Community Reference Laboratory for Antimicrobial Resistance, National Food Institute, Technical University of Denmark, Copenhagen V, DENMARK, [2]WHO International Salmonella and Shigella Centre, National Institute of Health, Department of Medical Sciences, Ministry of Public Health, Bangkok, THAILAND.

Background *Shigella* is an important cause of acute diarrheal disease and occurs worldwide in an estimated 164.7 million people per year, resulting in around 1,100,000 deaths, especially among children in developing countries. *Shigella flexneri* and *Shigella sonnei* are the predominant species in developing countries, while *S. sonnei* is predominant in industrialized countries. This study describes the trends in *Shigella* serotypes isolated from different medical centers in Thailand from 1993 - 2006.**Methods** A total of 9,063 *Shigella* isolates were submitted to the WHO International Salmonella and Shigella Centre in Bangkok from different medical centers in Thailand in the period 1993 through 2006. All isolates were speciated and serotyped. **Results** A total of 1,315 (37%) cases were from children from 0-2 years and 684 (19%) from children between 3-6 years. Most infections were recorded during 1993 and 1994, with more than 1,500 isolations each year, where after the number of isolations decreased to <200 in 2006. The relative species distribution has also changed. During 1993-1994 *S. flexneri* accounted for 2,241(65%) of the 3,474 isolations. This proportion decreased to 64 (36%) of 176 infections in 2006. Most of the infections occurred during July and August, with the lowest number of infections being diagnosed in December. For *Shigella dysenteriae* and *Shigella boydii* which accounted for less than 2% of the cases registered, spatial clusters were restricted to Bangkok and North of Bangkok. Both *flexneri* and *sonnei* clustered in Bangkok and west of Bangkok. *flexneri* also clustered North of Bangkok and *sonnei* clustered in zones in the Southern part of Thailand. Most *S. flexneri* infections were caused by serotype 2a (1,590 of 4,035) followed by seroptype var X (1,249). For both of these serotypes a pronounced decrease in the number of isolates took place over time. A much smaller, even though still significant, decrease could be observed for isolates of serotype 3a. **Conclusion** This study shows that when looking at the *Shigella* species Thailand changed from being a developing country to a developed country between 1995 and 1996. In addition, differences in the spatial clustering of *S. flexneri* and *S. sonnei* and serotypes of S. flexneri were observed. These aspects need further studies.

Immigrant & Refugee Health

Wednesday, March 19
12:00 PM – 1:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 312. Establishing Respiratory Disease Surveillance in Two Refugee Camps in Kenya, 2006-2007

J. Ahmed[1], E. Mulowayi[2], V. Kahi[3], M. Bunei[4], N. Kariuki[1], P. Muthoka[5], R. Kalani[5], K. Tsatsiyo[6], B. Swai[7], M. Qassim[7], D. Erdman[8], B. Fields[8], D. Feikin[9], H. Burke[1], M. Katz[1], B. Kapella[8], C. Baer[1], R. Breiman[1], R. B. Eidex[1], M. Weinberg[8];

[1]CDC, Nairobi, KENYA, [2]GTZ, Nairobi, KENYA, [3]IRC, Nairobi, KENYA, [4]IRC, Kakuma, KENYA, [5]MOH, Nairobi, KENYA, [6]UNHCR, Dadaab, KENYA, [7]UNHCR, Nairobi, KENYA, [8]CDC, Atlanta, GA, [9]CDC, Kisumu, KENYA.

Background: Dadaab and Kakuma refugee camps in Kenya house nearly 300,000 refugees. Acute respiratory infections (ARI) are leading causes of both morbidity and mortality in these camps. To guide prevention and therapeutic strategies, the burden and etiologies of respiratory disease must be established. CDC in collaboration with United Nations High Commissioner for Refugees, German Technical Cooperation and the International Rescue Committee, built upon the Kenya Ministry of Health's national influenza surveillance to establish ARI surveillance with enhanced diagnostic capacity. **Methods:** We targeted patients with ARI visiting the inpatient and outpatient medical facilities at each camp. Health-care workers were trained in standardized case definitions for ARI. For patients who met these case definitions, a questionnaire was administered, and combined nasopharyngeal and oropharyngeal samples were taken. Specimens were tested by real-time RT-PCR for Influenza A and B, Respiratory syncytial virus (RSV), Adenovirus (Ad), Parainfluenza virus (PIV) 1, 2, and 3, Human metapneumovirus (hMPV), *Chlamydia pneumoniae*, *Mycoplasma pneumoniae*, and *Legionella pneumophila*. **Results:** During May-September 2007, 286 samples were submitted from Dadaab refugee camp. A total of 2.4% were positive for Influenza A and 7.7% for Influenza B. Of 129 samples tested for other respiratory pathogens; 0 were positive for RSV; 0 for PIVs; 0.77% for hMPV, and; 11.6% for adenovirus. From October 2006 to September 2007, 628 samples were submitted from patients at Kakuma refugee camp. A total of 1.8%were positive for Influenza A and 9.4% for Influenza B. Of 117 samples tested for other respiratory pathogens; 17.9% were positive for RSV; 14.5% for Ad; 4.3% for PIV; and 2.6% for hMPV. Of these subsets, no samples were positive for *Chlamydia pneumoniae*, *Mycoplasma pneumoniae*, or *Legionella pneumophila*. **Conclusions:** A sentinel surveillance system for respiratory diseases was effective in identifying patients with respiratory illness at two refugee camps in Kenya. Sentinel surveillance systems can be implemented in refugee camp settings to detect the presence of specific pathogens and clusters of respiratory illness indicating outbreaks and to guide prevention strategies.

Board 313. Pyogenic Liver Abscesses with *Klebsiella pneumoniae* in a Public Hospital in Queens, New York

M. Pastagia[1], V. Arumugam[2];

[1]Mount Sinai Hospital, New York, New York, NY, [2]Elmhurst Hospital, Queens, NY.

Background: *Klebsiella pneumoniae* liver abscesses have become more common in US hospitals, based upon the demographics of the population served. **Methods:** We reviewed laboratory and clinical data for patients admitted to Elmhurst Hospital, New York from 2000-2007. **Results:** Of the 56 cases of pyogenic liver abscesses reviewed, twenty (35.7%) were secondary to *Klebsiella pneumoniae*, verified via radiographic imaging plus positive blood culture or liver aspiration culture. Liver drainage appeared to be the most important aspect for treatment. The mean age of the patients was 56.5 years. Fourteen (70%) were male. Twelve patients (60%) were of Asian descent. Hypertension was found in 9(45%) of the patients, diabetes mellitus and biliary disease were found in 5(25%) each, no medical history found in 4(20%). Solitary abscess was found in 16(80%) of patients, 15 of those in the right hepatic lobe. Of the 4(20%) with multiple abscesses, 2 were in the right hepatic lobe, and 2 in the left hepatic lobe. Positive blood culture was found in 65% and positive liver abscess culture in 70%. Eight patients had both positive blood cultures and positive liver abscess cultures (40%). Four patients experienced metastatic infection to the lungs (20%), and only one patient developed meningitis, bilateral

endophthalmitis, and pneumonia. Fifty per cent of patients received an infectious diseases consult. All of these cases were treated with ceftriaxone. The mean duration of intravenous antibiotics for these patients was 23.9 days. The mean duration of antibiotics for patients without an infectious diseases consult was 12.2 days. **Conclusions:** The majority of *Klebsiella pneumoniae* liver abscesses occurred in patients of Asian descent, many without any risk factors. Choice of antibiotics and length of treatment varied depending upon whether an infectious disease consult was called or not. Patient demographics should be kept in mind in patients with liver abscesses.

Board 314. Assessing Exposure to West Nile Virus in the Migrant Agricultural Workers of the Niagara Peninsula, Canada

R. Mergl, A. Duarte, A. L. Sanchez;

Brock University, St. Catharines, ON, CANADA.

Background: Since its introduction in 2001, the number of reported human clinical cases of West Nile virus (WNV) has consistently declined in the Niagara Peninsula. No WNV human cases have been reported in the region for 2007 but since infection in humans is usually either asymptomatic or causes mild febrile disease the possibility of undiagnosed infections is high, thus the question remains whether transmission to humans is occurring. The objective of this study was to determine transmission of WNV in a human population with increased exposure to mosquito bites. **Methods:** Niagara migrant agricultural workers with outdoor activities and therefore mosquito bite exposure from sunrise to late evening hours were chosen as study population. Workers who volunteered for the study answered a questionnaire and provided blood samples for serological evaluation. Antibody determination for WNV was done with an IgM capture ELISA and an IgG indirect ELISA with secondary avidity testing. Since participants may have had previous Dengue exposure, anti-Dengue IgG antibodies were also determined with an indirect ELISA (all tests were from PanBio Ltd., Brisbane, Australia). Plaque Reduction Neutralization Test (PRNT) for WNV and Dengue were requested for positive samples.**Results:** In total 92 participants originating from 21 states of Mexico completed the study (77% men; age range 22-65 years, mean 38). Less than 5% of participants were aware of the presence of WNV in Canada or knew about its transmission. Seropositivity was as follows: 2.17% for IgM WNV, 20.7% for IgG WNV, 17.1% for IgG Dengue, and 16.3% for both WNV and Dengue IgG. Avidity testing on 19 IgG WNV positive samples resulted in 68.4% past and 31.6% recent infections. **Conclusions:** IgM positivity suggests active WNV transmission most likely occurring in Canada since very few human infections have been detected in Mexico so far. The IgG cross-reactivity between WNV and Dengue was expected but the probability that some of this seropositivity might be due to WNV cannot be excluded until PRNT results are obtained. PRNT results in combination with avidity test results will provide definitive answers regarding exposure to WNV and its risk factors in Niagara. The lack of knowledge and awareness regarding WNV is concerning and the need for protective measures is warranted in this population.

Board 315. Being Free of Tuberculosis: Not Just a Matter of Health.

A. Duarte, A. L. Sanchez;

Brock University, St. Catharines, ON, CANADA.

Background: Although obviously a concern for developing nations, tuberculosis (TB) is also a concern for wealthy countries receiving permanent or temporary immigrants born in TB-endemic areas. The Canadian Seasonal Agricultural Workers Program (SAWP) presents >16,000 workers from the Caribbean and Mexico with an opportunity for secure employment to support family needs and increase living standards. Candidates to SAWP require active TB clearance thus eliminating the risk for local transmission; however, the rate of latent tuberculosis infection (LTBI) in this population is unknown. With a lifetime reactivation risk of 5-10%, it is important for LTBI-positive workers to be cognizant of their status and take actions to protect both their health and employment. This study aimed to determine the LTBI prevalence in a sample of Mexican migrant agricultural workers in Niagara Region, Canada and provide an educational program focused on healthy behaviours, prevention and recognition of TB reactivation, and a proactive attitude towards one's health. **Methods:** A convenience sample of Niagara Region's SAWP Mexicans workers in 2007 was invited to participate in the study. Participants answered a questionnaire assessing knowledge and perceptions about TB, BCG and TB history. Additionally, LTBI was determined by the tuberculin skin test, TST (Mantoux) and an Interferon-Gamma release assay (QuantiFERON®, QNF, Cellestis Inc, Valencia, CA). **Results:** A total of 82 participants (80% male; age range 20-65, mean 35) completed the study. None had symptomatology suggestive of respiratory disease, 42% correctly identified active TB symptomatology, 86% had received BCG, and 28 (34%) were TST positive, of which 15 (18%) were confirmed with QNF. Since few workers (6%) were aware of the existence of LTBI, the educational program emphasized risks factors for TB rea ctivation.**Conclusions:** Our study demonstrates a high prevalence (18%) of LTBI in healthy Mexican agricultural workers, none of whom were aware of their status. After the educational sessions, workers were aware of risk factors for TB reactivation particularly HIV/AIDS, alcohol abuse, and smoking; and expressed interest in keeping their annual health check-up including chest X-rays to confirm clearance of active TB, which is crucial for their continued enrollment in SAWP.

Influenza

Wednesday, March 19
12:00 PM – 1:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 316. Use of Hospital Discharge Data to Assess Completeness of Reporting of Adult Influenza-Associated Hospitalizations, Colorado, 2006-07

J. Sadlowski[1], K. Gershman[2], S. Burnite[2], A. Conroy[1], A. Juhl[1];

[1]University of Colorado Denver, Denver, CO, [2]CO Department of Public Health and Environment, Denver, CO.

Background: Hospitalization of persons with a positive test for influenza (flu) is a reportable condition in Colorado. As part of the CDC-sponsored Emerging Infections Program network surveillance for flu hospitalizations, The Colorado Department of Public Health conducted a retrospective audit using statewide hospital discharge data to assess completeness of reporting of adult flu hospitalizations during the 2006-07 influenza season in the Denver metro area. **Methods:** Reported cases of hospitalized flu from the 2006-07 flu season in persons ≥ 18 years in the 5 county Denver metro area were matched by date of birth and medical record number to hospital discharge database records with ICD-9 code 487 (influenza). A hospital- and age-stratified sample of the remaining unmatched discharge records with ICD-9 codes 480-486 (pneumonia) was created. Medical charts of all unmatched hospital discharge records with ICD-9 code 487 and the sample of records with ICD-9 codes 480-486 were reviewed for evidence of positive flu test results. Completeness of reporting was calculated as the number of cases reported divided by the number of cases eligible to be reported. **Results:** During the 2006-07 influenza season, 108 cases of adult flu hospitalizations were reported prospectively by hospitals in the Denver metro area. We identified 93 unmatched records with a 487

discharge code, of which 58 (62%) had medical chart documentation of positive flu test results and met the surveillance case definition. For 14 (24%) previously unreported cases, flu testing was performed at another facility/clinic prior to admission. Among the sample of 433 charts with 480-486 discharge codes, none had documentation of positive flu test results and only 11.8% had indication that flu testing was performed. Completeness of prospective adult flu hospitalization reporting was 65%. **Conclusions:** Prospective reporting of adult flu hospitalizations in the Denver metro area during 2006-07 was not optimal. Chart abstraction based on hospital discharge database ICD-9 code 487 was a sensitive method for identifying unreported cases, whereas, ICD-9 codes 480-486 were non-contributory. A low proportion of hospitalized adults with pneumonia were tested for influenza.

Board 317. Latitudinal Variations in Seasonal Patterns of Influenza and Respiratory Syncytial Virus (RSV): A Multinational Comparative Study

C. Viboud[1], W. Alonso[1], L. Simonsen[2], M. Miller[1], K. Bloom-Feshback[1];

[1]Fogarty International Center, National Institutes of Health, Bethesda, MD, [2]George Washington University, School of Public Health and Health Services, Washington, DC.

Background: For reasons poorly understood, influenza and RSV epidemics display marked winter seasonality in temperate areas and less-defined patterns in the Tropics. A global review of these patterns is needed to elucidate the mechanisms driving seasonality. Here we investigate latitudinal variations in seasonality and prevalence of influenza and RSV in more than 40 countries (latitude range, 60°N to 40°S). **Methods**: We searched the literature for laboratory studies of acute respiratory infections conducted between 1990 and 2007, reporting influenza and RSV relative prevalence in children under 5 yo (% positive among all specimens tested), or seasonal patterns (peak timing and epidemic duration). Additional seasonal data for 10 countries were compiled from influenza surveillance websites. Meta-regression was used to test the relationship between latitude and prevalence, adjusting for socio-demographics and study settings. **Results**: Despite substantial heterogeneity across studies, relative prevalence in young children was substantially higher for RSV (n=96, mean, 28.2%, range 0.1% - 78%) than influenza (n=51, mean 9.6%, range 0.4% - 49%, P<0.01). High latitude (above 25°) was associated with a ~40% higher prevalence of influenza and RSV infections in adjusted models (P<0.01). Epidemics consistently peaked during winter months in high latitude locales, with longer epidemic seasons for RSV than influenza (2.9 vs 1.9 months, P<0.001). Seasonal patterns were more diverse among Tropical countries, ranging from marked seasonality to persistent year-round activity. Epidemic duration varied inversely with absolute latitude for influenza (R^2= 26%, P=0.0002), but not for RSV (P=0.15). Biannual peaks were relatively common in South-East Asian countries for influenza (60%, n=10) and RSV (23%, n=13, P=0.06). **Conclusion**: A variety of pathogens contributing to acute respiratory infections may explain the lower relative prevalence of influenza and RSV in children from Tropical countries (eg, measles, dengue, malaria). For both viruses, a universal threshold at ~25° latitude appears to limit activity to wintertime. By contrast, local factors could drive the diversity of seasonal patterns in Tropical areas, including climate, altitude, seasonal changes in contacts, and international population fluxes.

Board 318. Effectiveness of Inactivated Influenza Vaccines Varied Substantially with Antigenic Match in the United States During the 2004-05 to 2006-07 Seasons

D. K. Shay[1], B. A. Kieke[2], J. G. Donahue[2], R. T. Greenlee[2], A. Balish[1], A. Foust[1], S. Lindstrom[1], E. A. Belongia[2];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Marshfield Clinic Research Foundation, Marshfield, WI.

Background: Timely information on the effectiveness of influenza vaccine for preventing laboratory-confirmed infection has not been routinely available. We estimated the effectiveness of licensed trivalent inactivated influenza vaccines during 3 consecutive seasons with variable antigenic match between viruses isolated from patients and vaccine strains. **Methods:** Prospective case-control studies were performed within Wisconsin population cohorts during the 2004-05 through 2006-07 seasons. The seasonal cohorts included 11,565 (2004-05) to 20,693 (2006-07) children and adults for whom influenza vaccine was recommended. Consenting individuals with medically attended acute respiratory illness were tested for influenza by culture and RT-PCR. Separate case-control analyses were performed using asymptomatic controls and ill controls with a negative influenza test. Vaccine effectiveness (VE) was calculated as 100 x (1 - adjusted odds ratio) for vaccination in patients with laboratory-confirmed influenza. Influenza isolates were antigenically characterized by hemagglutination inhibition and compared with vaccine strains. **Results:** The proportion of enrolled patients with influenza was 20% (167/818) in 2004-05, 14% (51/356) in 2005-06, and 11% (102/932) in 2006-07. In 2004-05, VE for medically-attended, laboratory confirmed influenza was 5% using ill controls and 3% using asymptomatic controls. In 2005-06, VE was 14% and 3%, respectively. The 95% confidence intervals (CI) included zero during these seasons. In contrast, during 2006-07 VE was 53% (95% CI, 26% to 71%) and 31% (95% CI, -20% to 60%), respectively. In each season, VE did not vary significantly by age group. VE was 90% (95% CI, 4% to 100%) for preventing influenza hospitalization in 2006-07. The proportion of viruses isolated from patients that were antigenically matched to vaccine strains was 5% in 2004-05 and 2005-06, and 91% in 2006-07. **Conclusions:** Influenza vaccine effectiveness varied significantly by season. Substantial effectiveness was found during the 2006-07 season, when vaccine strains and viruses isolated from patients were antigenically closely matched. Repeated assessments of vaccine effectiveness against laboratory-confirmed influenza are needed in populations at highest risk for severe outcomes from influenza.

Board 319. Variations in Primary Care Physician Influenza Testing Practices

R. Belflower[1], C. Long[1], A. Detty[2], G. Dumyati[1], C. Piper[3], N. Spina[3], N. Bennett[1];

[1]University of Rochester, Rochester, NY, [2]Yale University, New Haven, CT, [3]New York State Department of Health, Albany, NY.

Background To understand the true burden of influenza and prepare for an influenza pandemic, differences in testing capacity and practices must be understood. For example, the Rochester and Albany regions of the New York State (NYS) Emerging Infections Program have vastly different rates of hospitalization (5 vs. 0.6 per 100,000) for laboratory-confirmed influenza. Data collected for a national survey of provider practices related to influenza testing were examined for differences in the two regions and to identify factors associated with testing patterns. **Methods** Primary care physicians (PCPs) from Albany and Rochester, NY, were randomly selected from active licensure lists and surveyed between June and August 2007. Physicians were eligible for the survey if they practiced Internal Medicine, Pediatrics, Family Medicine or

Obstetrics/Gynecology in one of 8 counties in the Albany region and 7 surrounding Rochester, and performed 8 or more hours of direct patient care. Through a mailed survey, PCPs were asked about testing and antiviral prescribing practices during the 2006-07 influenza season. Data were analyzed by specialty and practice setting. Various factors were examined for their role in predicting testing practices. **Results** Surveys were mailed to 953 PCPs, 488 (51%) were returned complete and 357 (73%) of these met eligibility criteria. Significant differences in influenza testing practices were found between the two regions. Rochester PCP's (69%) were more likely than Albany PCPs (53%) to report ordering tests for flu (p =.02) while significantly more PCP's in the Albany region (61%), compared to 41% in Rochester, report prescribing antivirals (p=.008). On-site rapid influenza testing was available to more Albany (33%) than Rochester (13%) PCPs (p=.002), although overall 49% of responding PCPs had access to some type of rapid influenza tests. Factors associated with influenza testing included practicing in an academic setting compared to outpatient/private, HMO/managed, or hospital-based settings, and practicing in Rochester compared to Albany. **Conclusions** Differences in testing practices of Albany and Rochester may account for differing influenza hospitalization rates. Such differences must be considered in determining disease burden based on laboratory reporting.

Board 320. The 1918 Pandemic Experience in Japan: Age and Geographic Mortality Patterns

S. A. Richard[1], N. Sugaya[2], L. Simonsen[3], M. Miller[1], C. Viboud[1];

[1]National Institutes of Health / Fogarty International Center, Bethesda, MD, [2]Keiyu Hospital, Yokohama, JAPAN, [3]George Washington University, Washington, DC.

Background: The 1918 influenza pandemic had a devastating public health impact worldwide, with an unusual concentration of mortality among young adults. Here we describe the Japanese experience of the 1918 pandemic, focusing on age and geographic mortality patterns. **Methods:** Monthly and annual all-cause and pneumonia and influenza (P&I) mortality data by age were compiled for Japan and each of the 47 administrative prefectures for 1915-1923. Serfling seasonal regression on monthly data was used to estimate excess mortality for the 1918-19 and 1919-20 pandemic seasons. Furthermore, we compared pandemic to pre- (1915-17) and post-pandemic (1921-23) annual age-specific P&I mortality to determine excess mortality. **Results:** Annual and monthly approaches gave consistent estimates of all-cause excess mortality across the 47 prefectures (correlation=0.79, P<0.001, average difference between methods 5.5%). The excess all-cause mortality rate in Japan was 5.4/1,000 in the first pandemic season (1918/19) and 3.3/1,000 in the second season (1919/20). Over the three year pandemic period (1918-20), the excess P&I mortality rate in young adults (20-40 years of age) was 10.3/1,000, over 650% higher than the three year baseline rate of this age group. By contrast, excess P&I mortality rate in seniors aged ≥60 years was 5.9/1,000, only about 65% higher than baseline rate. While excess mortality rates declined in most (43/47) of the prefectures during the second season, several prefectures around Tokyo suffered equivalent or higher excess mortality rates during 1919/20. The 1918-20 excess all-cause mortality rates varied more than 2-fold between prefectures, but there was no association between pandemic impact and baseline mortality rates, under 5 mortality rates, or population demographics (correlation<0.20, P>0.15). **Conclusions:** During the 1918 pandemic, young Japanese adults suffered unusually high mortality rates, similar to patterns found in the US, UK and Denmark. Densely populated areas in and around Tokyo partially escaped the first pandemic season, and the second season was more severe in Japan than in the US or UK. Finally, variations in pandemic mortality rates across Japan's administrative units appear only mildly affected by socio-economic factors.

Board 321. Use of Pyrosequencing for rapid sequence confirmation and characterization of real-time RT-PCR amplicons of A/H5N1 highly pathogenic avian influenza viruses

B. Shu, V. Deyde, J. Winter, T. Sheu, L. Gubareva and S. Lindstrom;

Virus Surveillance and Diagnosis Branch, Influenza Division, Centers for Diseases Control and Prevention, Atlanta, GA.

Background: Ongoing circulation of A/H5N1 highly pathogenic avian influenza (HPAI) viruses in poultry as well as infrequent infections in humans emphasize the need for rapid and sensitive diagnostic methods for detection of this virus. Real-time RT-PCR (rRT-PCR) is currently used in many public health laboratories for diagnostic testing for A/H5N1 HPAI virus infections in humans. However, confirmation of rRT-PCR results and further characterization of viruses is often difficult because of problematic issues with the specimens, such as limited volume, low viral load, or poor quality. In such cases, confirmation of rRT-PCR diagnostic results and generation genetic data for additional strain characterization may only be achieved by genetic sequencing of rRT-PCR amplicons. Also, sequence confirmation of rRT-PCR products can be used to rule out false positive results that are due to contamination by positive control RNA. Unfortunately, fluorescence-based dideoxy-mediated termination methods for nucleotide sequencing are time consuming and labor intensive. We have explored the use of pyrosequencing as an alternative method to increase the throughput of sequencing analysis of rRT-PCR amplified DNA products. **Methods:** Pyrosequencing is an alternative method for performing nucleotide sequencing that allows for rapid sequence analysis of short DNA fragments that are similar in length to those amplified by rRT-PCR. In order to allow for post-amplification sequence analysis of the HA gene by pyrosequencing, the CDC rRT-PCR assay for detection of A/H5N1 HPAI viruses was modified by biotinylation of one of the two amplification primers. **Results:** Modification of the rRT-PCR assay by biotinylation of amplification primers did not have any detectable affect on assay performance. High quality sequence data were obtained by standard pyrosequencing of amplified DNA products from all rRT-PCR positive reactions. **Conclusions:** Real-time RT-PCR assays for detection of A/H5N1 HPAI viruses were modified to allow for post amplification analysis of DNA products by pyrosequencing. Combined use of rRT-PCR and pyrosequencing technologies make it possible to rapidly generate confirmatory sequence data that can provide additional genetic information for further characterization of the HA gene of A/H5N1 HPAI viruses.

Board 322. Title: Respiratory Outbreaks Identified by Ongoing Surveillance at US Military Basic Training Centers

K. Butler-DeRose, K. L. Russell, D. Metzgar, M. Osuna, A. W. Hawksworth, D. J. Faix;

NHRC, San Diego, CA.

Background: The Department of Respiratory Disease Research at the Naval Health Research Center (NHRC), San Diego conducts population-based surveillance for febrile respiratory illness (FRI) at 8 US military basic training centers. High FRI rates are common among basic trainees with the majority of cases being caused by adenovirus and occasionally by influenza. Persistent FRI surveillance identified an emerging adenovirus (type 14) and out-of-season outbreaks of both influenza A/H3N2 and A/H1N1. **Methods**: NHRC uses molecular and culture methodologies to identify and characterize respiratory pathogens. Samples are collected from consenting recruits that present for medical care with an oral temperature ≥38.0°C (100.5 °F) plus any respiratory symptom, such as a cough or sore throat. During outbreaks or periods of elevated

FRI rates, NHRC increases the amount of patient sampling and gives the highest priority to processing of those samples. **Results**: In early 2006, Ad14 (subspecies B2) simultaneously emerged at 5 of the 8 training centers under surveillance. Ad14 consistently maintained a presence at 3 of the centers during the summer of 2006. Following the outbreak an early detection and screening process along with isolation of patients facilitated the reduction of more severe cases. An off-season cluster of influenza A/H1N1 was identified at the Marine Corps Recruit Depot, San Diego in the summer of 2006. A total of 9 cases were identified, none had been vaccinated, and nearly all were from the same unit. Once early vaccination was instituted no new cases were reported. In late August of 2007 an A/H3N2 influenza outbreak was detected at Fort Benning, Georgia. A total of 9 cases were identified from five different units; none of the trainees had been vaccinated. Continued collaboration with the CDC revealed that the A/H3N2 at Ft. Benning was the same strain that circulated in the area the previous year. Sequencing data for both influenza incidents and adenovirus serotypes were shared with the CDC. **Conclusions**: Despite decades of study and a large body of literature, there are still unknowns in the dynamics of FRI pathogen transmission in military populations. The discovery of these out-of-season influenzas and the emergence of Ad14 validate the need for active, ongoing respiratory surveillance at military training sites.

New or Rapid Diagnostics

Wednesday, March 19
12:00 PM – 1:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 323. Potential Point of Care Technology Tested as Part of an Avian Influenza Pandemic Preparedness Initiative

E. A. McDonough, C. A. Myers, C. Hansen, M. Irvine, D. J. Faix, K. L. Russell;

Department of Respiratory Disease Research at the Naval Health Research Center (NHRC), San Diego, CA.

Background: As part of a US Department of Defense Global Emerging Infections Surveillance (DoD-GEIS) initiative, the Department of Respiratory Disease Research at the Naval Health Research Center (NHRC) has been tasked with evaluating new technologies for pandemic preparedness as it pertains to avian influenza. Having the ability to quickly and accurately diagnose an avian influenza outbreak could reduce the spread of a potential pandemic. Meso Scale Discovery (MSD) has developed a multiplex antibody panel for detection of influenza A & B. MSD's technology couples an 'antibody sandwich' assay with electrochemiluminescenct detection. Capture antibodies localize the antigen to the electrical field-generating base while an electrochemical dye on the detection antibodies emit light as a signal when excited; multiple excitation cycles improve sensitivity. **Methods:** MSD's platform and influenza A panel were evaluated by NHRC for strengths in: accuracy, deployability (shipboard and field), ability to adapt to a point of care setting, and ease of use. Evaluation was done with a standardized sample panel of clinical specimens consisting of 20 seasonal Influenza A, 20 Influenza B, 20 Adenovirus, 15 Parainfluenza, 5 RSV, and 20 Negative samples as determined by PCR and/or Culture. All samples tested were throat swab patient specimens in Viral Transport Media collected from military trainees with febrile respiratory illness (FRI) at recruit camps around the United States as part of our FRI surveillance program. **Results:** The machine has a relatively small footprint with few outside supplies needed (plate shaker, vacuum pump, pipettes). A newer version is in development that integrates all outside equipment. Initial influenza results show high sensitivity (88%) and specificity (96%). Evaluation of a panel with specific antibodies for H1, H3 & H5 is ongoing. **Conclusions:** The ability to quickly and efficiently diagnose seasonal influenza and distinguish it from avian strains is crucial for pandemic preparedness. This test shows promise, with the ability to distinguish avian strains from seasonal strains. The test is user friendly and rapid, with a total test time of less than two hours.

Board 324. Development of a High-Throughput Multiplex PCR and Capillary Electrophoresis Technique for Serotype Determination of *Salmonella Enterica* Food Animal Isolates

J. G. Frye[1], B. T. Leader[2], P. J. Fedorka-Cray[1], J. Hu[2], D. S. Boyle[2];

[1]USDA, Athens, GA, [2]Washington State Department of Health, Shorline, WA.

Background: Previously, a multiplex PCR technique, which employed two 5 product PCR reactions and gel electrophoresis, was developed to identify the top 30 human clinical serotypes of *Salmonella enterica*. To improve the speed, ease of use, utility and discriminatory ability of the technique, additional primers were added and the PCR product discrimination and analysis was automated by capillary electrophoresis. **Methods:** Fifteen genes, whose distribution reflects the different serotypes of *Salmonella enterica*, were targeted for amplification in a single multiplex PCR reaction. All forward primers incorporated a universal sequence complementary to a carboxyfluorescein (FAM) linked universal primer used to label all products for detection. The primer pairs and the universal primer were combined in a master mix containing a Hot Start Taq polymerase (Bioline, USA Inc, Randolph, MA, USA). Templates were prepared by the boiled colony method and thermocycling parameters were 94°C 15 min, (94°C 30s, 57°C 90s, 72°C 30s) x 25, 72°C 5min, (94°C 30s, 68°C 90s, 72°C 30s) x 15, 72°C 5min. Samples were diluted 1:100 (v/v) in formamide containing carboxy-X-rhodamine (ROX) labeled GENEFLO 625 DNA Ladder (CHIMERx, Milwaukee, WI, USA) and separated in an ABI 3100 Avant gene analyzer on a 50 cm capillary. **Results:** Fifty-four *Salmonella* isolated from raw pork were analyzed by the multiplex PCR analysis technique (PCR) and by traditional serotyping (TS). PCR resulted in serotypes for 49/54 isolates, while TS resulted in 53/54 serotypes with one isolate failing identification by both techniques. Results were the same for the 49 isolates that were serotyped by both techniques, (28 serotype Typhimurium, 18 Infantis, and 3 Seftenberg). Traditional serotype determination also identified four isolates as serotype Muenchen. Overall use of PCR resulted in a 92% (49/53) accuracy, lower cost (~$5 for PCR versus ~$39 for TS), and quicker turn-around time (6 h for PCR versus weeks for TS) as compared to TS. **Conclusions:** Automated multiplex PCR successfully determined the serotype of *Salmonella enterica* isolated from pork 92% of the time as compared to traditional serotyping indicating that a rapid and more economical alternative to TS is available. The inclusion of additional primers will increase the identification of additional serotypes.

Board 325. Rapid Molecular Determination of Serotype from Clinical Isolates of *Salmonella Enterica*

D. S. Boyle[1], B. T. Leader[1], J. G. Frye[2], D. Russell[1], P. Fedorka-Cray[2], J. Hu[1];

[1]Department of Health, Shoreline, WA, [2]USDA, Athens, GA.

Background: The conventional serotyping of *Salmonella Enterica* is time-consuming, costly, and requires highly-skilled staff. In the present study, we report a multiplex PCR typing method using capillary electrophoresis for fragment analysis that allows for the identification of the 30 most common clinical serotypes of *S.*

Enterica. The use of capillary electrophoresis dramatically improves the throughput, accuracy, discrimination, and sensitivity of this technique compared to conventional agarose gel electrophoresis. This new method of *Salmonella* typing has been used to test clinical isolates from Washington State and offers an alternative to conventional serotyping. **Methods:** Fifteen genes were identified based on their distribution's ability to discriminate different serotypes of *S. Enterica*. Regions of these genes were targeted for amplification in a single multiplex PCR reaction. All forward primers incorporated a 5' universal sequence to fluorescently-label the forward strand via a complementary universal probe containing FAM. Hot Start PCR was performed with template DNA extracted from either boiled PFGE plugs or from boiled colonies. Samples were diluted 1:100 (v/v) in formamide containing CHIMERx 625 DNA Ladder and separated in an ABI 3100 Avant gene analyzer. Data was analyzed using ABI GeneMapper v3.5. **Results:** Multiple isolates representing the thirty most common serotypes were analyzed by the multiplex PCR assay to determine representative amplicon codes for each serotype. Using the representative codes, we correctly typed 83% of 400 previously serotyped clinical isolates. Eight percent of the 17% of isolates that we were unable to type with our assay represented rare serotypes that we had not initially screened with our assay. **Conclusions:** Our fragment analysis-based multiplex PCR typing method is comparable to conventional serotyping in its accuracy, especially when used in conjunction with PFGE. Most importantly it is faster, more cost effective, and avoids the current QC issues arising from the availability, storage, and validation of the numerous reagents required for serotyping. We propose that this method will allow for the rapid and highly accurate typing of extremely large collections of specimens, thus providing an effective alternative to conventional serotyping.

Board 326. *Salmonella* Molecular Serotyping with a DNA Microarray : an Approach for Non Agglutinable *Salmonella enterica* Serotypes

A. Brisabois[1], M. Marault[1], A. Dekker[2], A. Kerouanton[1], S. Fremy[1], F. Moury[1], P. Vos[3], R. Van Santen[2], J. Fabre[4];

[1]afssa Lerqap, Maisons - Alfort, France, [2]dsm, Delft, The Netherlands, [3]check Point, Wageningen, The Netherlands, [4]phylum, Labege, France.

Background: *Salmonella* serotyping is an important tool for classification of strains, identification of sources and epidemiological purposes. In addition, regulations require monitoring of certain serotypes. Traditional serotyping is based on the Kauffmann-White antigen-antibody scheme. Application of this method is limited by the high costs, deviations in quality of sera, time-consuming and presence of non-typable isolates. Therefore, a fast molecular serotyping system based on DNA chips based on the Clondiag technique has been developed by Check-Points (The Netherlands). This new procedure (Premi-Test Salmonella (PTS) has been evaluated for its ability to determine the "molecular serotype" (genovar) of non-typable *Salmonella* isolates. **Methods:** Thirty three *Salmonella* strains isolated from various sources were analysed to determine the genovar using the PTS method. All the 33 tested strains were non typable by slide agglutination. Moreover, strains were subtyped by pulsed field gel electrophoresis (PFGE) after DNA macrorestriction according to the standardized PulseNet protocol. A *Salmonella* PFGE database was used to determine an expected serotype based on the PFGE patterns obtained. These PFGE results were compared with the PTS results. **Results:** PFGE sub-typing: Thirty isolates shared in 19 PFGE patterns associated to a genomic cluster corresponding to a given serotype: Typhimurium (15 strains), Enteritidis (3), Kottbus (2), Virchow, Mbandaka, Derby, Saint Paul, Newport, Goldcoast, Hadar, Senftenberg, Bredeney and Montevideo (1 strain each). Only three isolates gave unknown PFGE types. PTS genovars: Thirty one isolates were assigned to a certain serotype, the same as those found with PFGE were encountered. Only two strains yielded an unknown genovar. The results obtained with both methods were concordant for 29 isolates. Two strains harbouring an unknown PFGE pattern were determined as "Livingstone" serotype with the PTS. **Conclusions**: The PFGE and PTS methods were able to identify the serotype of 30 and 31 isolates respectively. The concordance between both methods was 91% and by combining both methods, a serotype was accessible for 32 out of the 33 strains. This study demonstrates the suitability of the PTS method for *Salmonella* molecular serotyping including non agglutinable isolates.

Nosocomial Infections

Wednesday, March 19
12:00 PM – 1:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 327. An Application of Social Network Theory to Optimize Influenza Vaccination among Healthcare Workers

P. M. Polgreen[1], T. L. Tassier[2], S. V. Pemmaraju[1], A. M. Segre[1];

[1]University of Iowa, Iowa City, IA, [2]Fordham University, New York, NY.

Background: Influenza vaccination is the most effective measure for preventing nosocomial spread of influenza, and the CDC recommends vaccination for all healthcare workers. Yet, in the US, only 36% of workers with direct patient contact are immunized annually. Interventions exist to increase vaccination rates, but they are costly to implement, and there are no data to identify the groups of healthcare workers who should be the primary focus of such interventions. Similarly, there are no data to guide vaccination efforts in the event of a vaccine shortage, nor is there a theoretical framework to inform such decisions. **Methods:** At the University of Iowa Hospital and Clinics (UIHC) we shadowed individuals from16 different healthcare-worker groups for 40 hours over different times of day and counted all contacts of the observed healthcare workers with patients and other healthcare workers. All contacts (direct touch and within three feet) were recorded. Using these data, we constructed a network representative of the contact structure at UIHC. We then performed an agent based SIR model of influenza transmission across the network assuming no vaccination, in order to observe baseline infection rates among worker groups. We then introduced vaccinations, varying the vaccination rates of healthcare worker groups in order to measure the marginal effect of each vaccination (the number of secondary infections prevented by inoculating a given individual in a given group). **Results:** In the simulation we observe a large degree of heterogeneity in the infection rates of worker groups. Thus, not surprisingly, the effectiveness of vaccinations also varies greatly. We find that vaccinating individuals from groups whose members have large numbers of contacts (such as residents, medical students, and floor nurses) or groups whose members have contacts within many different hospital groups (such as unit clerks) provides the greatest benefit. **Conclusions:** The degree and structure of contacts among healthcare workers contribute greatly to the size of outbreaks in our simulations. Our results suggest that social network theory can help inform interventions to target and optimize vaccination strategies to protect patients against nosocomial spread of influenza.

Board 328. Using Active Microbiologic Surveillance During an Outbreak of Healthcare-Associated Extended Spectrum Beta-Lactamase-Producing *Klebsiella pneumoniae* Infections --- New Jersey, 2007

A. J. Langer[1], P. Lafaro[2], C. A. Genese[3], P. McDonough[2], R. Nahass[2], C. Robertson[3];

[1]Epidemic Intelligence Service assigned to the New Jersey Department of Health and Senior Services, Centers for Disease Control and Prevention, Atlanta, GA, [2]Somerset Medical Center, Somerville, NJ, [3]New Jersey Department of Health and Senior Services, Trenton, NJ.

Background:Extended spectrum beta-lactamase-producing (ESBL) bacteria are an important cause of healthcare-associated infections. During April-July 2007, a regional hospital identified six patients with ESBL *Klebsiella pneumoniae* infections in its 12-bed private-room intensive care unit (ICU). Normally, this ICU expects fewer than three cases for such a period. Infection sites included the urinary tract (three), surgical wounds (two), and central venous catheter (one). We investigated this outbreak to characterize its extent and to implement control measures. **Methods**: We reviewed all patients' medical records to identify common exposures, including equipment and hospital staff as well as antibiotic usage patterns. The hospital instituted enhanced infection control (EIC) measures, including contact precautions, cohorting of infected patients (IP), and weekly terminal cleaning of all patient rooms. We collected active surveillance cultures (ASC) from all ICU patients weekly. We cultured ICU staff common to all infected patients. We submitted all isolates for pulsed-field gel electrophoresis (PFGE). **Results**: We identified three colonized ICU patients (CP) through ASC, for a total of nine patients during the outbreak period. This represented an infection rate of approximately 8.6 cases/1,000 patient-days. Common ICU exposures included endotracheal or tracheostomy tube placement; no intubation personnel were common to all patients. All isolates but two (one IP, one CP) were indistinguishable by PFGE. We identified no colonized staff. No patterns in antibiotic usage were identified. A suspected source-patient's infection was initially identified 4 weeks before the other affected patients; this patient was in ICU concurrently with two other affected patients. One patient became infected after EIC implementation, but we identified no additional cases after 5 weeks. **Conclusions**: These findings support that this outbreak was likely caused by transmission among infected patients. Because each patient had a private room and was relatively immobile, transmission likely occurred through contaminated fomites or healthcare workers' hands. EIC measures halted the outbreak, highlighting the effectiveness of EIC practices even in the absence of a clearly defined source.

Board 329. Microbiological Agents as a Contributing Cause of Death in Wounded Service Members During Iraqi Freedom and Enduring Freedom

R. N. Potter[1], L. M. Pearse[1], C. T. Mallak[1], J. C. Gaydos[2];

[1]Office of the Armed Forces Medical Examiner, Rockville, MD, [2]Global Emerging Infections Surveillance System, Silver Spring, MD.

Background: During the Global War on Terror (GWOT), many more Service members suffer battle-related injuries than are killed in action. A small fraction later die of those injuries after evacuation to military medical facilities in Germany or the United States. Some of those deaths are directly due to a secondary infection. **Methods**: The Mortality Surveillance Division (MSD) of the Armed Forces Medical Examiner System tracks the cause of death in all military personnel, including combat-related deaths. Service members who die after evacuation while still on active duty are identified by the MSD office, and an autopsy report is obtained. Those autopsy reports list the cause(s) of death, and usually include the results of relevant peri-mortem cultures. The autopsy reports are used by the authors to determine the relative role of infectious agents in those deaths. **Results**: From October 1, 2001 through September 30, 2007, there have been a total of 3,307 combat deaths. Of those, 113 (3.4%) have died of their wounds after medical evacuation from theater. Fifty-eight of the 113 autopsy reports have been extracted (review of the remaining is ongoing). Preliminary analysis of 58 deaths shows 24 (41%) with no infectious component. Of the remaining 34 deaths, 30 had an infectious process (sepsis, pneumonia, wound infection, meningitis, etc.) that was either the immediate cause of death (9 deaths) or was one of several other non-infectious immediate causes, such as hemorrhage, severe brain injury or multi-organ failure. Eighty-five positive peri-mortem cultures were seen in the 30 cases, with Klebsiella (19%), Acinetobacter (19%) and Pseudomonas (15%) most often identified. Seven of the 30 had only one agent identified, while over half (16) had 3 or more agents. **Conclusions**: Although these fatalities occurred after evacuation from theater, the injuries were frequently devastating and many of the 113 deaths experienced months of hospitalization before succumbing to their wounds. Other than Acinetobacter, the identified agents are those commonly seen in the setting of prolonged hospitalization. Acinetobacter, either acquired from theatre or nosocomially, is a significant contributor to delayed combat trauma deaths. However, its role appears to be comparable to Klebsiella and Pseudomonas in this patient population.

Outbreak Investigation: Lab & Epi Response

Wednesday, March 19
12:00 PM – 1:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 330. PulseNet International and WHO Global Salm-Surv: A Collaborative Effort to Reduce the Global Burden of Enteric Diseases

A. M. ElSedawy[1], N. T. Maxwell[2], N. Binsztein[3], E. Perez[4], F. J. Angulo[5], P. Gerner-Smidt[1];

[1]Enteric Diseases Laboratory Branch, Centers for Disease Control and Prevention (CDC), Atlanta, GA, [2]Enteric Diseases Epidemiology Branch, Centers for Disease Control and Prevention (CDC) and United States Veterans Administration, Atlanta, GA, [3]Bacteriology Department, Instituto Nacional de Enfermedades Infecciosas - ANLIS "Carlos G Malbran", Buenos Aires, ARGENTINA, [4]Area of Health Surveillance and Disease Management, Pan American Health Organization (PAHO), Rio de Janeiro, BRAZIL, [5]Enteric Diseases Epidemiology Branch, Centers for Disease Control and Prevention (CDC), Atlanta, GA.

Background WHO Global Salm-Surv (WHO GSS), with 14 international training sites, promotes integrated, laboratory-based surveillance among human health, veterinary, and food disciplines and enhances laboratory capacity to isolate, identify, and subtype foodborne and other infectious enteric pathogens. PulseNet International (PNI), consisting of six regional networks, is a global early warning system to detect foodborne disease clusters and investigate outbreaks using Pulsed-Field-Gel-Electrophoresis (PFGE). WHO GSS serves as a platform to introduce PFGE and PNI concepts globally. Both networks are dedicated to enhancing the capacity of countries to detect, respond to, and prevent foodborne diseases. **Methods** To guide the WHO GSS and PNI collaboration, the following strategic steps were developed: 1) identify and

assess PNI involvement and PFGE capacity among WHO GSS member institutions, 2) launch WHO GSS/PNI training courses to introduce the importance of collaboration among microbiologists and epidemiologists using PFGE data, and 3) encourage and assist course participants to develop projects and advocate for funding to conduct and use PFGE. **Results** A questionnaire to assess PNI involvement and PFGE capacity among WHO GSS member institutions was distributed to microbiologists from 50 institutions from 20 countries at the WHO GSS courses held in Russia and East Africa. Plans for a joint WHO GSS/PNI International Training Course for 32 microbiologists and epidemiologists from 10 South American countries have been initiated. PulseNet concepts were introduced to 160 participants from 30 countries at WHO GSS courses held in Brazil, Russia, and East Africa; WHO GSS was also presented and discussed at PNI meetings held in the Middle East, the United States and Latin America **Conclusions** This collaborative effort between two independent networks enhances the overall integrated surveillance activities of both WHO GSS and PNI members and builds synergy to facilitate stronger capacity building for foodborne diseases globally. Future joint courses will be launched in additional regions and will facilitate strengthened communication and collaboration between microbiologists and epidemiologists. This relationship acts as an example of a horizontal partnership among global networks.

Board 331. The Usefulness of a Web Forum and Online Questionnaire in the Investigation of an Outbreak of *Campylobacter jejuni* Associated with a Mountain Bike Race, British Columbia, Canada, June-July, 2007

T. L. Stuart[1], J. Sandhu[2], J. Corder[3], A. Ellis[4], R. Stirling[1], E. Galanis[5];

[1]Canadian Field Epidemiology Program, Public Health Agency of Canada (PHAC), Ottawa, ON, CANADA, [2]Office of the Chief Medical Health Officer, Vancouver Coastal Health Authority, Vancouver, BC, CANADA, [3]Squamish Community Health Centre, Vancouver Coastal Health Authority, Squamish, BC, CANADA, [4]Foodborne, Waterborne and Zoonotic Infections Division, PHAC, Guelph, ON, CANADA, [5]British Columbia Centre for Disease Control, Vancouver, BC, CANADA.

Background: An international *C. jejuni* outbreak associated with a June 16, 2007 mountain bike race occurred in British Columbia. Following the race, messages regarding ill racers were posted on a race-related web forum. The use of this forum and an online questionnaire represent innovative investigation strategies employed in this outbreak investigation. **Methods:** To determine the role that the web forum played in the outbreak investigation, we compared the date of outbreak detection using the forum to the date of laboratory confirmation of the first cases. We reviewed all forum postings for hypotheses on possible sources of *Campylobacter* exposure during the race. An online questionnaire was developed and a link sent to race participants via their race registration email addresses. Questionnaire response rates and speed of response were determined. **Results:** The first web forum posting mentioning ill racers was on June 18. The race organizer notified public health officials about the forum on June 20. On June 25, public health officials received the first laboratory reports of *C. jejuni* infection in ill racers. Thirty-four individuals posted 58 entries in the forum. The hypotheses discussed regarding sources of *Campylobacter* exposure included inadvertent mud consumption, consumption of certain food items, and the use of a common cloth to wipe riders' faces. Questions were designed to address these and other hypotheses. The online questionnaire was designed, piloted and launched in less than 48 hours. Within two hours of sending the email invitation, 69 questionnaires had been completed; after 48 hours there were 293 responses. Within 11 days, 537 (68%) race participants completed the questionnaire. **Conclusions:** The web forum identified the outbreak prior to laboratory results and aided in questionnaire development. The use of an online questionnaire eliminated the need for time consuming phone interviews and data entry. The ease of completing the questionnaire online combined with interest generated by the forum likely played a role in the high response rate. Internet technologies such as these can play important roles in the identification and investigation of outbreaks. Web forums can also be used to relay recommendations, provide accurate sources of information and encourage participation in investigations.

Board 332. An Outbreak of Acute Respiratory Disease Caused by *Mycoplasma pneumoniae* In a Shipboard Environment.

J. A. Sliman[1], D. Asseff[2], D. Faix[3], S. Lizewski[4];

[1]NEPMU6, Pearl Harbor, HI, [2]Naval Medical Center, San Diego, CA, [3]Naval Health Research Center, San Diego, CA, [4]NEPMU5, San Diego, CA.

Background: Acute respiratory disease (ARD) is the leading cause of lost training time among military populations. *Mycoplasma pneumoniae* is a common cause of acute respiratory infections in young adults. Transmission of *M. pneumoniae* probably occurs through close contact with contaminated respiratory droplets. Shipboard populations, due to close-quarter living and work environments, are particularly susceptible to the rapid spread of respiratory pathogens. We investigated an outbreak of acute respiratory illness aboard a U.S. Navy ship in May 2007. **Methods:** Based upon review of routine surveillance data, a U.S. Navy epidemiological investigation team embarked aboard the affected ship between the dates of 20 and 30 May 2007. Activities included medical record review, patient interviews, and oropharyngeal swab and serum specimen collection. Information was analyzed for demographics, temporal and spatial association of cases, and significance of associations. Specimens were sent to Naval Health Research Center where they were tested for respiratory pathogens using real time PCR. **Results:** A total of 179 cases of respiratory illness occurred on the affected ship between 1 February and 28 May 2007. Of these, 55 (30.7%) had documented fever (oral temperature >100.4F) on presentation. Sixty-six patients received a chest x-ray during their evaluation, with 50/66 (75.8%) positive for infiltrate by radiologist-confirmed reading. PCR testing identified the presence of *M. pneumoniae* in 23 of 31 respiratory specimens obtained. None of the specimens were positive for adenovirus or influenza virus. Habitation in female centerline berthing compartment, the rating of Storekeeper, and the rank of Chief Petty Officer were all significantly associated with development of respiratory illness. **Conclusions:** Based upon epidemiological and laboratory data, the outbreak of respiratory illness aboard the affected ship implicated *M. pneumoniae* as the causative organism. The outbreak likely originated within the compartment where the two index cases habitated. Once established aboard ship, disease was transmitted throughout the crew through person to person transmission via close quarter exposures. This investigation suggests that *M. pneumoniae* is a significant source of respiratory illness aboard ships.

Board 333. Challenges to Contact Tracing Investigations Following International Airline Travel by Persons with Infectious Tuberculosis

D. Scholten[1], K. Marienau[2], C. Kim[2], J. Neatherlin[2], C. Schembri[2], M. Russell[2], K. Buckley[2], E. Ellis[1];

[1]Public Health Agency of Canada, Ottawa, ON, CANADA, [2]Centers for Disease Control and Prevention, Atlanta, GA.

Background: Several recent high profile events related to cases of tuberculosis (TB) on international flights have underscored the importance of rapid and coordinated public health response. The WHO *Tuberculosis and Air Travel Guidelines* recommend

threshold criteria for public health action but lack clear roles and responsibilities for jurisdictions/partners. These guidelines are currently under revision and will incorporate input from several international stakeholders. The purpose of this work was to identify factors affecting such investigations and to inform the revision of the WHO guidelines. **Methods:** A qualitative review was conducted of 40 Canadian and 90 US TB contact investigations involving commercial air travel that were initiated by Public Health Agency of Canada and U.S. Centers for Disease Control and Prevention (CDC) from January 2006 though October 2007. An overall impression of potential problems and delays in investigation was determined based on the investigators experience. **Results:** Four situations were identified as problematic: 1) the country where the case was diagnosed is not the country where the flight arrived; 2) more than one flight and country of destination is involved; 3) the airline is foreign-based and passenger information available to the country of destination is limited; and 4) one of the involved countries has a TB and air travel policy that is more strict than the WHO guidelines and needs assistance from a country whose policy is to follow WHO guidelines. These resulted in delays in initiating investigations. **Conclusions:** A number of factors may impact the effective completion of TB contact investigations involving commercial air travel. The roles and responsibilities of the public health authorities involved with TB contact investigations that involve more than one country are unclear. Consensus on clear roles and responsibilities of the public health authorities for the countries involved will facilitate successful and timely completion of these international contact investigations.

Board 334. *E.coli* O157 and Non-O157 Shiga Toxin-Producing *E.coli* (STEC) Testing Among Clinical Laboratories Serving the FoodNet Catchment Area

D. Hoefer[1], S. Hurd[2], C. Medus[3], S. Shin[4], A. Cronquist[5], T. Hayes[6], K. Larson[7], K. Edge[8], J. Hatch[9], S. Hanna[10], P. Snippes[3], H. Gould[11];

[1]New York State Health Department, Albany, NY, [2]Connecticut Emerging Infections Program, Yale, CT, [3]Minnesota Department of Health, MN, MN, [4]California Emerging Infections Program, SF, CA, [5]Colorado Department of Health, Denver, CO, [6]Georgia Emerging Infections Program, Atlanta, GA, [7]Maryland Department of Health, MD, MD, [8]New Mexico Emerging Infections Program, NM, NM, [9]Oregon Department of Health, OR, OR, [10]Tennessee Department of Health, TN, TN, [11]Enteric Diseases Epidemiology Branch, CDC, Atlanta, GA.

Background: Shiga toxin-producing *Escherichia coli* (STEC) infection causes severe diarrhea and may result in life-threatening hemolytic uremic syndrome. *E. coli* O157:H7 (O157) is the most widely recognized STEC in the United States; however, studies suggest that infection caused by non-O157 STEC may be as prevalent. In 2006, the CDC published guidelines for STEC testing to improve both routine surveillance and outbreak response. Guidelines include simultaneous testing for Shiga toxin (Stx) using non-culture methods and culturing for O157. We evaluated adherence to published guidelines, as well as changes over time in clinical laboratory practices to better understand surveillance trends. **Methods:** In 2007, all clinical laboratories serving the ten FoodNet sites were surveyed about their practices for identification of STEC. The surveys were conducted in person, by telephone, or via a web-based survey tool. The survey addressed procedures related to culture- and non-culture methods. The results from this survey were compared to a similar survey conducted by FoodNet in 2003. **Results:** Responses were received from 668 (99%) of 675 labs surveyed; 433 (65%) tested on-site for O157/STEC. Sixty-nine (16%) labs tested on-site using non-culture methods, up from 9% in 2003. Forty-five labs (10%) used a method that would detect non-O157 STEC, up from 2% in 2003. Thirty-eight labs (9%) used both culture and non-culture methods; 8 (2%) set up these tests simultaneously. Among labs using non-culture methods, 62 (94%) sent a specimen or clinical material on to the state public health lab (SPHL) for further testing. At the time of the survey, 39 (11%) labs had plans to add non-culture methods for testing STEC in the next six months. **Conclusions:** Laboratory methods for STEC testing are changing rapidly with increasing use of non-culture methods for Stx detection. Only 2% of the labs reported simultaneously using non-culture and culture based methods as recommended in CDC guidelines. Barriers to following published guidelines should be explored to improve the identification of STEC. All Stx positive specimens and O157 isolates should continue to be forwarded to the SPHL for further testing, including PFGE, to aid in the rapid identification of O157 and non-O157 outbreaks.

Board 335. Laboratory and Epidemiologic Description of Children Infected with *Shigella sonnei* in Northwest Georgia

S. Crim[1], D. Abercrombie[2], M. Atkins[2], M. M. Park[3], B. Wallace[3], C. M. Shuler[1], M. Tobin-D'Angelo[1];

[1]Georgia Division of Public Health, Atlanta, GA, [2]Northwest Georgia Health District 1-1, Rome, GA, [3]Georgia Public Health Laboratory, Decatur, GA.

Background: *Shigella sonnei* outbreaks frequently occur in school and childcare settings creating an opportunity for public health education. During previous outbreaks, antibiotic resistance has developed and multi-drug resistant *Shigella* infections have been reported. Information about drug resistance, combined with pulsed field gel electrophoresis (PFGE) results, is necessary to control the spread of *Shigella* infections. In April of 2007, the Northwest Health District (HD 1.1) of Georgia (GA) saw an increased number of *S. sonnei* cases and outbreaks. We described *S. sonnei* cases in GA during March-September 2007 and evaluated case and isolate characteristics from HD 1.1 compared with other reported infections in GA. **Methods:** Clinical and epidemiological information gathered from routine notifiable disease interviews and reports were combined with PFGE and antibiotic resistance data from the Georgia Public Health Laboratory when available. An outbreak was defined as two or more culture-confirmed cases with a common school or childcare exposure. Previously identified antibiotic resistance patterns from outbreaks in similar settings were used for the analysis. **Results:** The mean age for reported infections in HD 1.1 (10 years) was significantly ($p < 0.05$) less than in the rest of GA (13 years). Twenty-three school or childcare outbreaks were reported from March to September. One of 33 PFGE patterns was significantly more common in HD 1.1 ($p<0.05$). Isolates resistant to amoxicillin/clavulanic acid, ampicillin, cephalothin, and streptomycin (a common pattern during GA's 2000-2002 outbreaks) were rarely identified (6/132, 4.6%) in 2007. The other pattern of interest, ampicillin and trimethoprim/sulfamethoxazole resistance, was significantly less common in HD 1.1 than in the rest of GA (6% vs. 18%, $p<0.05$). **Conclusions:** Antibiotic resistance and PFGE patterns are valuable tools in describing *Shigella sonnei* outbreaks. The 2007 outbreaks investigated in GA Health District 1.1 were not characterized by multidrug resistance and had different antibiotic resistance patterns compared to childcare/school outbreaks in the past. PFGE patterns were diverse with minimal clustering. Laboratory data, along with clinical and epidemiologic information may be useful for treatment and outbreak control.

Social Determinants of Infectious Disease Disparities

Wednesday, March 19
12:00 PM – 1:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 336. Predictors of Household Water Treatment among a Rural Population in Kenya

J. D. Vojdani[1], P. C. Juliao[1], L. Ruth[2], R. Otieno[2], I. Sadumah[2], R. E. Quick[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Safe Water and AIDS Project, Kisumu, KENYA.

Background: In response to the lack of access to safe water by over a billion people in the developing world, CDC developed the Safe Water System (SWS), a household based intervention that includes water treatment, safe storage, and behavior change techniques. The SWS is socially marketed in 19 countries, but has had limited uptake in rural areas. To enhance SWS use in rural Kenya, a local non-governmental organization, the Safe Water and AIDS Project (SWAP), empowers HIV self help groups to sell SWS products, which include bleach (brand name WaterGuard) and a flocculant-disinfectant (brand name PuR®), as an income generating activity. In November 2006, we evaluated use of the two products among clients of SWAP groups. **Methods:** We surveyed a random sample of SWAP clients in 30 communities in five districts of Nyanza Province about household demographic and socioeconomic characteristics, and water, hygiene, and sanitation practices, and tested stored water for residual chlorine. **Results:** Among 471 respondents, the mean age was 33 years (range 9 to 85), 90% were female, and 89% were literate; 88% of households had ≥1 child under 5 years old. All respondents stored drinking water, 99% had heard of WaterGuard, and 75% had heard of PuR®. Of 471 respondents, 79% had ever used and 47% were currently using WaterGuard, and 19% had ever used and 2% were currently using PuR®. We confirmed, through observation of detectable chlorine residuals in stored water, that 32% of respondents had treated their water, 30% with WaterGuard and 2% with PuR®. Confirmed water treatment was more likely to be found in the three richest than the two poorest socioeconomic quintiles (odds ratio [OR], 1.8; 95% confidence interval [CI], 1.2 to 2.7) and among literate than illiterate respondents (OR, 2.5; 95% CI, 1.2 to 5.5). Respondent age and gender were not significantly associated with confirmed water treatment.**Conclusions:** Awareness of at least one household water treatment product was universal among SWAP clients and confirmed use in the population was relatively high. Despite a higher risk of disease, poor and illiterate people were less likely to treat their water. Promotion of water treatment should target poor and illiterate populations; alternate product delivery strategies may be required for those who cannot pay.

Board 337. Occupational Brucellosis in Xilinhaote, Inner Mongolia, China, 2007

S. Hui;

CFETP, Beijing, CHINA.

Background: As a kind of reemerging disease, Brucellosis is attached more and more importance in Inner Mongolia. Usually most of the cases occurred in the village. But, Xilinhaote, a city of Inner Mongolia has reported 438 brucellosis cases in 2006. About half of them are residents in the city. Why so many cases had occurred in city ? To find the reason and the risk factor of this cases , We made a field investigation in the city in September. **Methods:** We analyzed the information of notifiable infectious disease about the brucellosis in 2006. Then we conducted a case-control study in Xilinhaote. According to the standard of brucellosis diagnosis, we made a case definition. One or more symptom of fever, fatigue, sweats, myalgia, arthralgia, headaches, and serum tested positive, onset from August 1 2006 to July 31 2007. The control is belong to the same factory ,and serum negative is needed. We have interviewed 76 cases and 458 control. We asked the case and control about occupational factors and exposure to animals and animal products. Logistic regression was used to study the association between exposure variables and brucellosis. **Results:** Among the 438 cases in 2006, 234(53.4%) cases are not belong to the herd or farmer(The cases are shepherd or farmer mostly in other district of Inner Mongolia.). Most of them are occupational person who served for flocks and herds business. It's different with other district. Through case-control analysis we found some risk factors, contact with dead lamb(OR = 19.91; 95% CI= 9.39~42.60), incorrect method for wound treatment(OR = 10.71; 95% CI= 4.17~29.18),. contact with coat(OR = 8.20; 95% CI= 3.98~16.92), flocks and herds carry(OR = 7.63; 95% CI= 3.67~15.89), contact with placenta(OR = 4.45; 95% CI= 1.51~12.80), and so on. And we found some protective factors for the occupational person, such as mask wearing(OR = 0.12; 95% CI= 0.03~0.59), hand washing with soap(OR = 0.23; 95% CI= 0.10~0.56). Through multivariate analysis, we found which contact with dead lamb(OR = 12.89;),is the most significant risk factor. **Conclusions:** Contact with dead lamb, incorrect method for wound treatment are risk factor for brucellosis.The protect measure like mask and hand washing with soap should be taken for occupational person. And we should provide normal wound treatment for them.

Surveillance: International and New Strategies

Wednesday, March 19
12:00 PM – 1:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 338. WHO Global Salm-Surv Country Databank

S. M. Pires[1], A. R. Vieira[1], H. C. Wegener[1], S. Karlsmose[1], D. M. Lo Fo Wong[2], WHO-GSS Members;

[1]National Food Institute, Mørkhøj, DENMARK, [2]Department of Food Safety, Zoonoses and Foodborne Disease, WHO, Geneva, SWITZERLAND.

Background: WHO Global Salm-Surv promotes integrated, laboratory based surveillance and inter-sectoral collaboration among human health, veterinary and food-related disciplines. Created in 2000, the program enrolls now over 1,000 members from 151 countries. WHO GSS members annually report the 15 most frequently isolated *Salmonella* serotypes to a secured web-based databank. This program is the only foodborne disease surveillance that is global in scope and surveys all components of the food chain, from animal feed to humans. **Methods:** Data are updated annually and are publicly accessible for members and the scientific community (www.who.int/salmsurv). The objectives are to provide an overview of the most important *Salmonella* serotypes in the different countries and regions, evaluate trends over the years and analyze the worldwide epidemiology of the serotypes. **Results:** We describe the number of members that provided data to the database, the frequency of reporting and the comprehensiveness of the information in the food chain between 2003 and 2006. From 141 member institutions within 89 countries, 54 reported the most frequent *Salmonella* serotypes. Among these, data from both human and non-human sources are available for only part of the countries.

In the analysed period, around 55.3% of the reported datasets refer to human isolates, while data from animals represented 13.9%, from food isolates 19.2%, from feed 6.3% and environment 5.3%, . Information on the reporting is shown by year and by type of data, allowing the evaluation of the trends over time and space. **Conclusions:** The frequency of contribution of the countries is variable, with some of the members reporting every year whereas others update information sporadically. Data for 2005 and 2006 is available for few countries. Nevertheless, the available data provides useful information when evaluating the globally most important *Salmonella* serotypes in humans and animals/ food, as well as geographical and temporal trends, and the Country Databank is a powerful tool that combines information from a wide range of countries worldwide.

Board 339. WHO Global Salm-Surv: *Salmonella* Surveillance in China 2006-2007

L. Ran[1], B. K. Gu[2], M. Chen[2], S. L. Xia[3], Z. Q. Xie[3], Q. Li[4], Z. F. Li[4], X. L. Deng[5], B. X. Ke[5], M. Lin[6], M. L. Wang[6], H. Y. Wu[7], X. R. Yang[7], J. M. Ou[8], W. W. Chen[8], Z. J. Wang[1], Z. J. Feng[1], WHO Global Salm-Surv;

[1]Chinese Center for Disease Control and Prevention, Beijing, CHINA, [2]Shanghai Centers for Disease Control and Prevention, Shanghai, CHINA, [3]Henan Centers for Disease Control and Prevention, Zhengzhou, CHINA, [4]Chongqing Centers for Disease Control and Prevention, Chongqing, CHINA, [5]Guangdong Centers for Disease Control and Prevention, Guangzhou, CHINA, [6]Guangxi Centers for Disease Control and Prevention, Nanning, CHINA, [7]Sichuan Centers for Disease Control and Prevention, Chengdu, CHINA, [8]Fujian Centers for Disease Control and Prevention, Fuzhou, CHINA.

Background: *Salmonella* is one of the leading causes of foodborne illness in the world including China. WHO Global Salm-Surv (GSS) promotes integrated laboratory-based foodborne disease surveillance. The Chinese Center for Disease Control and Prevention is a member of WHO GSS and has performed Enhanced *Salmonella* Surveillance from 2006. Henan, Fujian, Shanghai in 2006, Guangdong, Guangxi, Sichuan and Chongqing in 2007 were selected to join the Enhanced Salmonella Surveillance Project. This will help to understand the epidemiology of *Salmonella* in China and affect the public health action. **Methods:** Stool specimens of diarrhea patient who were fitted in the salmonellosis cases definition were collected and *Salmonella* was recovered. *Salmonella* isolates were shipped to the Provincial CDC for serotyping, antimicrobial susceptibility testing, and pulsed-field gel electrophoresis (PFGE). The Provincial CDCs have been enrolled in the External Quality Assurance System of WHO GSS 2006 and 2007. **Results:** Totally, 24895 of stool samples were screened and 807 *Salmonella*.spp isolates were recovered and further confirmed by API 20 E test, among which 776 (96.2%) were serotyped. Seventy serotypes were identified. The fifteen most common serotypes were Typhimurium (22%), Enteritidis (19%), Senftenberg (6%), Derby (5%), Aberdeen (3%), Agona (3%), Indiana (2%), Thompson (2%), Braenderup (2%), Litchfied (2%), Infantis (2%), Lomita (2%), Cholerae-suis (1%), Anatum (1%) and Kottbus (1%). Eleven to 93 percent of *Salmonella* isolates were resistant to Nalidixic Acid and 1 % to 14% of *Salmonella* isolates were resistant to ciprofloxacin in seven provinces. Ten *Salmonella* outbreaks were detected from 55 diarrhea outbreaks in Chongqing city 2007, among which four *S. Typhimurium* outbreaks were caused by preserved eggs. *S.Senftenberg* was an emerging serotype in Shanghai city and increasing dramatically in 2006 and 2007. *S.Litchfied* clusters of illness were detected in Henan Province. **Conclusion:** These data provided important informations for *Salmonella* prevalence among diarrhea patients in seven provinces of China.

Board 340. FDA Tomato Safety Initiative: Virginia Preliminary Finding, 2007

P. McCarthy, M. Smith, N. Fogg, Jr., T. Hill, S. Assar, J. Guzewich, FDA Tomato Assessment Team;

FDA, College Park, MD.

Background: In response to Salmonella outbreaks associated with tomatoes, FDA began a Tomato Safety Initiative in cooperation with the States of Virginia and Florida, several universities, and members of the produce industry. The goal of the initiative is to minimize the incidence of illness associated with consumption of tomatoes. **Methods:** Packing facilities and farms in Eastern Virginia were assessed to characterize current conditions and to determine the degree to which Good Manufacturing Practices (GMPs), Good Agricultural Practices (GAPs), and other practices designed to minimize the contamination of tomatoes have been implemented. Assessments focused on the dump tank, employee hygiene, and cleaning practices in packing facilities. Environmental factors included irrigation water source, procedures for mixing chemicals, weather events, worker hygiene, and animal proximity. Florida farms will be assessed in 2008. **Results:** Operations at five tomato packing facilities and 58 tomato farms were assessed. Ten of the farms were also harvesting. Assessments revealed evidence that resources are being committed to implement GMPs and GAPs. SOPs have been written and workers are being trained to follow procedures. Some facilities use a secondary chlorine dioxide system to treat wash water. Several newly drilled wells are in use and there is a high percentage of cross-connection controls in-place on wellheads. Pond water is no longer used to mix spray chemicals. Additional improvements can be made in dump tank monitoring and recordkeeping. Some tomatoes had higher internal temperatures than dump tank water temperatures increasing the potential for internalizing contaminated water when they are placed in the dump tank. Cleaning of equipment, restrooms, and worker hygiene issues were also observed. Some wells were close to ponds and some portable toilets were close to ponds and wells which raised questions about the potential impact of pond water and other run-off on well aquifer water quality. **Conclusions:** FDA is working cooperatively with industry, universities, State and local partners to identify conditions and practices that can lead to tomato contamination. Information from the assessments will be used to improve guidance, and to ascertain research, education, and outreach needs.

Board 341. An International Survey of Bioscience Research and Biosecurity Practices

L. M. Astuto-Gribble[1], R. Salvat[1], D. Aceto[1], S. Caskey[1], J. Gaudioso[1], T. Zemlo[2];

[1]Sandia National Laboratories, Albuquerque, NM, [2]BioInformatics, LLC, Arlington, VA.

Background: In the past decade, the United States has enacted extensive federal legislation to regulate the possession, use, and transfer of dangerous biological agents and toxins. Unfortunately, few international laboratories have implemented similar safeguards. Limited data is available concerning the types of pathogens researched in non-US laboratories, and the biosecurity practices employed to maintain those agents. To address these knowledge gaps, a survey was administered to 765 scientists from 86 countries in Asia, Eastern Europe, Latin America, and the Middle East. **Methods:** In 2005, *BioInformatics, LLC* conducted a 30-question online survey to members of The Science Advisory Board, an international community of more than 28,000 scientists, physicians, and healthcare professionals who actively study infectious diseases and/or toxins. Survey questions pertained to the types of pathogens used in the laboratory, as well as laboratory biosafety and biosecurity measures, risks, and perceptions. **Results:** Survey results revealed that participants are actively engaged in research with a wide variety of biological agents. Most respondents in Asia, Eastern Europe, and

the Middle East study bacteria more frequently than viruses; Latin American researchers report studying viruses more commonly. Some of the most commonly studied agents include *S. typhi*, *E. coli O157: H7*, *M. tuberculosis*; HIV, HPAI, Japanese encephalitis, botulinum and toxin and *S. aureus* toxin. Overall, respondents in all regions reported using only simple physical security, such as posted guards (53.5%), locked doors (51.1%) and cabinets (49.5%), all the time. Information security and material accountability were fairly robust in all regions; however, most admitted to poor personnel biosecurity. Breaches of security were generally not feared; accidental rather than deliberate contamination was a more significant concern. **Conclusion:** This survey provided unique insight into the variety of dangerous agents studied worldwide and uncovered a consistent weakness in laboratory biosecurity and biosafety. Because many of these facilities are located in volatile areas of the world, these findings indicate a significant risk and future actions are warranted to improve the safe and secure handling of biological agents internationally.

Board 342. Evaluation of an Animal Health Electronic Laboratory Reporting Surveillance System (Characterizing an Outbreak of Anthrax in North Dakota)

J. L. Goplin[1], T. K. Miller[1], B. Carlson[2];

[1]North Dakota Department of Health, Bismarck, ND, [2]North Dakota Board of Animal Health, Bismarck, ND.

Background: The North Dakota Department of Health (NDDoH) and the State Board of Animal Health (BOAH) developed an electronic laboratory reporting system using data streams exported from the North Dakota Veterinary Diagnostic Laboratory (NDVDL) for animal and public health surveillance. This report describes the system and characterizes an outbreak of anthrax in North Dakota in 2005. **Methods:** Laboratory records are exported real time from the NDVDL and uploaded to a secure File Transfer Protocol website at the NDDoH. Records are imported into an Access database (Microsoft® Office Access 2003) and further processed using SAS 9.1 (SAS Institute Inc., Cary, NC) programming code. The CDC Early Aberration Reporting System (EARS) V4r5 was used to retrospectively illustrate distribution and frequency of positive anthrax results reported in 2005. The electronic laboratory reporting system was qualitatively evaluated against traditional reporting methods. **Results:** Five-hundred fifty-six *B. anthracis* infected animals were reported to the BOAH (136 laboratory confirmed) between June 30 and Sept. 30, 2005. One hundred and nine premises were affected in 16 counties. Animal species most frequently reported were cattle, farmed elk, horse, bison and sheep. The median length of time of premise quarantine was 61 days (range: 32 - 192). Reports were faxed to the BOAH every day at 4 pm. Data was hand entered into a database for de-duplication and identification of new cases and premises. Evening phone calls were then made to new premises and area veterinarians. Maps and graphs were developed as time permitted. Retrospective analysis shows that electronic laboratory reports would have been received earlier in the day (every hour if needed), along with automatic data entry. Using EARS, the tempo of the outbreak was graphed and the system also provided a map of infected counties.**Conclusions:** The animal health surveillance reporting system is a timely and secure electronic laboratory reporting system that will replace the current paper reports sent by the NDVDL to the BOAH. The system provides for faster reporting and avoids the need for data entry allowing more time to focus resources on target areas such as quarantine, vaccination and public education.

Board 343. Forecast and Validation of the Rift Valley fever outbreak in East Africa: 2006-2007

A. Anyamba[1], J. Chretien[2], J. Small[1], C. J. Tucker[1], P. Formenty[3], J. H. Richardson[4], E. Pak[1], S. C. Britch[5], D. C. Schnabel[6], R. L. Erickson[2], A. Hightower[7], R. Breiman[7], K. J. Linthicum[5];

[1]NASA Goddard Space Flight Center, Greenbelt, MD, [2]Department of Defense Global Emerging Infections Surveillance & Response System,, Division of Preventive Medicine, Walter Reed Army, MD, [3]World Health Organization, Department of Epidemic and Pandemic Alert and Resp, SWITZERLAND, [4]U.S. Army Medical Research Unit –Kenya, Department of Entomology & Vector-borne Disease, KENYA, [5]USDA-ARS, Center for Medical, Agricultural, & Veterinary Ent, FL, [6]U.S. Army Medical Research Unit –Kenya, Greenbelt, KENYA, [7]CDC-KEMRI, Unit 64112, Nairobi, KENYA.

Background: The instantaneous occurrence of El Nino / Southern Oscillation (ENSO) warm events and anomalous warming of the equatorial western Indian Ocean (WIO) are associated with elevated and widespread rainfall over East Africa. Such, sustained, heavy rainfall in East is associated with the emergence of large populations of virus infected Aedes spp mosquitoes and the Rift Valley fever (RVF) outbreaks. **Methods**: The Department of Defense Global Emerging Infections System (DoD-GEIS) collaborating with NASA Goddard Space Flight Center, operate an near-real time environmental monitoring and RVF risk mapping system for Africa/Middle East, DoD-GEIS. Using a combination of sea surface temperature [SST], outgoing longwave radiation [OLR], rainfall, and satellite derived normalized difference vegetation index [NDVI] to map areas conducive to the emergence of RVF-mosquito vectors. **Results:** The development of warm ENSO conditions with anomalous warming of SSTs in the central and eastern Pacific (CEP) region and the concurrent anomalous warming of SSTs in the WIO region during the September - November 2006 period enhanced rainfall over the oceans and East Africa. The excess moisture resulted in anomalous growth and green-up in vegetation, creating ideal ecological conditions for the emergence of virus-infected mosquitoes. Using a RVF monitoring and risk mapping algorithm the December 2006-May 2007 RVF outbreak in, the Horn of Africa region was forecast as early as September 2006 A mapping of human case locations shows that 64% of the cases were reported in areas mapped to be at risk within the RVF potential epizootic area. **Conclusions:**The ability to monitor key climate indicators, including SSTs in the CEP and WIO regions and rainfall and NDVI over the Horn of Africa, enabled prospective warning of a RVF outbreak and enabled a regional-level assessment of RVF risk that was critical in guiding early entomological investigations and control activities.

Board 344. WHO Global Salm-Surv: Providing a Platform for Training on Zoononsis, Food Security, and Antimicrobial Resistance Issues, 2006-2007

T. N. Maxwell[1], K. Glynn[2], D. Lo Fo Wong[3], M. Elmi[4], L. Kaftyreva[5], N. Singh[6], M. Gouali[7], B. Lopez[8], S. Kariuki[9], T. Chalermchaikit[10], F. J. Angulo[11], and WHO Global Salm-Surv;

[1]Centers for Disease Control and Prevention, Enteric Disease Epidemiology Branch and US Veterans Administration, Atlanta, GA, [2]Centers for Disease Control and Prevention, Bacterial Zoonosis Branch, Atlanta, GA, [3]Food Safety, Zoonoses and Foodborne Diseases, Health Security and Environment, World Health Organization, Geneva, SWITZERLAND, [4]World Health Organization Regional Office for the Eastern Mediterranean, Cairo, EGYPT, [5]Pasteur Institute, St. Petersburg, RUSSIAN FEDERATION, [6]Secretariat of the Pacific Community, Suva, FIJI, [7]Institut Pasteur de Madagascar, Antananarivo, MADAGASCAR, [8]Universidad del Valle, Guatemala City, GUATEMALA, [9]Kenya Medical

Research Institute, Nairobi, KENYA, [10]Chulalongkorn University, Bangkok, THAILAND, [11]Centers for Disease Control and Prevention, Atlanta, GA.

Background: WHO Global Salm-Surv strengthens the capacity of public health, veterinary, and food national reference laboratories and ministries of health and agriculture to conduct integrated, laboratory based surveillance, and rapidly detect and respond to outbreaks of foodborne and other infectious enteric diseases. WHO Global Salm-Surv is coordinated by a Steering Committee that includes representatives from the World Health Organization and eight other public health, veterinary, or food-related agencies. **Methods:** From 2000-2005, WHO Global Salm-Surv activities focused on enhancing surveillance and outbreak detection and response for infections caused by non-typhoidal *Salmonella*, *Campylobacter*, *E. coli* O157, *Shigella*, and *V.* cholera surveillance and response systems globally. In 2006-2007, additional activities related to other zoonoses, food security, and antimicrobial resistance were added to the WHO Global Salm-Surv platform. **Results:** Training modules on *Brucella* were presented at courses for the Middle East, Russia and Eastern Europe. for 81 microbiologists and epidemiologists from 19 countries. Training on *Clostridium botulinum* was given at a course in Southeast Asia for 57 microbiologists and epidemiologists from 13 countries, and an additional workshop was conducted on botulism detection and response in Thailand. An in depth microbiologic and epidemiologic module on antimicrobial resistance (AMR) was introduced at a course in Central America for 68 microbiologists and epidemiologists from 9 countries; microbiologic bench-top modules on AMR related to *Salmonella* were provided at courses in the Pacific, Indian Ocean Islands, and East Africa for 58 microbiologists from 25 countries. **Conclusions:** WHO Global Salm-Surv is providing a platform for additional activities related to other zoonosis, food security, and antimicrobial resistance testing. Adding these activities to WHO Global Salm-Surv further enables national public health, veterinary and food-related institutes to conduct laboratory-based surveillance and outbreak detection and response for an increasingly broad group of animal and food related diseases.

Board 345. Identification of Respiratory Disease Cases Using Outpatient ICD-9-CM Codes

S. Lee, M. S. Bloom, S. Tobler;

U.S. Army, Silver Spring, MD.

Background: U.S. Army recruits are at high risk for acute respiratory disease (ARD). In 2006 alone, there were approximately 8,800 ARD cases with a median incidence rate of 5.3 cases/1,000 recruit-weeks. Due to the high attack rate among military recruits, continuous monitoring for ARD is necessary. Active surveillance can be both time and cost intensive. We sought to determine whether routinely collected ICD-9-CM diagnostic code data could be used to accurately capture ARD cases. **Methods:** Outpatient ARD cases, among U.S. Army recruits between August and December 2006, were identified using data from the Acute Respiratory Disease Surveillance Program. Controls were identified from among non-ARD diagnosis outpatient medical visits. Each case was matched to up to four controls by military treatment facility, time from accession, and date of outpatient medical encounter. These data were abstracted from the Defense Medical Surveillance System. Following the selection of those ICD-9-CM codes with biological relevance, Mantel-Haenszel χ^2 testing was used to select codes significantly associated ($P<0.05$ using false discovery rate) with ARD. Correlations (r) between ARD and significant codes were evaluated for positive coefficients. The selected codes were entered into a multiple logistic regression model using GEE to estimate robust standard errors and discriminatory ability evaluated with the receiver operating characteristic (ROC) analysis. **Results:** Among 377 unique ICD-9-CM codes identified from case and control records, 26 were considered biologically relevant. Fifteen were significantly associated with ARD, seven of these (034.0, 079.99, 462, 463, 465.9, 466.0, 780.6) with positive correlation coefficients (r=0.08-0.20). Each of the latter seven codes was a statistically significant independent predictor of ARD in the multiple logistic regression model. The area under the ROC curve was 0.78. **Conclusions:** Seven routinely collected ICD-9-CM codes accurately classified approximately 78% of ARD case-control pairs. This passive surveillance approach may provide a cost-effective alternative to active surveillance efforts. Military and civilian populations may benefit from using these alternative methods for ARD surveillance

Board 346. The Development of a Pediatric Population-based Encephalitis Study

S. Honarmand[1], R. Baxter[2], L. Walter[2], B. 0. Brown[2], N. Khetsuriani[3], A. L. Fowlkes[3], L. J. Anderson[3], J. Hayward[2], C. A. Glaser[1];

[1]California Department of Public Health, Richmond, CA, [2]Kaiser Permanente of Northern California, Oakland, CA, [3]Centers for Disease Control and Prevention, Atlanta, GA.

Background: Encephalitis is a complex syndrome and its etiology is often not identified. In 2006, the California Encephalitis Project initiated population-based surveillance within Kaiser Permanente of Northern California facilities (KPNC). KPNC is a large health maintenance organization providing healthcare for approximately 785,000 pediatric members. **Methods:** To evaluate the burden of pediatric encephalitis within a defined population, an automated listing of all patients whose physician requested a HSV PCR was obtained along with the corresponding admit text strings and ICD-9 data from April 2006 - April 2007. Patients were excluded after review of the automated data and medical records based on the following criterion: normal mental status, no hospital admission, HSV PCR on a non-CSF specimen, patient < 6 months of age or ≥ 19 years, severe immunosuppression, or severe baseline neurological impairment. **Results:** From April 2006 to April 2007, an HSV PCR was ordered for 306 pediatric patients hospitalized at KPNC. After applying the exclusion criteria, 14 pediatric patients were identified with evidence of mental status changes or acute central neurologic impairment (incidence: 1.8 per 100,000 pediatric members). The median age was 9.2 years (range: 1.1-17.5) and 57% were male. CSF results were available on 8 patients; median WBC=1.0 cells/mm^3 (range: 0-215), median protein=23.0 mg/dl (range: 17-36), median glucose=53.0 mg/dl (range: 47-73) and 4 of 9 (44%) patients had an abnormal neuroimaging. All 14 patients had a negative CSF HSV PCR. A cause for the encephalitis was identified in 3 patients: metabolic encephalopathy (1), enterovirus (1), and bartonella *spp* (1). The etiologic agent was unknown or not recorded for the remaining cases. **Conclusions:** Utilization of HSV PCR orders in conjunction with admit text strings and ICD-9 data is a feasible method for examining rates of encephalitis in a defined population. The incidence rate in this study is similar to the average rate of 4.3 per 100,000 for patients 1-19 years reported by Khetsuriani, et al in their analysis of the National Hospital Discharge Survey data. Approximately 80% of the cases did not have an agent identified; this is similar to other studies published.

Board 347. Risk Factors for Brucellosis in Samarqand Oblast, Uzbekistan

A. K. Soliman[1], J. A. Tjaden[1], A. A. Michael[1], S. Vafokolov[2], N. Yarmohamedov[2], E. Musabaev[3], K. C. Earhart[1];

[1]US Naval Medical Research Unit-3, Cairo, EGYPT, [2]Samarqand Fever Hospital, Samaqand, UZBEKISTAN, [3]Virology Institute, Tashkent, UZBEKISTAN.

Background: This study was conducted to identify the potential risk factors in Samarqand Oblast in Uzbekistan for human Brucellosis infection. Methods: Clinically identified cases admitted to different hospitals within the Oblast (n=144), and age, sex and

residence matched control patients (n=288) with other unrelated conditions, were used for this study during 2004-2006. Structured questionnaires and consent forms were filled out and blood samples from patients and controls were collected and tested on site for Brucella infection by standard tube agglutination tests and culture. Statistical analysis was performed with Stata software; univariate analysis was carried out by computing the adjusted matched odds ratios (AMOR) and their 95% confidence interval (CI) to compare cases and controls for each variable. Multivariate analysis was conducted through conditional logistic regression to identify specific animal or food exposures independently associated with Brucellosis. The level of significance was set to <0.05. Results: Among the 144 patients (Median age was 25) with confirmed brucellosis during the study period, 137 (95.1%) owned farm animals, 135 (93.8%) were from rural areas, and 119 (82.6%) enrolled during the spring/summer animal breeding season. Multivariate analysis indicated that Brucellosis was highly associated with handling aborted products (AMOR=87.19; CI= 9.35-911.85; p<0.001), slaughtering/butchering animals (AMOR=35.35; CI= 6.25-199.77; p<0.001) in the household, consumption of raw milk (AMOR=54.13; CI=1.98-1476.13; p<0.018), and exposure to a family member that had Brucellosis (AMOR=15.93; CI=1.37-184.97; p<0.027). The least association was through milking animals (AMOR=7.66; CI= 1.15-50.93; p<0.035). In conclusion: to reduce the burden of Brucellosis in Samarqand Oblast, veterinary services, such as surveillance and management of infected animals, should be strengthened. In addition public health education programs should be increased. Implementing these measures should reduce exposure to infected farm animals and the risk of infection from consumption of raw milk or milk products.

Tuberculosis

Wednesday, March 19
12:00 PM – 1:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 348. Detection of Nocardia from Patients Diagnosed as Tuberculosis in Egypt.

Z. H. Helal[1], M. I. Khan[2], M. Ashour[3], S. A. Eissa[4];

[1]Department of Microbiology and Immunology, Faculty of pharmacy, Al-Azhar University, Egypt & Molecular biology laboratory, Department of Pathobiology and Veterinary Science, University of Connecticut, Storrs, CT, [2]Molecular biology laboratory, Department of Pathobiology and Veterinary Science, University of Connecticut, Storrs, CT, [3]Department of Microbiology and Immunology, Faculty of pharmacy, Al-Azhar University, Cairo, EGYPT, [4]Center of Tuberculosis, Department of Microbiology and Immunology, Faculty of Medicine, Cairo University, Cairo, EGYPT.

Background: Pulmonary tuberculosis and pulmonary nocardiosis are similar in most clinical symptoms and radiological manifestation. In the developing countries like Egypt where tuberculosis is very common, antituberculosis drugs are started on basis of radiology and clinical symptoms. During our study of the molecular diagnosis and genotyping of tuberculosis, we found that four DNA samples extracted from sputum specimens from tuberculosis patients were of *Nocardia* species. The objective of this study was to confirm the presence of *Nocardia* species. **Methods:** The study included 600 sputum specimens collected from 200 patients diagnosed as pulmonary tuberculosis from three chest hospitals in Egypt. IS6110 specific primers were selected for PCR to identify the *Mycobacterium* species. In addition, hsp65 gene specific primers were used for PCR and sequencing for the differentiation of *Mycobacterium* and *Nocardial* species. Furthermore, 16S rRNA specific for *Nocardia* species were selected as genus specific primer sequences for a PCR and Real Time PCR assays. **Results:** Our result confirmed that four genomic DNA samples, extracted from sputum specimen from the pulmonary tuberculosis patient, were *Nocardia* species. No cross reaction were observed using Real Time PCR with other closely related genera for confirming nocardia. **Conclusions:** The present study highlights the need for detecting of pulmonary nocardiosis in Egypt especially among tuberculosis patients, due to the similarity of clinical and radiological examination between pulmonary nocardiosis and pulmonary tuberculosis especially with patients not responding to anti-tuberculosis drugs.

Board 349. Brazilian tuberculosis surveillance and health information system, 2001-2003

J. U. Braga;

Universidade do Estado do Rio de Janeiro, Rio de Janeiro, BRAZIL.

Background: Tuberculosis Epidemiologists, health planners and policy makers must evaluate the quality of tuberculosis surveillance information to qualify the epidemiologic measures calculated from health information system data. **Methods:** This study it is based on tuberculosis municipality information system data in the period of 2001 the 2003 and aims to evaluate the epidemiologic surveillance of the tuberculosis in Brazil according to (i) the quality of case detention and patient follow-up information, (ii) the quality of the information produced for the case notification system data and (iii) the tuberculosis disease burden. Four groups of municipalities had been created: Group I (GI) - municipalities with regular tuberculosis epidemiologic burden (for example: moderate to low incidence rate) and good quality of surveillance information. Group II (GII) - municipalities with severe tuberculosis epidemiologic burden and good quality of surveillance information. Group III (GIII) - municipalities with severe tuberculosis epidemiologic stage and low quality of surveillance information. Group IV (GIV) - municipalities with regular tuberculosis epidemiologic stage and low quality of surveillance information. **Results:** In about 8% of the Brazilian municipalities, more than 10% of tuberculosis cases were notified by heath services of another municipality. In a great number of municipalities the frequency of pulmonary tuberculosis patients who had carried sputum acid fast exam was low. In the North region, the states of Amazonas, Pará and Amapá have more municipalities with low quality of surveillance (GIII and GIV) than the others. In the Northeast, the poorest surveillance quality information was detected in the states of Pernambuco, Ceará and Bahia. The South and Mid-West regions have greatest number of municipalities with best tuberculosis surveillance information levels. The state of Mato Grosso had highest frequencies of municipalities classified as GIII and GIV. **Conclusions:** The outcomes of the present study were enabled to stratify the Brazilian districts according to their quality of surveillance. This classification may help building control strategies in areas that have not been seen as priority, such as the improvement of surveillance actions.

Board 350. Tuberculosis among Non-Residents Receiving Treatment in Brazil, 2001 - 2006

M. L. Lise, F. Malaspina;

Brazilian Ministry of Health, Brasilia, BRAZIL.

Introduction: Brazil shares borders with 10 South American countries; 105 municipalities are located on the frontiers. Three of these neighboring countries have tuberculosis (TB) incidences higher than Brazil: Paraguay, Guyana and Bolivia. The true impact of this proximity on public health in Brazil is unknown. We describe TB cases in individuals not residing but receiving treatment in Brazil (TBnr) by time, place and person during 2001-2006. **Methods:** We analyzed new cases of TBnr in Brazil reported to

the National Notifiable Disease Information System during 2001-2006. A case of TBnr was a TB infection in a person that reported residence outside Brazil but received treatment in Brazil. **Results:** We evaluated 465,900 TB new cases, of which 172 (0.16%) were TBnr from 15 countries: 74 (43%) from Paraguay, 40 (24%) from Guyana, 26 (15%) from Bolivia, 16 (9%) from Venezuela and 16 (9%) from elsewhere. TBnr cases were concentrated in the States of Roraima (33%), located in the Northern region; Paraná (33%), in the Southern region, and Mato Grosso do Sul (22%), in the Mid-Western region. Sixty (35%) TBnr cases occurred in 2003, 44 (26%) in 2004, 25 (15%) in 2005 and 19 (11%) in 2006. The majority (87%) of TBnr cases were aged ≥ 15 years and 110 (64%) were male. Supervised treatment by Brazilian public health services was provided to 55 (32%) case-patients; 106 (62%) had cure of TB, 23 (13%) abandoned treatment, 19 (11%) died and for 24 (14%) outcome data was missing, or the patient had transferred treatment to another health service. **Conclusions:** The majority of TBnr cases in Brazil came from border countries in South America and were males aged ≥ 15 years. The main borders were in the Northern and Southern regions. Reinforcing bi-national technical cooperation between Brazil and these countries is important for implementing a monitoring system for TBnr cases in border municipalities to reduce abandonment of treatment and increase cure rates.

Board 351. Determining the impact of HIV infection on the outcome of patients infected with Tuberculosis meningitis

M. Louisias[1], S. Madhi[2], S. Nachman[1], M. Edginton[3], E. Lazarus[2], C. Cutland[2], X. Poswa[4];

[1]Stony Brook University Medical Center, Stony Brook, NY, [2]Chris Hani Baragwanath Hospital, Soweto, SOUTH AFRICA, [3]University of the Witwatersrand, Johannesburg, SOUTH AFRICA, [4]Johannesburg Hosptial/Wits Medical School, Parktown, SOUTH AFRICA.

Background: TB meningitis (TBM) is of grave concern in the HIV positive population due to the risk of long term neurological sequelae and even death. There is also limited data on the impact of the TB-HIV co-infection on perinatal and neonatal outcomes. The lack of information is apparent in TBM whose peak incidence is in infants and children up to 4 years of age and has high mortality rates and neurological sequelae. We sought to determine the effect of HIV co-infection on TBM presentation, to compare the short-term outcome and to determine the burden of TBM between HIV infected and HIV uninfected individuals. **Methods:** After IRB approval, charts were collected for patients with positive auramine and/or TB culture on CSF exam from National Health Laboratory Service and for patients notified to the TB Care Centre as TB meningitis at Chris Hani Baragwanath Hospital during 2005. Chart reviews were performed to obtain information on HIV status, neurological history, neurological state on admission, in-hospital deaths, treatment course and clinical condition on discharge. Data was entered on data collection forms and then transferred to Epi Info Database Version 3.3.2. **Results:** Data was extracted from 354 charts. There were 17 pediatric [greater than and less than 12 years of age] patients (4.8%), 222 patients alive at discharge, 132 patients died during admission and in subsequent admissions - (40% mortality)**.** There were 283 patients notified to TB Care Centre, 71 patients were not notified. Thirty adult patients were examined for results. Fifty seven percent (n=17) had a positive HIV status, 3 had a negative HIV status, and 9 were unknown. Forty-three percent (n=13) patients died during admission, and 17 were discharged. Thirty-seven percent (n=11) of patients presented with main complaint of headache or vomiting "days" before admission. Thirty percent (n=9) presented with main complaint of confusion from "days" to "weeks" prior to admission. **Conclusion:** We demonstrate that there is severe under-reporting of tuberculosis meningitis to the South African DOH when the number of cases from the NHLS and TB Care Centre are compared to SA DOH data. We also demonstrated a high mortality (40%) in patients admitted with TBM, high prevalence of HIV infection and most patients present with main complaint of headache, vomiting or confusion.

Board 352. Febrile Respiratory Illness and Tuberculosis in the CNMI: a Perspective Over a Decade

J. A. Sliman[1], J. L. Young[2], R. Brostrom[3];

[1]NEPMU6, Pearl Harbor, HI, [2]University of Hawaii, Honolulu, HI, [3]Department of Health, Saipan, NORTHERN MARIANA ISLANDS.

Background: Tuberculosis (TB) remains a leading disease threat throughout the Asia-Pacific region. This threat extends to U.S. military populations stationed in and deployed throughout the region. Concern exists for the transmission of multidrug resistant forms of the pathogen (MDR TB) for several reasons, including increasing migration from countries with a high endemicity and inadequate, incomplete or inappropriate treatment. The Commonwealth of the Northern Marianas Islands (CNMI) has had a screening policy for legal workers with industry-sponsored work visas for the past nine years (1998-2007), and an extensive amount of data covering all cases of active and latent TB (LTBI) during that timeframe. We collated and analyzed that clinical data to better determine the prevalence rate and antimicrobial sensitivities of the various populations in the CNMI. **Methods:** We used available information from all referred cases of active TB and LTBI in the CNMI since 1997 to create a new TB database. Information was analyzed for demographics, temporal and spatial association of cases, and significance of associations. **Results:** A total of 8967 cases of TB and LTBI were referred to the Commonwealth Health Center (CHC) between 1998 and 2007. Of the referrals, 34.3% were Filipino nationals and 17.8% were Chinese nationals, all of whom legally entered the CNMI on work visas. Of these, 469 (5.2%) had radiographic evidence of active pulmonary TB and were placed on antimicrobials. A total of 223 of these cases were culture-confirmed, of which 169 (76%) were pan-sensitive to all typical anti-tuberculosis antimicrobials. **Conclusions:** Based upon epidemiological and laboratory data, we have determined that foreign nationals on legal work visas in the CNMI are somewhat more likely to be diagnosed with TB or LTBI versus those of local Chamorro or Carolinian Islander ethnicity. We have further determined that the majority of these diagnoses are made within the first year after arriving in the CNMI, and that more than three-quarters of all active pulmonary TB cases in this population are sensitive to all common anti-tuberculosis antimicrobials. This information will provide great insight into the nature and sensitivity of tuberculosis cases imported into the CNMI, many of which originate in Southeast Asia.

Vector-Borne Diseases

Wednesday, March 19
12:00 PM – 1:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 353. Dengue Outbreak at a Fishing Port: Guangdong Province, China, 2007

F. M. Dou[1], H. Sun[1], Z. J. Wang[1], Z. Xu[1], L. F. Lin[2], F. Lin[2], Z. Zhang[2], L. Lu[2], Z. G. He[3], G. Q. Ye[3], X. P. Lu[3], J. Chen[4], H. S. Chen[4], H. L. Ma[1], L. J. Zhang[1];

[1]Chinese Center for Disease Control and Prevention, Beijing, CHINA, [2]Guangdong Center for Disease Control and Prevention, Guangzhou, CHINA, [3]Zhangjiang Center

for Disease Control and Prevention, Zhangjiang, CHINA, [4]Leizhou Center for Disease Control and Prevention, Leizhou, CHINA.

Background: Since 1950, Wushi , a fishing port in Guangdong Province, China, had two dengue fever (DF) epidemics with thousands of cases but has had no DF for the past 20 years. On October 6, 2007, a new outbreak in Wushi was reported and we began an investigation to identify the source of the outbreak, describe the epidemiology of disease, and recommend and evaluate control measures. **Methods:** We defined a case as onset of the following symptoms since September 1, 2007 in a resident of Wushi: acute febrile, headache, retro-orbital pain, myalgia, arthralgia, asthenia and rash, and were conformed by serology. We selected 28 DF and 44 asymptomatic control-persons with IgG and IgM negative from the neighbor randomly. Habit and home sanitation were collected by using a structured questionnaire. We also surveyed the Breteau Index(BI) during the outbreak. **Results:** From September 19 to October 25, 1% (185) of Wushi residents developed DF. We identified a solitary DF with onset on September 19. Following this DF we identified a secondary generation of 53 cases with a peak 18 days later (October 7) and a tertiary generation of 131 DF 10 days (October 17) after the secondary peak and this periodicity approximated the combination of the extrinsic and intrinsic incubation period for DF. The cases infected in the home. In the case-control study 21% of cases have visited the family of patient in two week before the onset compare to 2.3% of control-persons(odds ratio [OR] _ 4.3, 95% CI _ 2.5–7.3) and 48% cases lives in poor home sanitation compare 22% of control-persons (OR_13, 95%CI_1.3-335). Adulticiding and source reduction were initiated on October 7. The onset of new cases began declining abruptly 7 days (the intrinsic incubation period) after initiation of adulticiding. Similarly, the BI reduced from 76 to <5 twelve days after adulticiding and source reduction began. **Conclusions:** This DF outbreak probably began from a single case resulting in large secondary and tertiary generations. Our data suggest that community cleanup campaigns, and adult mosquito control can effectively curtail a DF outbreak despite a high basic reproductive rates.

Board 354. Serologic Evidence Of *Ehrlichia Chaffensis* Infection In Peru

P. L. Moro[1], J. Shah[2], M. H. Moro[3], R. H. Gilman[4];

[1]Immunization Safety Office, Centers for Disease Control and Prevention, Atlanta, GA, [2]IIGeneX Inc, Palo Alto, CA, [3]Department of Diagnostic Medicine/Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, KS, [4]Department of International Health, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD.

Background: Serologic evidence for human ehrlichiosis has been found in certain South American countries such as Argentina, Brazil, Chile and Venezuela. No study has documented any cases of human ehrlichiosis in Peru though *Ehrlichia canis* infection was recently demonstrated in Lima city dogs. Given the absence of data, we conducted a serosurvey in different communities of Peru to determine the possible presence of *Ehrlichia chaffensis*. **Methods**: A serosurvey for human ehrlichiosis caused by *Ehrlichia chaffensis* was performed in different regions of Peru. Those regions included an urban shantytown in Lima city, a rural community in the northern coast of Peru, Department of Piura; a rural community in the southern Peruvian Andes, near the city of Cuzco, Department of Cuzco; and a rural community in the jungle Peruvian region, near the city of Iquitos, Department of Loreto. **Results**: An overall seroprevalence for human ehrlichiosis of 16.9% (27/160) was found using an indirect immunofluorescent assay. Seroprevalences in the Lima city, northern coastal, Andean and jungle communities were 5% (2/40), 25% (10/40), 23% (9/40), and 15% (6/40) respectively. Seroprevalence in the Lima city community was significantly lower than in any other surveyed regions ($p < 0.01$). No associations were noted between seropositivity and gender or age of study participants. **Conclusions**: Our findings suggest that human infection with *Ehrlichia chaffensis* occurs throughout Peru. Further studies are needed to characterize ehrlichia species in Peru, their vectors and their clinical significance.

Board 355. Occupational Risk Factors Associated with a Large Increase in Malaria Cases on the Brazil-French Guiana Frontier, 2006

E. V. Rossetto[1], M. L. Pereira[2], G. S. Dimech[1], G. A. Silveira[2], R. M. Braz[2], J. L. Ladislau[2], W. N. de Araujo[1];

[1]Field Epidemiology Training Program, SVS, Brazilian Ministry of Health, Brasilia, BRAZIL, [2]National Malaria Control Program, SVS, Ministry of Health, Brasilia, BRAZIL.

Background: Oiapoque (pop, 16,827), located on the Brazil-French Guiana frontier, is a town dominated by gem mining, with large mobile migrant populations on both sides of the border. Between July and December 2005, 6,507 suspect malaria cases and 2,070 confirmed cases were reported. In July 2006 we noted an increase in cases compared with the same period of 2005, and initiated an epidemiologic investigation. **Methods:** The study period was July 2_December 2, 2006. A suspected case was defined as a suspected malaria infection reported from Oiapoque, in a person exposed to an area of known malaria transmission 8-30 days before fever onset. A confirmed case was defined as *Plasmodium* in the blood of a person reported from Oiapoque. The investigation included interviews, blood sample collection, and an entomological survey. Cases were reported to the National Epidemiologic Surveillance Information System for Malaria. Data were analyzed in Epiinfo. **Results:** During the study period, 8,030 suspect cases and 3,414 (42%) confirmed cases were reported. Of confirmed cases, 2,236 (65%) were caused by *P. vivax* and 944 (28%) by *P. falciparum*. The incidence was 203/1,000 inhabitants; 3,307 (97%) confirmed case-patients reported residence in Brazil. The highest incidence was in persons aged 20-29 years (359/1,000), with Relative Risk=2.1 (95%CI=2.0-2.6) compared with other case-patients (169/1,000). Of confirmed cases, 1,892 (55%) worked in gem mining, and of these 753 (40%) were aged 20-29 years, and 1,277 (67%) were males. Of 1,200 (35%) confirmed case-patients who were women, 74 (2%) were pregnant and these had a median age of 22 years (range, 14-40 years). The suspected location of infection was, in 1,882 (99%) confirmed cases, in French Guiana but 1,876 (99%) of these patients reported their residence was in Brazil. The entomological survey identified areas favorable for vector propagation, and the presence of *Anopheles albitarsis s.l.* and *Anopheles darlingi* **Conclusions:** The increase in malaria cases affected principally young adult male residents of Brazil who cross the border to engaged in gem mining in French Guiana. Treatment is available and cases are reported on the Brazilian side of the border. Vector control activities have been implemented in the community.

Board 356. Downregulated Expression of IL-4 and IL-10 in mice brain during Japanese Encephalitis virus infection

T. N. Dhole, Sr.[1], V. Saxena, Jr.[1], A. Mathur, Sr.[2], N. K. Krishnani, Sr.[1];

[1]Sanjay Gandhi PGI, Lucknow, INDIA, [2]KGMU,Lucknow, Lucknow, INDIA.

Background: Japanese Encephalitis (JE) remains the most important cause of acute epidemic viral encephalitis and continues to spread to the so far unaffected regions like Indonesia, Pakistan and Australian continent. The innate and adaptive immune response with special reference to cytokines during JE infection is not precisely known and no reports exist describing the sequence of pathological changes and their correlation to the immune response in the brain

following infection with JE virus (JEV). **Methods:** We analyzed inducible nitric oxide synthase (iNOS) mRNA, proinflammatory (IFN-γ, TNF-α), anti-inflammatory (IL-4, IL-10) cytokines' expression at transcript as well as protein level by RT-PCR and ELISA respectively in the brain of JEV challenged mice at different time points during infection. Viral replication was detected by plaque assay. Inflammatory changes in the brain of JEV challenged and mock infected mice were recorded during histological analysis. **Results:** Expression of iNOS mRNA was found to be upregulated in virus infected mice at 3 days post infection (d.p.i.) followed by a progressive decline at 5 and 6 d.p.i. We report for the first time that in JE, there is a progressive decline in level of IL-4 along with IL-10 that is inversely correlated to the increased level of proinflammatory cytokines and histopathological changes. In contrast, proinflammatory mediators like IFN-γ and TNF-α were significantly upregulated ($P<0.05$). A negative correlation between IFN-γ and iNOS is suggestive of their independent actions during JEV infection. **Conclusion:** To conclude, there is an insufficient anti-inflammatory cytokine response indicated by decreased expression of IL-4 and IL-10 in the brain is associated with increased tissue pathology and viral load during JEV infection

Board 357. Detection of *Rickettsia typhi* and *R. felis* in *Xenopsylla cheopis* from Hawaii

S. E. Karpathy[1], W. R. Warashina[2], M. M. Sturgeon[1], Y. Zaldivar[1], A. Williams[1], A. E. Buchholz[2], S. Y. Park[2], P. V. Effler[2], M. E. Eremeeva[1];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Hawaii Public Health State Laboratory, Honolulu, HI.

Background: Murine typhus is a zoonotic disease endemic to Hawaii, where increases in human cases have been occurring since 2002. *Rickettsia typhi* is the etiologic agent of murine typhus; classically it circulates in a zoonotic cycle involving rats, *Rattus rattus* or *R. norvegicus*, and their fleas, *Xenopsylla cheopis*. Humans become infected accidentally in rat infested areas or by encounters with fleas seeking alternative hosts during declines in rat populations. **Methods:** *X. cheopis* (n=121) were collected from *Mus musculus* trapped in peridomestic environments in 2004 on the island of Oahu. DNA was extracted from the fleas and a multiplex TaqMan assay detecting *R. typhi* and *R. felis* was used for testing the DNAs. DNA sequencing of amplicons was done to confirm the species identification. **Results:** Screening was completed for 121 fleas, of which 6 were positive for DNA of *R. typhi* (4.9%) and 48 were positive for DNA of *R. felis* (39.6%). Both organisms were detected at similar Ct values with averages of 38.88 and 40.94 for *R. typhi* and *R. felis*, respectively (p value = 0.0263). Amplicons shared 98 to 100% nucleotide sequence identity with *R. felis* or *R. typhi* reference sequences. **Conclusions:** Detection of both *R. typhi* and *R. felis* DNA in association with *X. cheopis*, the classic vector for murine typhus, suggests that two different flea-borne rickettsial diseases probably occur in Hawaii. In the continental USA, *R. felis* is associated with a peridomestic cycle involving opossums, cats, and cat fleas. However, whether *R. felis* can be maintained transovarially by rat fleas and thus exist without any need for animal reservoir is unknown.

Board 358. The Potential for Introduction of *Japanese Encephalitis Virus* into California

R. J. Nett[1], G. L. Campbell[2];

[1]F.E. Warren AFB, Cheyenne, WY, [2]Division of Vector Borne Infectious Diseases, Centers for Disease Control and Prevention, Fort Collins, CO.

Background: Japanese Encephalitis Virus (JEV) is a mosquito-borne virus endemic to Southeast Asia that when transmitted to humans can lead to Japanese Encephalitis (JE), a disease affecting mostly children with a fatality rate up to 30 percent. The continued geographical expansion of JEV across Southeast Asia along with the recent introduction and rapid spread of West Nile Virus (WNV) across the United States, demonstrates the ability of arboviruses to spread quickly across the globe. To date, no review has analyzed the potential for introduction of JEV into California or North America. **Methods:** We performed a descriptive analysis of the scientific literature. **Results:** California is a large state, which functions as a hub for international travel and commerce with Asia, potentially allowing for the introduction of mosquitoes infected with JEV, most likely by importation of an infected adult female mosquito via marine or air transportation. If JEV is introduced into California, the virus may quickly become established due to the significant number of preadapted mosquito vectors and viral amplifying vertebrate hosts that exist within favorable climates. The two most likely JEV vectors, *Culex tarsalis* and *Culex pipiens quinquefasciatus*, are common mosquitoes in California that feed readily on birds, but also on man, and are efficient laboratory vectors of JEV. In contrast to Asia where pigs serve as the primary amplifying hosts, common passerines in California, such as the tricolor redwing blackbird and the house finch, efficiently amplify JEV in the laboratory and would likely act as primary amplifying hosts. Once introduced, the lack of active surveillance for JEV, the ambiguous clinical presentation of JE, the cross reactivity of serological testing between JEV and other flaviviruses, and the probability that clinicians and laboratories would not consider JE as a possible diagnosis would likely lead to a delay in recognition. **Conclusion:** As exemplified by WNV, the introduction of JEV to California or other parts of North America could result in rapid spread throughout North America and significant morbidity and mortality. Arbovirus surveillance programs within California should be modified to increase the probability of detecting JEV introduction in a timely manner, especially in mosquitoes and birds.

Zoonotic & Animal Diseases

Wednesday, March 19
12:00 PM – 1:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 359. Anthrax in Wabessa village in the Dessie Zuria district of Ethiopia

G. S. Ejigu;

Medical Faculty, College of Health Sciences, Hawassa University, Awassa, ETHIOPIA.

Background: In Ethiopia, Anthrax is an endemic disease which occurs every year 'anthrax season' in several farming localities, causing disease both in humans and livestock. This study was therefore undertaken with the objective of examining the impact of the disease in one village in the Dessie Zuria district, by isolating and characterizing the causative agent, and by assessing the views and practices of farmers as regards the control and prevention of this zoonotic disease. **Methods:** An investigation of sudden death in a goat in Wabessa village in the Dessie Zuria district of Ethiopia was undertaken using fresh blood brought to the Kombolcha Vet. Laboratory. The sample was examined using standard bacteriological techniques and animal pathogenicity tests. Participatory approaches were employed to gain information on the magnitude of the problem, villager's knowledge of the disease, and the control measures practiced. **Results:** The laboratory investigation revealed *Bacillus anthracis* as the cause of sudden death. Information gathered from stockowners in the same village revealed other similar recent cases and deaths, both in animals and humans, with farmers clearly describing the clinical signs and necropsy findings of anthrax. The disease occurs annually in this area in May and June, and in the 2002

outbreak mortality rates of 7.7%, 32.7% and 47.1% were observed in cattle, goats and donkeys, respectively. This study indicates that the community of this particular village neither knows of, nor practices, any of the conventional methods for anthrax control. The disease in humans and the environmental contamination associated with the practice of opening cadavers are briefly described and the findings are discussed with the epidemiology of anthrax in Ethiopia and elsewhere. **Conclusions:** This study and the retrospective national district disease outbreak reports revealed that anthrax is still a serious public health and economic concern for farming communities in Ethiopia. The key to reducing environmental contamination, preventing public health issues and controlling the disease is to have appropriate handling and removal practices for dead animals, but these do not exist.

Board 360. Animal Rabies Surveillance in Jordan, 2000-2007

H. Khazally[1], R. Gerber[2], A. Mhedat[3], A. Majali[4], M. Al-Rashdan[3], M. Al-Nsour[5], B. Hijawi[3];

[1]Field Epidemiology Training Program, Amman, JORDAN, [2]Resident Advisor, Field Epidemiology Training Program, Jordan & Coordinating Office for Global Health, Centers for Disease Control and Prevention, Atlanta, GA, [3]Directorate of Disease Control, Ministry of Health, Amman, JORDAN, [4]Department of Veterinary Medicine, Jordan University of Science & Technology, Irbid, JORDAN, [5]Field Epidemiology Training Program & Directorate of Disease Control, Ministry of Health, Amman, JORDAN.

Background: Rabies is a fatal viral zoonosis. In developing countries, accurate data about animal rabies is lacking due to incomplete reporting systems. This report describes the incidence of animal rabies in Jordan during the period January 2000 to July 2007. **Methods:** A retrospective investigation was carried out on data collected by the Division of Vaccines and Sera, Ministry of Health, which is the referral rabies diagnostic laboratory in Jordan. The confirmatory test used was direct fluorescent antibody testing by standard protocol. Data on date of testing, animal species, and geographic location were analyzed. **Results:** During the study period, 89 cases of rabies in animals were identified in Jordan; 48 (54%) were in dogs, 18 (20%) in cattle, 6 (7%) in goats, and 5 (6%) in sheep. No human cases were reported. The yearly number of animal cases increased sharply from 2003 (1 case) to 2007 (31 cases through July). There was no change in surveillance procedures for animal rabies. Cases occurred in 16 of the 21 health directorates in Jordan, but most were geographically concentrated in the north (Ajloun, Irbid, Mafraq, and North Badia) (respectively, 15%, 18%, 10%, and 9%). Cases varied by month of occurrence; most cases (37; 64%) were from July to December and few cases (10; 17%) were from February to May. **Conclusions:** The increase in the incidence of reported and confirmed cases, especially after 2003, is of public health concern and efforts are being directed towards immediate implementation of effective control programs. Prevention of animal rabies, and subsequently human infections, will require the joint efforts of veterinary and public health officials in Jordan. Routine mass immunization, licensing of pet animals, and spay-neuter programs, especially in dogs, should reduce rabies cases and assist in rabies prevention. Such campaigns are underway in health directorates in north Jordan.

Board 361. Host Ecology in Urban and Rural Habitats: Modeling Exposure Risk to Rabies in the Midwest

S. E. Bowe, S. M. Wisely;

Kansas State University, Manhattan, KS.

Background: Urbanization is a global phenomenon that alters the epidemiological landscape. To understand the altered epizootic potential of rabies in the Midwestern United States due to urban and suburban development, we are constructing a model of human exposure risk based on ecological parameters of the host species, striped skunk (*Mephitis mephitis*), and current and predicted anthropogenic changes. As a first step towards model development, we are comparing habitat use, survival, and fecundity of striped skunks in urban and rural habitats. These data will allow us to estimate the number of susceptible animals and habitat-specific encounter rates in each environment. **Methods:** A total of 1482 trap nights were carried out on the Konza Prairie Biological Station, a tract of tall-grass prairie. Captured skunks were immobilized and fitted with a collar transmitter. Using triangulation methods, nighttime location data were collected. **Results:** Eight striped skunks were captured (3 females). Individual skunk movement ranged from 171 m to 2114 m between consecutive points with an average of 620 m. There was an average distance of 3633 m between locations of different skunks, ranging from 113 m to 7949 m. Of the traps, 16% were set in gallery forest, 73% were set in prairie and 11% were set near human habitation. Although only 11% of the traps were set within 500 m of human habitation, 38% of the skunks were trapped in these areas. The locations of these skunks were an average distance of 763 m from one another. **Conclusions:** Although trapping in the urban site has yet to begin, we are already observing the affinity of skunks for human habitation. Many urban adapted species occur at higher densities in urban environments and have increased contact rates as compared to rural areas. All movements of collared skunks near human building sites were less than 1.6 km of one another and multiple skunk captures in a single trap suggest home range overlap. Movements of skunks on prairie far from human sites were an average of 3.2 km from one another. The risk of rabies transmission increases with an increase in host contact rates and the risk of human exposure increases due to greater contact with companion animals. By comparing skunk ecology in urban and rural environments, we can develop vaccination strategies that reduce human exposure risk in urban areas.

Board 362. A Comparison of the Impact of Rabid Foxes with Rabid Raccoons, New York State

K. Yousey-Hindes, A. Newman, B. Cherry, M. Eidson, C. V. Trimarchi, R. J. Rudd;

New York State Department of Health, Albany, NY.

Background Rabies virus, an RNA virus of the Lyssavirus genus, causes an acute, incurable encephalomyelitis with a case-fatality rate approaching 100%. The virus is transmitted through the saliva of infected mammals. In New York State (NYS), terrestrial rabies is found in the greatest numbers among raccoons, skunks, and red and grey foxes. Anecdotal evidence suggests that rabid grey foxes are more aggressive and are more likely to attack humans than rabid raccoons. The purpose of this investigation was to employ the NYS rabies surveillance data to determine whether rabid foxes were more likely than rabid raccoons to have been involved in a human exposure and whether they were more likely to have caused a direct exposure (such as a bite). **Methods** The NYS Department of Health's rabies laboratory data and human exposure and treatment data from 1999-2007 were examined. Data analysis was performed in SAS 9.1. **Results** From 1999 to 2007, rabies was laboratory-confirmed in 3015 raccoons, 227 grey foxes, and 61 red foxes. Raccoons were associated with 1487 human exposure incidents and 2192 post-exposure prophylaxes (PEPs), compared to 156 human exposure incidents and 210 PEPs for foxes (red and grey foxes combined). Among all animals that caused a potential rabies exposure in NYS, foxes were more likely than raccoons to be linked to a human exposure (OR: 9.96; 95% CI: 5.63-17.62). Among the subset of animals linked to a human exposure, foxes were more likely than raccoons to have caused a bite (versus non-bite) exposure (OR: 4.58; 95% CI: 3.47-6.05). Similarly, rabid foxes were more likely to have had direct (versus indirect) contact with a human (OR: 4.37; 95%

CI: 3.17-6.02). **Conclusions** Although raccoons remain the leading terrestrial wildlife source of potential rabies exposures and PEPs in NYS, rabid foxes appear to be more likely to cause direct human exposures than rabid raccoons. More research needs to be done to determine whether the difference in human exposures is caused by the rabies infection or is indicative of inherent differences between the infected animal species. The findings should inform educational campaigns for the public as well as for animal control and law enforcement officials who are often called to investigate wildlife issues.

Additional Poster Abstracts

Wednesday, March 19
12:00 PM – 1:00 PM
(authors present 12:00 PM – 1:00 PM)
Exhibit Hall

Board 363: Profile of Meningococcal Infection-Report from a Developing Country

N. Agarwal, .R. Guleria, P. Agarwal, .S. Bhoi

Background: Neisseria meningitides has been recognized to be the cause of frequent worldwide outbreaks of meningococcemia and meningococcal meningitis. In India an increase in the number of outbreaks has been observed since early 2005.Meningiococcal infection is a potential cause of morbidity and mortality globally .The present study was done to see the clinical profile of patients presenting with meningococcemia like illness to emergency department from March 2005 – June 2007. **Methods:** 112 suspected cases of meningococcal infection that had presented to Emergency Medicine from March 2005 -June 2007, with fever and symptoms suggestive of meningococcal infection were analyzed. Details of the clinical profile, course of treatment in the hospital, investigations and the final outcome as in morbidity and mortality was recorded. **Results:** Out of 112 patients who had come 97 were male .Mean age was 25.6 years. Majority of patient's i.e.85 presented with 1-3 days of fever. 66(58.92%) patients had headache, 41(436.60%) myalgia, 61(54.47%) vomiting and 17(15.17%) backache. Classical erythematous macular skin rash was seen in 52(46.42%), petechiae in 45(40.17%) and erythematous papule in 29(25.89%).Bleeding occurred in 2 patients. None of the patients in the study gave history of seizures at admission. Meningeal signs were seen in 51 patients and only 10 patients had focal neurological deficit. Average systolic blood pressure noted was 101mmHg and diastolic of 68mmHg. 13(11.6%) patients also developed Lower Respiratory Tract Infections. Hemoglobin was 12.1gm%, Mean Total leukocyte count was 20027cells/mm3, and platelet count ranged from 11000 – 493000/mm3.CSF study was done in 58(64.96%) patients and in 52(89.65%) it was positive for meningitis. CSF culture was positive in only 1 patient. In 11 patients skin scrapping was positive. Blood culture was not positive in any of the patients. Patients were treated mainly with 3rd generation cephalosporins, aminoglycosides, & fluroquinolones based on clinical symptoms. 77(68.75%) patients also received parenteral steroids. 74 patients were discharged and 22 died.**Conclusion:** Meningococcal meningitis continues to be endemic in parts of Asia. The diagnosis is mainly clinical and diagnostic yield of the tests is low. It is still associated with high mortality.

*Department of Medicine ,AIIMS ,New Delhi ,India
**Department of Emergency Medicine , AIIMS ,New Delhi ,India

Board 364: Influenza

W. L. Jackson,

CDR, USPHS, Quarantine Medical Officer, CDC Liaison Officer, US PACIFIC COMMAND, J07

Left side of poster: Background: Tripler Army Medical Center is the DoD tertiary treatment facility serving the Pacific Command area of responsibility. Hawaii also serves as a major travel hub between Asia, the current epicenter for Influenza A H5N1 (or "Bird Flu"), and North America. As such, Hawaii is potentially a sentinel site for the emergence of the next influenza pandemic. Successfully managing an influenza pandemic in real time requires greater capacity for surveillance and monitoring so leaders can make better choices on managing scarce resources and mitigating the effects of a pandemic. **Methods:** Clinical Informatics and Preventive Medicine established the requirements for an application: an easy to use graphical user interface using existing Electronic Medical Records for providers, a command dashboard to give leaders real time view of the pandemic, an interface for public health officers to acquire more detailed information that allows univariate, bivariate, and multivariate analysis to spot trends that could change treatment or management during a pandemic, and the capacity to use demographic data to generate a geographic information system map of cases that would allow for better allocation of resources. A multidisciplinary approach with weekly meetings was undertaken with input from all Armed Services on island as well as CDC and with collaboration of the Pacific Disaster Center on Maui toward the development of the tracking database tools. **Results:** Development of a graphical user interface form for AHLTA (the current DoD electronic medical record program). This form, called an Alternate Input Methodology (AIM) allows for easier clinician data input. Outputs include a command "dashboard" that allows leaders an easier overview of several variables of interest; a restricted site "dashboard" for public health officials that allows more detailed analysis including exporting to standard sophisticated software tools; and a Geographic Information Systems proof of concept. These form the major products of this project that allow a comprehensive overview of pandemic and seasonal influenza. **Conclusions:** The goal of this project was to develop a pandemic influenza tracking tool that would benefit clinicians, decision-makers, public health officials, and ultimately our patients. We sought to test the concept and components of the tool by using real data during an influenza season. This project has proven a useful tool for tracking seasonal influenza and has already yielded helpful data on the distribution of cases by month as well as age, clinic, and strain distribution of influenza over time. One important result is that we do not appear to have a clear peak influenza season in the DoD population in Hawaii in contrast to that reported in the Continental United States (November-April). Potential explanations include DoD populations traveling to Southern Hemisphere and tropical locations for duty and that we may need more data to see a clear seasonal variation. The diagnosis of influenza should be entertained all year long and vaccine should be offered all year long. **Right side of poster, Background at top: Background:** Tripler Army Medical Center (TAMC) is the tertiary Department of Defense (DoD) Medical Treatment Facility for the Island of Oahu and the Pacific Region. Oahu is the island hub for air travel between the Pacific Basin and the United States. Given Hawaii's proximity to the current Influenza A H5N1 epicenter in Southeast Asia and air travel patterns, we are especially vulnerable if and when an influenza pandemic occurs. Anticipating such a potentially devastating outbreak, we recognized the need to be able to track and manage such an outbreak as it happens. We convened a working group within our Clinical Informatics and Preventive Medicine sections to develop an automated system that would hopefully facilitate our management efforts using existing technology and medical information systems. **Results to Date:** The AHLTA graphical input AIM form provides a simpler method for clinicians to record history, symptoms, signs, contact information,

as well as order entry for influenza and influenza-like illnesses.The Command "Dashboard" provides leaders and clinicians an overview of many variables of an evolving pandemic in near real-time, allowing for improved situational awareness and clinical diagnostic acumen. The restricted "Dashboard" site allows public health officials to conduct case tracking and complex statistical analysis that will help clinicians better diagnose and manage pandemic or seasonal influenza cases. A Geographic Information System (GIS) proof of concept was performed with the Pacific Disaster Center on Maui and demonstrated the feasibility and usefulness of case mapping.Using real influenza and influenza-like illness cases, we were able to speculate that the influenza season in our DoD population in Hawaii spans the entire year compared to the US mainland and this has practical consequences: the diagnosis of influenza should be considered year-round and vaccination against seasonal influenza should continue throughout the winter into spring and perhaps continuously until the next seasonal vaccine is available.

Board 365: Diversity of picornaviruses in rural Bolivia, 2002-2003

Nix WA[1], **Oberste** MS[1], Peñaranda S[1], Maher K[1], Khetsuriani N[1], Venczel L[1], Cselko Z[1], Freire MC[2], Cisterna D[2], Lema C[2], PAHO/BOL, Rosales P[3], Halkyer P[4], Pallansch MA

[1] Centers for Disease Control and Prevention, Atlanta, GA, USA; Instituto Nacional de Enfemedades Infecciosos C. Malbrán, Buenos Aires, Argentina; Pan-American Health Organization, Bolivia; Ministry of Health and Sports, Bolivia

Background: Despite the eradication of wild poliovirus in the Americas in 1991, acute flaccid paralysis (AFP) remains a public health concern in many countries. AFP surveillance identified a persistently high occurrence of AFP cases in a small geographic area of eastern Bolivia. These cases were seasonal (beginning after the rainy season) and, anecdotally, often coincided with apparent neurologic disease in domestic pigs. Diagnostic studies in these cases ruled out poliovirus, but no other etiology was identified. **Methods:** We tested stool specimens from 49 AFP cases and 32 healthy household or community contacts collected via AFP surveillance during 2002-2003, as well as six porcine specimens from the area. Viral genomes of four picornavirus genera, *Enterovirus*, *Parechovirus*, *Cardiovirus*, and *Teschovirus*, were detected and identified directly in stool RNA by real-time RT-PCR and nested RT-PCR coupled with amplicon sequencing. **Results:** Picornaviruses were found in 52 of 81 individuals (32 cases and 20 healthy contacts), including 37 positive for enteroviruses, 23 for parechoviruses, and 13 for cardioviruses; 20 contained 2 or more picornaviruses. There were no significant differences in positivity rates between cases and contacts. All 6 porcine stools contained picornaviruses: 2 contained enterovirus, 4 had parechovirus, and 5 contained teschovirus; 4 of 6 were mixed infections. Teschovirus was not detected in human specimens and cardiovirus was not detected in porcine specimens. In addition to 19 previously known enterovirus and 4 parechovirus serotypes, sequence comparisons identified 4 enterovirus types (2 human, 2 porcine), 3 parechovirus types, and 2 cardiovirus types which have not been previously detected in humans or animals. In all but one case, picornaviruses from humans were different from those found in pigs. **Conclusions:** We identified a high prevalence and great variety of picornaviruses in AFP cases and their contacts in Bolivia, but there was no single virus, or combination of viruses, that specifically correlated with disease. A prospective case-control study is underway to determine the etiology of AFP cases in this area of Bolivia. Further studies are also needed to determine the clinical and public health importance of the new picornaviruses identified in this study.

Board 366: Analysis of genetic diversity and natural selection in the apical membrane antigen 1 of *Plasmodium falciparum* and *P. vivax* from India

M. T. Alam, A. Thakur, S. Vinayak, S. Garg, and Y. D. Sharma,

Department of Biotechnology, All India Institute of Medical Sciences, Ansari Nagar, New Delhi, India

Background: Apical membrane antigen 1 (AMA1) is a potential vaccine candidate, and a number of vaccines based on this molecule are currently at different stages of clinical trials. Genetic polymorphism studies on Plasmodium antigens in natural population need to be done prior to conducting clinical trials of a malaria vaccine. Accumulating evidence suggests that antigenic polymorphisms may influence immunogenicity and protective effect of a vaccine. Here we report characterization of AMA1 polymorphisms in both P. falciparum and P. vivax from India. **Methods**: Part of the AMA1 gene from both species was analyzed from large number of isolates collected from different regions of the country. We sequenced only domain I of P. falciparum AMA1 while both domain I and II of P. vivax AMA1. The software packages DnaSP and MEGA3 were used to analyze the sequencing data. Signatures of natural selection on these antigens were estimated by the ratio of non-synonymous (dN) and synonymous (dS) mutations as well as Tajima's D and McDonald-Kreitman test statistics. Three-dimensional structures of AMA1 were made using MODELLER routine incorporated in Discovery studio. **Results**: A total of 57 AMA1 haplotypes with 29 polymorphic residues were found among 157 P. falciparum isolates. Whereas 49 haplotypes with 25 polymorphic residues were found among 61 P. vivax isolates. Most of the observed haplotypes from both species were new as they were not reported from any other regions. The dN/dS ratio for PfAMA1 domain I and PvAMA1 domain II were >1, indicating that they are under positive natural selection while, it was <1 for PvAMA1 domain I. Results from PfAMA1 show moderate level of genetic differentiation and limited gene flow (Fixation index ranging from 0.048 to 0.13) between populations studied here. Three-dimensional structures of PfAMA1 and PvAMA1 were made showing that all observed polymorphisms were distributed at only one surface of the molecule. **Conclusion**: Apical membrane antigens in both Plasmodium species show extensive diversity in India and are under positive natural selection. The extent of genetic diversity and selection were higher in high malaria transmission areas as compared to low malaria transmission areas. Moderate levels of gene flow were predicted amongst populations. The data reported here will be valuable for the development of AMA1-based malaria vaccine.

Board 367: Analyzing Global Trends in EIDs, and Predicting the Origin of the Next New Zoonosis

P. Daszak[1], K. Jones[2], M. Levy[3], V. Mara[3], J. Gittleman[4],

[1]Consortium for Conservation Medicine, New York, NY, USA, [2]Institute of Zoology, London, UK, [3]Center for International Earth Science Information Network, Palisades, NY, USA, [4]University of Georgia, Athens, GA, USA.

EIDs are a significant burden to public health and global economies. In particular, a series of high case-fatality zoonoses have caused significant mortality (e.g. HIV/AIDs, influenza virus) and represent a growing threat (e.g. Nipah virus in Bangladesh, H5N1 avian influenza). Despite this, there has been little quantitative analysis of global spatial and temporal trends in disease emergence, and virtually no attempts to predict the origins of the next zoonosis. Here we present analyses using a new database of 335 disease emergence 'events' (origins of EIDs) between 1940 and 2004 (Jones et al. *Nature*, in press). After correcting for reporting biases, we show for the first time definitive evidence that the incidence of new EIDs has increased significantly since 1940, with the highest number in the 1980s concomitant with the rise in HIV incidence

in Europe and North America. As previously shown, EIDs are dominated by zoonoses (60.3%), the majority of which originate in wildlife (71.8%), with this latter group increasing significantly over time. We also show that 54.3% of EID events are due to bacterial and rickettsial pathogens, reflecting a large number of drug-resistant microbes. We analyzed the causes of EIDs and show that EID origins are significantly correlated to socio-economic, environmental and ecological factors. We then used these results to identify regions where new EIDs are most likely to originate (Emerging Disease "Hotspots"). For high-impact zoonoses, these are tropical countries with high wildlife biodiversity, whereas other groups show different predicted global risk distributions. We conclude that global resources for EID surveillance and investigation are poorly allocated, with the majority of the scientific and surveillance effort currently focused on countries from where the next important emerging pathogen is least likely to originate.

Board 368: Increasing Resistance to Antimicrobials Among Neisseria Gonorrhoeae Isolates in Developing Country

[1]K. Panday, [2]R.P.Sukla,[3]S.D.Joshi,

[1]Nepal Medical College and Teaching Hospital, Kathmandu, NEPAL, [2]All India Institute of Medical Sciences,New Delhi, India, [3]Public Health Office, Kailali

Background: Increasing antimicrobial resistance among N. gonorrhoeae isolates in many developing countries in recent years has become a major global public health concern in a high-risk population. **Methods:** Gonococcal isolates from consecutive male and female patients with urethral / cervical discharge attending 4 STD clinics and 2 hospitals through september 2004-October2007, were tested for antimicrobial susceptibility to penicillin, tetracycline, norfloxacin and ceftriaxone by disk diffusion method using NCCLS guidelines. MIC?s were determined for resistant strains by the agar dilution technique. Penicillin resistant isolates were tested for lactamase production by nitrocefin method. Linear yearly trend in the proportions of resistant strains to individual antibiotics was studied by trend chi-square test using the statistical package, EPI INFO program. **Results:** 277 N. gonorrhea isolates were obtained during the period of seven years. Resistance to penicillin was observed in 63(22.74%) of which, 31 (44.2%) were penicillinase producing N. gonorrhoeae (PPNG). 137 (49.45%) of the isolates were resistant to tetracycline of which 73 (43.9 %) were tetracycline-resistant N. gonorrhoeae (TRNG, MIC >/=16 ug/Ml). A significant increasing trend in the resistance to penicillin and tetracycline ($p< 0.001$) was observed over the seven years. Resistance to norfloxacin was seen in 40(14.44%) of strains with an increasing prevalence of resistant strains observed though not significant ($p=0.2$). Overall 10(3.6%) isolates showed resistance to ceftriaxone by disc diffusion technique. **Conclusion:** An overall increase in N. gonorrhoeae strains resistant to the commonly used antimicrobials was observed. The high percentage of GC isolates resistant to quinolones and the emerging resistance to ceftriaxone highlights the need for periodic susceptibility monitoring and proper patient management

Board 369: Prevalence of Hepatitis B Amongst Healthy Pregnant Women in Developing Country

[1]K. Panday, [2]R.P.Sukla, [3]S. Joshi,

[1]Nepal Medical College and Teaching Hospital, Kathmandu, NEPAL, [2]All India Institute of Medical Sciences,New Delhi, India, [3]Community Health and Environmental society Nepal.

Background: The routine Antenatal screening of pregnant women for HBsAg and identification of Chronic Hepatitis B in pregnant women with subsequent immunoprophylaxis of newborns has come up with promising results over the years. However, there are limited data in this regard as far as studies are concerned .To determine the Hepatitis B infectivity amongst a large population of pregnant women,the socio-demographic profile and the risk factors if any present in these group of women and to correlate maternal with that of maternal HBVDNA levels. **Methods**: Pregnant women at any gestation coming for antenatal checkup in one of the largest tertiary care centers in 5 regions of Nepal were included in this study from Sept. 2004 till Nov. 2007. After an informed consent and a detailed history serological study including HBV markers and moleculer assays of the women were done and results analysed. Results: Out of a total 36,379 antenatal registrations ,11,000 pregnant women were screened, of which 125 women tested positive for HBsAg .The prevalence of HBsAg 1.13% (11 in 1000) .The age of the HBsAg positive women varied between 18 and 25 yrs (mean 21 ?3.1 yrs) with majority (90%) between 21 and 25 yrs. Seventy percent of them were multigravida. The socioeconomic status in majority was low (52%). Most of them (75%) were illiterate.. Majority (60%) were healthy carriers of HBsAg. HBsAg was incidentally detected in 9%. Family history of Hepatitis B was given by five women (4.5%) and history of blood transfusion(8%) , tattooing(9%) and surgery (8%),The prevalence of HbeAg positivity was 21.6%. The estimation of HBVDNA levels showed that in majority it was undetectable (<0.5 pg/ml) to low levels(0.5 pg/dl -5 pg/ml)(30% and 50%).It was moderate(5 pg/dl '1000 pg/dl) in 6% and high (>1000 pg/dl) in 14% of women.There was a linear correlation between levels of HBVDNA and HbeAg Status in HBsAg positive women . Women with a positive HbeAg had in majority(75%) high to moderate circulating levels of HBVDNA as compared to those who had a positive Hbe antibody in whom HBVDNA was undetectable to low levels(93%)($p<0.001$). **Conclusion**: Although the Prevalence of Hepatitis B in healthy pregnant women in our population is not high but its prevalence in younger age group and a high infectivity is definitely alarming depicting a major route of transmission from mother to the newborn .Hence to detect, identify and treat these subgroup of population with use of available sensitive methods could really pave a path in preventing Chronic HepB infection on a large scale basis especially in developing country like Nepal.

Board 370: The Preven Urban Community Randomised Trial Of A Combined Intervention For Sexually Transmitted Disease Prevention In Nepal

[1]K. Panday, [2]R.P.Sukla,[3]S.Kumar BK,

[1]Nepal Medical College and Teaching Hospital, Kathmandu, NEPAL, [2]All India Institute of Medical Sciences,New Delhi, India, [3]Public Heath Office,Nepal

Background: A community randomized trial, (PREVEN trial), was conducted to explore the impact of combined sexually transmitted disease interventions in urban Nepal in ten intervention and ten control cities. **Methods:** The intervention were: (1) improved syndromic management of vaginal and urethral discharge available through pharmacies, with social marketing of condoms and treatment packages and referral to previously trained physicians for cases of pelvic inflammatory disease and genital ulcers, and (2) screening and treatment of sex workers (SW) reached through a mobile team every two months, along with presumptive treatment for trichomoniasis (TV) and bacterial vaginosis with metronidazole, and provision of free condoms. A baseline survey of STIs prevalence was undertaken in the general population (GP) and amongst SW and their clients in 24 cities in 2002 to stratify cities for randomisation to intervention and control arms of the trial. Twenty cities were selected for the trial. The impact of the interventions, was evaluated through surveys of STI prevalence after 2 years and 3 years of intervention, in an interim household based survey in 2005 and a final survey in 2006 along with concomitant surveys in a sample of SW. Testing for syphilis, GC, CT, TV and HIV were undertaken in the 20 randomised cities. Data analysis was blinded with respect to city identity until results were available for each infection where upon the prevalence of each infection in the matched intervention and control cities could be compared. **Results:** In 2006, the overall prevalences of STIs in

the general population across the 20 cities were as follows: males: gonorrhea 0.11%, Chlamydia 4.7%, syphilis (titer > 1:8) 0.29%, HIV 0.51%; females: gonorrhea 0.24%, Chlamydia 8.6%, syphilis (titer > 1:8) 0.20%, trichomonas 2.4%, HIV 0.17%. The overall prevalences of STIs in the female sex workers in 2006 across the 20 cities were as follows: gonorrhea 1.2%, Chlamydia 17.6%, syphilis (titer > 1:8) 1.3%, trichomonas 3.7%, HIV 0.41%. **Conclusions:** Final analyses of the differences in STI prevalences by intervention arm are ongoing and will be presented. The implications of these results for sexually transmitted disease control programmes will be discussed with an invited panel.

Board 371: Modeling the effects of land-use changes on the emergence of Hendra virus

R. Plowright[1], P. Foley[2], A. Dobson[3], J. Foley[1], H. Field4, P. Eby[5], P. Daszak[6],

[1] School of Veterinary Medicine, Department of Medicine and Epidemiology, University of California, Davis, CA, 95616, [2]Department of Biological Sciences, California State University, Sacramento, CA, [3]Department of Ecology and Evolutionary Biology, Princeton University, Princeton, NJ, USA, [4]Department of Primary Industries & Fisheries, Moorooka, Queensland, Australia, [5]Independent consultant, Australia, [6]The Consortium for Conservation Medicine, 460 West 34th Street, New York, NY, USA

Hendra virus (HeV) is a lethal paramyxovirus that that recently emerged from Pteropus spp. fruit bats (flying foxes) in Australa. Despite a high case fatality rate in people, and lack of effective therapy or vaccines, there is little known about the underlying causes of its emergence. Hendra virus outbreaks have occurred sporadically, in a pattern that coincides with dramatic changes in flying fox ecology, including changes in spatial population distribution, population fragmentation, decreasing migratory behavior, and aggregation in urban areas. We used computational models to evaluate how these anthropogenic environmental changes may have changed HeV dynamics in flying fox populations, and ultimately led to emergence. Our models predict that decreased migratory behavior and increased population fragmentation lead to a decline in herd immunity, and thus to more intense outbreaks after local reintroduction of HeV. Aggregation of flying fox populations into urban centers results in regional pulses of infected individuals. These processes could increase the likelihood of viral transmission from flying foxes to spill-over hosts such as humans and horses and may have created the 'perfect storm' that allowed a poorly-transmissible virus to emerge via sporadic, explosive outbreaks into at least two new host species.

Board 372: S. Woo-Jin

Influenza virus continues to emerge and re-emerge as new threat to human population. We have tested various Korean medicinal plant extracts for antiviral activity against influenza viruses. Among them, one (total extract of *Agrimonia pilosa*) was shown to be highly effective, as tested in MDCK cell culture, against all three types of influenza viruses that are currently circulating globally (H1N1 and H3N2 influenza A subtype and influenza B virus). The extract also exhibited strong inhibitory effect on avian influenza virus as tested in embryonated chicken eggs. The antiviral effect of Agrimonia pilosa total extract on influenza A virus as tested by plaque reduction assay was about 14-23 /□ of 50% inhibitory concentration (IC50) for both influenza A and B viruses. Agrimonia pilosa total extract also exhibited virucidal effect at concentration of about 160-570 ng/ against influenza A and B viruses when the viruses were treated with the extract prior to plaque assay. Similarly, the extract exhibited virucidal effect against H9N2 avian influenza virus in embryonated chicken eggs at concentration of 280 ng/□ . Moreover, the extract exhibited hemagglutination inhibition effect against all three types of viruses tested, including influenza A, B viruses and avian influenza virus, at high concentration. However, the sensitivity in hemagglutination inhibition was widely different among four different subtypes of influenza viruses tested. The quantitative RT-PCR analysis data showed that the extract suppressed viral RNA synthesis in MDCK cells whereas amantadine failed to show similar effect. The results suggest that the major target for the observed antiviral effect is viral surface antigen and/or the viral membrane, and merits further investigation as an alternative strategy for controlling influenza infections.

Board 373: Nipah Virus Emergence in Malaysia 1998-9 Was Due to Epidemic Enhancement in The Domestic Pig Population

J. R.C. Pulliam[1], J. Dushoff[2], H. E. Field[3], J. H. Epstein[4], the Henipavirus Ecology Research Group (HERG) 4, A. P. Dobson[5], and P. Daszak[4] ,

[1] Emory University, Atlanta, GA, USA, [2] McMaster University, Hamilton, ON, Canada, [3] Biosecurity Sciences Laboratory, Department of Primary Industries and Fisheries, Queensland, Australia, [4] The Consortium for Conservation Medicine, New York, NY, USA, [5] Princeton University, Princeton, NJ, USA

Nipah virus (NiV) is a recently discovered emerging zoonotic paramyxovirus that has caused human mortality across southern Asia and is a particular threat due to its broad host range, wide geographical distribution, and high case fatality, as well as the lack of available vaccine or effective therapy. It first emerged in Ipoh, Malaysia, 1998-9 and the index cases were traced to a large pig farm in this town. As part of an NIH/NSF Ecology of Infectious Disease award (Fogarty International Center), we analyzed livestock production data from this index farm and modelled within-farm infection dynamics. Results suggest that *repeated* introduction of NiV from the wildlife reservoir into this intensively managed pig population led to changes in infection dynamics in the pigs. Initial viral introduction produced a partially immune population and led to an "enhanced" epidemic upon reintroduction of the virus. Long-term within-farm persistence permitted regional spread of the virus, ultimately producing widespread human infection. Thus, the cause of emergence of NiV can be essentially characterized as due to agricultural intensification. These findings have two important implications for the prevention and control of NiV. First, they suggest that prophylactic vaccination of commercial pig populations is unlikely to be a cost-effective option for the prevention of NiV emergence, as failure to uphold expensive, rigid vaccination schedules could produce enhanced epidemics and promote widespread infection. Second, epidemic enhancement is most likely to occur on large farms, as these farms have sufficient population numbers and turnover to sustain long-term transmission. Targeted surveillance of these farms in areas where flying fox distributions overlap commercial pig farms is therefore extremely important to detect spillover events early-on and prevent widespread infection.

Board 374: Five- Year Review of Etiology of Food and Waterborne Disease Outbreaks in the Philippines

J. G. GERONIMO, Ma. C. Dela Cruz, L.T. Sombrero, G. Reclusado, Z. Mojares,

Department of Health- Research Institute for Tropical Medicine Alabang, Muntinlupa City, Philippines

Background: This study reviewed the occurrences of the etiologic agents of food and waterborne disease (FWBD) outbreaks in the Philippines from 2001 to 2005 based from the referred FWBD samples for bacterial culture by public health officials from different regions in the Philippines to the National Reference Laboratory for Bacterial Enteric Diseases (NRL-BED) at the Research Institute for Tropical Medicine (RITM). The number of

samples of FWBD outbreak cases were analyzed to know the trends of occurrences of FWBD outbreaks and the commonly isolated bacterial etiologic agents from year 2001 to year 2005. **Method:** Restrospective review of data of food and waterborne disease outbreak cases was done and results were determine using descriptive type of analysis. **Results:** A total of 6,145 FWBD outbreak cases were analyzed and data showed fourteen (14) regions in the Philippines have occurrence of food and waterborne diseases outbreaks; namely regions I, II, III, 1V, V, VI, VII, VIII, IX, X, XII, National Capital region (NCR), Coldillera Autonomous Region(CAR), and CARAGA. By comparing each year ,it was observed that 2004, has the highest number of cases (2,602 cases) followed by 2002 (974); third by 2005 (969); fourth by 2003 (875) and least was 2001 (725). Totality of cases from different regions showed that NCR has the most number cases referred (2,005 cases) followed by Region I (1,745 cases) ; third was Region IV (975 cases); fourth was Region III (576 cases) and fifth was Region VII (161 cases). No referred cases were observed from Regions XI, XIII, XIV, and Autonomous Region of Muslim Mindanao (ARMM). Regions III, IV and NCR have consistent number of cases in all years of observations while there was notable increase of cases in Regions I, V, CAR and CARAGA. The number of outbreak cases declines in five years of observations in Regions VI,VII, and IX while in Regions V, CAR and CARAGA the number of cases were rising although they were under control. **Conclusions:** The continuous high morbidity of FWBD outbreak cases in many parts of the country remains the same although reported mortality is low. Data showed the presence of the five most common etiologic agents in FWBD namely *V. cholerae* 01, Non-typhoidal *Salmonella* species, *S. aureus* , *V. parahaemolyticus* and *S. Typhi*.. Public health officials should be alarmed with the increasing isolation of toxin- producing organisms of *V. parahaemolyticus* and *S. aureus* as recognized etiologic agents of FWBD from human cases. The consistency of outbreaks from 2001-2005 in Regions III, IV, and NCR which showed isolation *V. cholerae* 01, *Salmonella* non-typhoidal species and *S. aureus* are indications that something needs to improve in the delivery of public health services in meeting the needs for basic provisions in our food and water safety system.

Board 375: Case report: Dual infection of H5N1 avian influenza and H3N2 human influenza in Jakarta Indonesia, April 2007

V. Setiawaty[1], K. N. A Pangesti[1], H. A. Prawestri[1], D. H. Mulyono[2], E. Burhan[3], Priyanti[3], E. R. Sedyaningsih[1],

[1]National Institute of Health Research and Development, Ministry of Health (NIHRD-MOH), Jakarta, Indonesia[2]Eijkman Institute, Jakarta, Indonesia, [3]Persahabatan Hospital, Jakarta, Indonesia

Background Human influenza A viruses are transmitted year round in Indonesia with a higher frequency detected among patients with influenza-like illness during the rainy season. In 2005, the Ministry of Health established a referral system for patients with avian Influenza A virus (H5N1) infection and identified 113 patients with laboratory-confirmed disease between 2005 and 2007. We are reporting a case-report of a patient with simultaneous infection with avian (H5N1) and human influenza A (H3N2) virus infection. **Methods** In April 2007, a 16 year old female patient was hospitalized with respiratory illness at a referral hospital in Jakarta. A case investigation form was used to collect clinical and epidemiologic data and clinical samples were collected for hematological profile and as well as acute and convalescent antibody titers for H1, H3, and H5 antigen using HAI assays. Throat & nasal swab specimens were collected on the 6th day of onset, when she visited NIHRD laboratory and tested with real-time and gel-based RT-PCR for H1, H3 and H5 at NIHRD-MOH. Patient was hospitalized after results showed H5N1 positive infection. Specimens were sent to the Eijkman Institute for confirmation of PCR results and genetic sequence analysis. **Results** The patient presented with moderate symptoms of fever > 38°C, sore throat, cough, rhinitis, headache and myalgia, but no dyspnoea. The thrombocyte counts were 250,000 - 269,000 cells/mm^3, leucocytes 4,700–5,800 cells/mm^3, lymphocyte 31 – 44.7%. X ray and CT scan of thorax showed no pneumonia. PCR results were positive from throat and nasal swabs for influenza A (H3N2) and influenza A (H5N1) by real-time and gel based RT-PCR. These results were confirmed by repeat testing at Eijkman. HAI antibody titers were negative for H3N2 and 1:10 for H5N1 from sera that was collected 6 days after onset of illness. HAI antibody titers from convalescence sera were 1:640 for H3N2 and negative for H5N1.**Conclusions** This is the first case-report of a human with both influenza A (H5N1) and influenza A (H3N2) co-infection. Such infections are of great concern due to the possibility of genetic reassortment leading to the emergence of a H5N1 strain that is more easily transmitted human to human and emphasizes the importance of advanced laboratory-based surveillance in geographic regions where both human and avian influenza viruses are co-circulating.

L1. New Rapid Diagnostics

Wednesday, March 19
3:00 PM – 4:30 PM
Centennial I

Application of Proteomics Methods for Pathogen Discovery

D. Wang, Y. Ye, E. Mar, S. Sammons, S. Tong, L. J. Anderson, B. P. Holloway;

CDC, Atlanta, GA.

Background: Proteomics has been widely used to study proteins in complex mixtures such as cells, body fluids, tissues, and organisms. Application of advance proteomics techniques in the characterization of disease-specific proteins should provide information for the detection of potential infectious agents. As a proof of concept, we applied two proteomics techniques, 1) two-dimensional differential gel electrophoresis (DIGE) and 2) one-dimensional gel electrophoresis and one-dimensional liquid chromatography coupled with mass spectrometry (GeLC/MS), to investigate viral proteins from cultured cells inoculated by virus obtained from an infected patient. **Methods:** A virus isolate was inoculated in human lung fibroblastic cells. In DIGE experiment, the proteins extracted from infected and uninfected cells were labeled with Cy5 and Cy3 dyes, respectively, and then combined and run on 2D PAGE gel. CyDye labeled proteins were visualized using a Typhoon 9100 scanner. The proteins of infected cells were directly subjected to 1D PAGE gel in GeLC/MS method. Selected spots in 2D gel or bands in 1D gel were subjected to in-gel trypsin digestion and the peptides were analyzed by LC-MS/MS for protein identification. **Results:** The DIGE method identified five viral proteins of *vaccinia virus* that are only present in infected cells, in agreement with the finding determined by nucleic acid based methods. In addition, the isolate was identified to be Copenhagen strain of *vaccinia virus* by high sequence coverage of the viral protein E3. Among 428 proteins detected by Gel-LC/MS method, eight were identified as *vaccinia virus* viral proteins. Two of these viral proteins were identified by both methods. **Conclusions:** These results demonstrate that proteomic techniques can be effectively used for the detection and strain identification of infectious agents. Given the techniques work on proteins of any sources, proteomics possesses a potential of being developed as a useful molecular tool in pathogen discovery and disease diagnosis of emerging infectious diseases and bioterrorism defense.

Evaluation of the QuickVue Influenza A+B rapid diagnostic test in a community setting

B. J. Cowling[1], K. Y. Cheng[1], K. H. Chan[1], R. O. Fung[1], V. Fang[1], C. L. Lam[1], L. M. Ho[1], W. H. Seto[1], R. Yung[2], T. M. Uyeki[3], P. M. Houck[4], J. S. Peiris[1], G. M. Leung[1];

[1]The University of Hong Kong, Hong Kong, HONG KONG, [2]Centre for Health Protection, Hong Kong, HONG KONG, [3]Influenza Division, CDC, Atlanta, GA, [4]Division of Global Migration and Quarantine, National Center for Preparedness, Detection and Control of Infectious Diseases, CDC, Seattle, WA.

Background: Rapid influenza diagnostic tests can be useful to facilitate optimal treatment of seasonal influenza, and in a pandemic scenario could potentially be important tools for control and mitigation as well as clinical management. We evaluated the performance of the QuickVue Influenza A+B test (Quidel Corp., San Diego, California) among a large community sample of patients presenting with influenza-like-illness in a sub-tropical setting. **Methods:** Patients older than 2 years whose chief complaint consisted of any combination of at least 2 influenza-like symptoms were recruited from 25 outpatient clinics in Hong Kong during the 2007 influenza season. Two sets of nasal and throat swabs were obtained using a standardized protocol from each patient. One set of swabs was combined and tested by QuickVue while the other was sent for viral culture (gold standard) by standard methods. **Results:** 946 subjects were enrolled, 11 of whom were excluded due to missing or contaminated laboratory samples. In the remaining 935 subjects, QuickVue had sensitivity 68% and specificity 96%, with positive predictive value 78% and negative predictive value 93%. Age stratification showed that the rapid test had lower sensitivity in adults aged 16 or above (67%) compared to children (73%); within children the sensitivity further increased with younger age (82% in under-5s). We also found higher sensitivity in subjects who were tested within 24 hours of symptom onset (69%) versus those tested 24-48 hours after onset (62%). **Conclusions:** Our findings suggest that QuickVue has slightly lower sensitivity in the community setting compared to most previous evaluations typically under more controlled conditions such as laboratories and hospitals. Our finding that sensitivity varies by age and time of symptom onset is likely explained by the greater degree of viral shedding in children and earlier in the course of illness.

Evaluation of an Antigen-capture ELISA to Detect *Histoplasma capsulatum* Antigenuria in Immunocompromised Patients

C. M. Scheel[1], B. Samayoa[2], L. Benjamin[1], P. Riley[1], M. D. Lindsley[1], A. Herrera[2], G. Raxcacoj[2], S. Lima[2], R. Miramontes[1], T. M. Chiller[1], M. Brandt[1], E. Arathoon[2], B. L. Gomez[1];

[1]Mycotic Diseases Branch, Centers for Disease Control and Prevention, Atlanta, GA, [2]Clinica Familiar Luis Angel Garcia (CFLAG), Hospital General San Juan de Dios, Guatemala City, GUATEMALA.

Background: *Histoplasma capsulatum* infection causes significant morbidity and mortality in HIV-infected individuals, particularly those in developing countries without access to sophisticated diagnostics or highly-active antiretroviral therapy. Symptoms of histoplasmosis are non-specific, yet most deaths occur in the first 2 weeks after diagnosis. Current diagnostic methods can be complex, expensive and slow. A simple, rapid method to detect *H. capsulatum* infection would dramatically decrease time to diagnosis and treatment and reduce morbidity and mortality. We evaluated an antigen-capture ELISA to detect antigen in urine of HIV patients with histoplasmosis in Guatemala. **Methods:** Urine samples were collected prior to treatment in HIV patients with culture-confirmed histoplasmosis ($n = 19$) or non-histoplasmosis fungal and non-fungal diseases ($n = 25$). Urine from healthy controls ($n = 33$) were used to define specificity. An antigen-capture ELISA was developed which utilizes polyclonal rabbit anti-*H. capsulatum* antibody as both capture and detection reagent. A standard curve was included in each assay plate to insure inter-assay reproducibility. Urine specimens were run twice on separate days and repeated a third time if the coefficient of variance (CV) was greater than 20%. **Results:** Preliminary results indicate that the *H. capsulatum* antigen-capture ELISA demonstrates a sensitivity of 84.2% for confirmed histoplasmosis and a specificity of 96.6% (all other disease controls, 96.0%; healthy controls, 96.9%) when tested against baseline urine specimens in these patient cohorts. Eight of the patients with follow-up urine specimens showed decreased antigenuria during the course of antifungal therapy. **Conclusions:** In this preliminary analysis, the antigen ELISA assay shows high sensitivity and specificity as a simple rapid diagnostic test for histoplasmosis in HIV-infected persons. Specimen collection and more detailed evaluation is ongoing. This assay has the potential to be easily adapted to laboratories across the world. A test using urine would allow for rapid, non-invasive diagnosis and initiation of treatment. Longitudinal analysis of *H. capsulatum* antigenuria in serial specimens during therapeutic intervention may prove useful for monitoring patient recovery in a clinical setting.

Mycobacterium tuberculosis: Direct from Sputum Identification and Determination of Drug Resistance within Hours for all Antimycobacterial Agents

N. Parrish, G. Osterhout, K. Carroll;

Johns Hopkins University, Baltimore, MD.

Background There is an urgent need for new, rapid diagnostics to stem the tide of multi-drug resistant (MDR-TB) and extensively-drug resistant (XDR-TB) tuberculosis (TB). No SINGLE, rapid, diagnostic method currently exists for identification, and determination of drug resistance in *Mycobacterium tuberculosis* (MTB). We have developed a new diagnostic test,"RAM" (Rapid Analysis of Mycolic Acids), for rapid identification of MTB and determination of antibiotic resistance for ALL 1st- and 2nd-line agents directly from sputum. "RAM" is an HPLC-based qualitative and quantitative measure of the mycolic acids present in the cell walls of Mycobacteria. **Methods** Processed, sputum samples were spiked with known quantities of MTB or other non-tuberculous (NTM) species. "RAM" assay detection limits and specificity were established. Viable counts were done to verify total CFU/ml/specimen. Drug susceptibilities were done by inoculating aliquots of spiked sputum into broth with and without 1st- or 2nd-line agents followed by incubation (72 h). Samples were saponified, protonated, extracted and derivatized prior to HPLC-"RAM" analysis. **Results** "RAM" detected / differentiated MTB from other NTM (e.g. *M. avium*) and normal flora directly from sputum. Detection limits paralleled smear (~10^3 CFU/ml). Total time for detection and identification of MTB from a smear positive sputum sample was < 2 h. Using known drug susceptible, MDR- and XDR-TB strains (n = 15), there was 100% agreement for "RAM" results directly from sputum to ALL 1st- and 2nd-line agents in 72 h. **Conclusions** We have shown definitive proof-of-concept that "RAM" detection, identification, and susceptibility testing of MTB with ALL 1st- and 2nd-line drugs can be achieved directly from sputum in ≤ 72 h. Since this is a phenotypic rather than a molecular-based test, resistance is identified irrespective of the genetic mechanism of resistance.

Rapid Identification of Class A Biothreat and Other Clinically Relevant Bacterial Pathogens using Universal PCR coupled with High Resolution Melt Curve Profile Analysis

S. Yang, P. Ramachandran, A. Hardick, R. Rothman, C. A. Gaydos;

The Johns Hopkins University, Baltimore, MD.

Background: Improved rapid diagnosis of systemic bacterial infections can significantly improve patient outcome. Broad-range PCR assay targeting the 16S rRNA gene using conserved primers allows universal Eubacterial pathogen detection in otherwise sterile body fluids. However, characterization of the amplicon inter-primer variable sequences for definitive identification of the etiologic pathogen has been associated with high cost and low throughput, when based on hybridization probes or sequencing. High-resolution melt curve profile analysis of the PCR products, used in tandem with 16S rRNA PCR, offers a simple high throughput workflow method that is highly accurate with reduced cost. **Methods**: DNA isolated from 42 clinically relevant bacterial species was analyzed. A single primer pair was designed to target the highly conserved sequences within the 16S rRNA gene with inter-primer hypervariable sequences being unique for each bacterium. PCR reactions were performed in the Idaho Technologies Rapid Cycler-2 instrument with LC-Green saturating dye. We performed high-resolution melting analysis of the PCR products with the High Resolution (HR-1) instrument and melting profiles were generated for each organism. **Results**: All 42 bacteria tested could be distinctly identified at the species level by their unique melting temperature (Tm) and melt curve profile. Even closely related species (e.g. *Bacillus anthracis* vs. *B. cereus*, *Francisella tularensis* vs. *F. philomiragia*, *Yersinia pestis* vs. *Y. pseudotuberculosis and Streptococcus pneumoniae* vs. *S. viridans*) with 1-2 nucleotide differences in their amplicon sequences could be clearly discriminated. Time to identification was less than 2 hrs for PCR and high-resolution melt curve analysis. **Conclusions**: This novel approach combining broad-based PCR with high resolution melt curve profile analysis provides a rapid and cost-effective diagnostic approach for detection and identification of biothreat, as well as other clinically relevant bacterial pathogens.

The Use of a Real-Time Multiplex PCR for Detection of Sporadic and Outbreak Cases Caused by Free-Living Amoeba

K. Bandyopadhyay[1], Y. Qvarnstrom[2], G. S. Visvesvara[2], R. Sriram[2], M. J. Beach[2], A. J. da Silva[2];

[1]CDC, Division of Parasitic Diseases, NCZVED and AREF, Atlanta, GA, [2]CDC, Division of Parasitic Diseases, NCZVED, Atlanta, GA.

Background: *Acanthamoeba* spp., *Balamuthia mandrillaris* and *Naegleria fowleri* are ubiquitous free-living amoebae that can cause infections in humans that often result in death. *Acanthamoeba* species are also associated with amoebic keratitis that can lead to blindness. Because of the severity of these diseases, timely, specific, and sensitive laboratory diagnosis is needed. The current study compares a triplex real-time PCR assay (simultaneous detection of 3 amoeba species in a single real-time PCR test) with culture and direct detection of amoeba using an IFA for laboratory identification of these amoebae. **Methods:** A total of 143 samples were tested for free-living amoebae. 75 samples were associated with the *Acanthamoeba* keratitis outbreak investigated by CDC in 2007; 68 were obtained from sporadic cases. DNA was extracted from these samples using Qiagen DNeasy kit (Qiagen, CA). A triplex real-time PCR, culture and IFA were performed following the published protocols. **Results:** Twenty of the 75 samples from the *Acanthamoeba* keratitis outbreak were positive by PCR and 11 of these were positive by culture; IFA was not performed on these samples. Of 68 clinical samples from sporadic cases, 22 were positive for *N. fowleri* by PCR, of which 21 were positive by culture. The PCR positive, culture negative specimen was positive by IFA. Three other samples were positive for *B. mandrillaris* by both real-time PCR and IFA. Four samples were positive using both PCR and culture for *Acanthamoeba* sp. **Conclusions:** Free living amoeba were detected in 40 samples by culture or IFA; all of these samples were positive using real-time PCR; 9 additional samples were detected using PCR alone. The added advantages of multiplexed identification, low cost and analysis time of 5-6 hours from specimen receipt to results, make this test an attractive complement to existing methods for detection of free living amoeba.

L2. Mobile Poulations and Infections Diseases

Wednesday, March 19
3:00 PM – 4:30 PM
Centennial II

Survey of U.S. Travelers to Asia to Assess Compliance with Recommendations for Japanese Encephalitis Vaccine

M. Duffy[1], C. Reed[2], P. Edelson[3], S. Blumensaadt[4], K. Crocker[5], A. Griggs[1], E. Hayes[1], M. Fischer[1];

[1]Division of Vector-Borne Infectious Diseases, Fort Collins, CO, [2]Division of Global Migration and Quarantine, Centers for Disease Control and Prevention, Atlanta, GA, [3]Division of Global Migration and Quarantine, Centers for Disease Control and Prevention, Jamaica, NY, [4]Division of Global Migration and Quarantine, Centers for Disease Control and Prevention, Chicago, IL, [5]Division of Global Migration and Quarantine, Centers for Disease Control and Prevention, Los Angeles, CA.

Background: Japanese encephalitis (JE) vaccination is recommended for travelers to Asia whose itineraries increase their risk of exposure to JE virus. The numbers of travelers with such itineraries and the proportion who receive JE vaccine are unknown. We performed a survey to estimate the proportion of U.S. travelers to Asia who receive JE vaccine according to the Advisory Committee on Immunization Practices (ACIP) recommendations. **Methods:** We surveyed U.S. residents >18 years old departing on 39 flights to Asia. Surveyed flights were selected through a stratified random sample of all direct flights to JE endemic countries from three U.S. airports (John F. Kennedy International Airport, Chicago O'Hare International Airport, and Los Angeles International Airport). We asked participants about planned itineraries and activities, source of travel health information, JE vaccination status, and potential barriers to vaccination. Participants planning to spend ≥30 days in Asia or >40% of their time in rural areas were defined as "at-risk" travelers for whom JE vaccination should have been considered. **Results:** Of 2,530 eligible travelers contacted, 1,737 (69%) responded. Among the 1,737 participants, 1,079 (62%) sought medical advice from one or more sources prior to travel, and 449 (26%) described itineraries for which JE vaccination should have been considered. Of these at-risk travelers, only 47 (11%) reported receiving >1 dose of JE vaccine; 374 (83%) did not receive JE vaccine, and 28 (6%) did not indicate if they had received JE vaccine. Among the 374 at-risk travelers who did not receive JE vaccine, 166 (44%) had visited a health care practitioner (HCP) to prepare for this trip. Of the 166 unvaccinated at-risk travelers who visited a HCP, 83 (50%) indicated their HCP had not offered or recommended JE vaccine. **Conclusions:** A majority of all travelers sought some medical advice prior to travel. A quarter of surveyed U.S. travelers to Asia reported planned itineraries for which JE vaccination should have

been considered. Few of these at-risk travelers received JE vaccine, even when they visited a HCP to prepare for the trip. These findings indicate both a need and an opportunity to better educate travelers and HCPs regarding the ACIP recommendations for the use of JE vaccine.

Brucella melitensis Infection Following Duty in Iraq

L. R. Carpenter[1], J. R. Dunn[1], S. K. Thomas[2], D. L. Smalley[3];

[1]Tennessee Department of Health, Communicable and Environmental Disease Services, Nashville, TN, [2]Tennessee Department of Health, Montgomery County Health Department, Clarksville, TN, [3]Tennessee Department of Health, Laboratory Services, Nashville, TN.

Background: *Brucella* spp. are zoonotic pathogens and potential bioterrorism agents which infect >500,000 persons worldwide each year. Of approximately 100 US brucellosis cases annually, most are associated with travel to endemic regions or consumption of certain high-risk foods. *B. melitensis* infection is widespread in humans, cattle, sheep, and goats in the Middle East, including Iraq. We describe a case of *B. melitensis* infection in a Tennessee soldier following recent duty in Iraq. **Methods:** We interviewed the patient and attending physicians and reviewed the patient's medical records to ascertain clinical features, diagnosis, and exposure history. Speciation of the isolate was performed by Tennessee Department of Health Laboratory Services. Ongoing post-exposure serologic monitoring among laboratory personnel is being conducted at one hospital where the patient had received care. **Results:** The 23-year-old soldier's onset of clinical signs was in December, 2006, one month after returning from Iraq. Prior to the diagnosis of brucellosis he was an inpatient at two different hospitals. Clinical signs included weight loss, cyclic febrile episodes, and severe, progressive hip pain. Numerous microbiologic tests yielded no results, until blood culture and cultures of a sacro-iliac abscess demonstrated *B. melitensis* in April, 2007. Despite widespread reports of soldiers eating locally prepared food, the patient reported eating only food from military-approved sources in Iraq. He also reported occasional, inadvertent contact with goats while carrying out his duties in Iraq. Following this patient's diagnosis, two of 25 laboratory personnel tested at the hospital where this patient was originally admitted displayed serologic evidence of recent exposure to *Brucella* sp. **Conclusions:** Brucellosis is an infrequent diagnosis in the U.S.; however, overseas travelers, persons consuming high-risk foods, and soldiers serving in endemic regions may be at increased risk for exposure. Education among these groups may help avoid infections. Additionally, providers should consider brucellosis as a differential diagnosis when dealing with episodic fever, especially among these populations, and laboratorians should emphasize proper precautions when attempting to identify potentially infectious agents.

Persistent Gastroenteritis Outbreak Due to New Variant Norovirus Spanning Multiple Cruises of a Domestic Riverboat and Affecting On-Shore Contacts--Ohio and Mississippi Rivers, 2006

A. Sheth[1], **G. Ewald**[1], K. Kornylo[1], K. Fleming[1], T. Allen[1], M. Menon[1], S. Harris[1], N. Seerpi[2], M. Sears[2], J. Vinjé[1], J. Sobel[1], and the Riverboat Outbreak Investigation Team;

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]Green River District Health Department, Owensboro, KY.

Background: Noroviruses are the leading cause of gastroenteritis outbreaks on international cruise ships, which are required to report gastrointestinal illnesses to public health authorities. In October 2006, we investigated an outbreak on a domestic riverboat on the Ohio and Mississippi Rivers. **Methods:** We defined a case as diarrhea or vomiting in a person who had illness onset while on board or within seven days of disembarkation. We reviewed the ship's illness log, conducted a cohort study, and surveyed for cases during the next cruise. We tested stool specimens for norovirus RNA by RT-PCR and DNA sequence analysis. **Results:** The ship's log revealed that 2%-12% of passengers and crew reported illness on five cruises preceding our investigation. During this cruise, 201 (53%) passengers and 26 (18%) crew members were ill. Increased risk of illness was noted among passengers who shared a dining table with an ill person [relative risk (RR) 2.8, 95% confidence interval (CI) 1.9 - 4.0], shared a cabin with an ill person (RR 2.2, CI 1.8 - 2.8), or witnessed a person vomiting (RR 2.3, CI 1.9 - 2.7). Cases peaked on day 5; the cruise was aborted on day 6 of 8. The next cruise began after a 1-day sanitization; 71 (19%) passengers and 3 (2%) crew members became ill, and the cruise was aborted on day 3 of 7. Among 216 responding passengers on both cruises, 77 (36%) reported illness onset in a hotel after leaving the ship, 13 (6%) in an airplane, 8 (4%) in a bus, and 7 (3%) in a rental car. Illness occurred in 9 hotel employees and 5 public health workers who had on-shore contact with ill passengers. After a 10-day sanitization, no cases were reported on future cruises. Norovirus RNA was detected in stool samples from 18 of 24 ill passengers on three consecutive cruises and 6 of 8 ill hotel and public health workers. Strains obtained from passengers of three cruises and a hotel employee shared the identical sequence of a new variant (GII.4) strain called Minerva that emerged nationwide in 2006. **Conclusions:** This norovirus outbreak spanned multiple cruises of a domestic cruise ship. Illness was transmitted to on-shore contacts of ill passengers. As with international cruise ships, public health officials should develop outbreak reporting and control plans for domestic cruise ships to prevent future outbreaks and decrease spread of illness to on-shore contacts.

Occurrence of Infectious Diseases in US Veterans of Recent Military Conflict

G. A. Roselle[1], S. M. Kralovic[1], L. A. Simbartl[2];

[1]US Department of Veterans Affairs, Veterans Health Administration (VHA) Central Office Infectious Diseases Program and Cincinnati VA Medical Center AND University of Cincinnati, Cincinnati, OH, [2]US Department of Veterans Affairs, Veterans Health Administration (VHA) Central Office Infectious Diseases Program and Cincinnati VA Medical Center, Cincinnati, OH.

Background: Conflict and strife predispose to emerging infectious diseases (ID) risks. Military personnel returning to civilian life after military service during times of war may have ID issues. **Methods:** Annually from 2005-2007, inpatient and outpatient encounters from VHA were assessed for ICD-9 ID diagnoses (001.00-139.99) osteomyelitis (OM) (730.00-730.99) and tuberculin skin test positivity (TST+) (795.5). Three groups of veterans were compared: those from the current US military conflict in SW Asia, all other served by VHA and an age-comparable subset of all others (<40 yrs of age) who had not served in the conflict. **Results:** Inpatient discharges with an ID diagnosis for length of stay were low (~1.5%) after removal of HIV-infection from all groups. Superficial skin and appendage infections (dermatomycoses, dermatophytoses) were the most common reported for all three groups. For those from the current conflict, warts, HSV, hepatidites and other venereal diseases completed the top 5. For the age-comparable group HIV-infection was the second most common, followed by warts, hepatidites and HSV, while for the all other group, hepatidites, HIV, zoster and warts were most prevalent. Percent of persons with a TST+ diagnosis was from 0.8% to 1.2%/yr for those from the current conflict compared to 0.3%/yr for all others and 0.6% to 0/7%/yr for the age-comparable group. OM encounters were lowest in the current veteran group (ranging from 9.4-16.4 encounters/10,000 pts/year) with similar results for the age-comparable group (16.0-18.6 encounters/10,000 pts/year), while much higher in the all other group (65.5-68.4 encounters/10,000

pts/year). Regional diseases such as leishmaniasis, show an increase in younger veterans. **Conclusions:** Veterans from recent conflict have similar overall ID issues compared to age-comparable veterans and all other veterans. Differences from the age-comparable group may define areas for prevention awareness. Increased TST+ needs to be further explored. Burden of disease from OM which might be expected from traumatic injuries, remains similar to age-comparable controls and much less for the all others. While ID burden from regional diseases for an affected individual is significant, overall burden of disease from these relative to all IDs for the VHA-served population is still low.

Five-Year Experience with Type 1 and Type 2 Reactions in Hansen's Disease at a US Travel Clinic

J. T. Jacob, P. Kozarsky, C. Franco-Paredes;

Emory University, Atlanta, GA.

Background: Although the worldwide prevalence of Hansen's disease (HD) has decreased in the era of multi-drug therapy (MDT), the annual reported in US has remained approximately 100-150 cases/year for 30 years. Leprosy reactions (type 1 or type 2) occur in 25-50% of patients with HD and represent both diagnostic and therapeutic challenges. Precipitating factors, outcomes, and optimal management of reactions remain elusive. **Methods:** We retrospectively examined our experience with HD reactions over a 5 year period (2002 to 2007). Medical records of patients with HD seen in Emory University's TravelWell Clinic were systematically reviewed to assess the frequency and outcomes of reactions. **Results:** Of the 543 patients seen in TravelWell for post-travel clinic visits from 2002 to 2007, 12 (2.2%) had HD. Among these patients, 9 (75.0%) were male with a median age of 47.1 years (range: 21.2-64.9). The median age at diagnosis was 39.0 (range: 21.8-64.4). Eight (66.7%) patients had lepromatous or multibacillary disease, and 4 had tuberculoid or paucibacillary disease. Seven patients originated from Brazil, 2 from Mexico, and 1 each from Trinidad & Tobago and Vietnam. All patients were treated with MDT; second-line therapy was used in 3 cases due to drug toxicity or resistance. Reactions occurred in 9 (75%) of patients, of which 4 (44.4%) were type 1 and 5 (55.6%) were type 2. The median time from initiation of treatment to onset of reaction was 16.2 months (range: 3.9-149.2). Reactions occurred prior the use of MDT in 2/9 (22.2%), during MDT 5/9 (55.6%), or after completion of MDT in 2/9 (22.2%). All patients with type 1 reactions were treated with prednisone and 3 (60%) of patients with type 2 reactions required both thalidomide and prednisone. Corticosteroid use lasting > 6 months was required in 4 (44.4%) of patients with reactions, with an average daily prednisone dose of 30 mg. **Conclusions:** HD is a reemerging infection in many areas of the world, including the US, due to increasing migration. HD is often complicated by reactions, often requiring chronic corticosteroid therapy. Reactions may be more common than previously thought and may occur prior to the initiation of MDT, during MDT, or even years after completion of therapy. Further research on the epidemiology and optimal clinical management of reactions is needed.

Exposure to Infectious Tuberculosis (TB) During Air Travel: Outcome of Passenger Contact Investigations Initiated June-October 2007

K. J. Marienau[1], M. Russell[2], J. Neatherlin[3], C. Schembri[4], C. Kim[5], K. Buckely[6];

[1]Centers for Disease Control and Prevention, ST PAUL, MN, [2]Centers for Disease Control and Prevention, Chicago, IL, [3]Centers for Disease Control and Prevention, Dallas, TX, [4]Centers for Disease Control and Prevention, Atlanta, GA, [5]Centers for Disease Control and Prevention, Detroit, MI, [6]Centers for Disease Control and Prevention, New York, NY.

Background: The Division of Global Migration and Quarantine (DGMQ) follows the 2006 WHO guidelines "*TB and Air Travel*" and works with state health departments (SHDs) using a standardized process for TB contact investigations (TB CI) involving air travel. DGMQ also collaborates with international partners, but international standards for this process have not been defined. Data about possible TB transmission among contacts (passengers seated within two rows of the index case) on flights >8 hours are limited. The large number of TB CIs involving air travel provide an opportunity to better understand TB transmission during flights >8 hours among airline contacts of an index case. **Methods:** U.S. health departments and foreign public health partners are asked to report passenger contact investigation outcome data to DGMQ for TB CIs. We analyzed data for TB CIs initiated from June 1 through October 31, 2007, to characterize the outcomes of passenger contact tracing and determine the extent of *Mycobacterium tuberculosis* transmission among these contacts. **Results:** From June through October 2007, 56 TB CIs were initiated. Of these, contact information has been provided for 42. DGMQ provided information for 1,069 contacts to SHDs and for 109 contacts to foreign public health officials (1,178 total). To date, DGMQ received outcome data for 185 contacts (16%). For 117 (63%) of these, TB skin test (TST) results were available. Of the 117 contacts with TST results, 88 (75%) had negative TST and 29 (25%) had positive TST. Of the 29 with positive TST, 23 (79%) had other known risk factors and 6 (21%) had none (2 of those were documented new converters). **Conclusions:** The paucity of outcome data reported from these TB CIs precludes determining the extent of *M. tuberculosis* transmission. Improved methods for national and international reporting on the outcomes of TB CIs are needed to better define TB transmission during air travel and provide data for evidence-based guidelines for TB CIs.

L3. Vaccine Preventable Diseases

Wednesday, March 19
3:00 PM – 4:30 PM
Regency VII

Reducing Global Disparities in the Use of Hib Vaccine

L. Ojo[1], R. O'Loughlin[1], A. Cohen[1], K. Edmond[2], S. Shetty[3], U. Griffiths[2], A. Bear[3], L. Privor-Dumm[3], P. Zuber[4], R. Hajjeh[3];

[1]Centers for Disease Control and Prevention, Atlanta, GA, [2]London School of Hygiene and Tropical Medicine, London, UNITED KINGDOM, [3]Johns Hopkins University Bloomberg School of Public Health, Baltimore, MD, [4]World Health Organization, Geneva, SWITZERLAND.

Background: *Haemophilus Influenzae* type b (Hib) is estimated to cause 3 million cases of meningitis and severe pneumonia and close to 400,000 deaths in children <5 years of age annually. Hib conjugate vaccines, widely used in developed countries, are underutilized in developing countries where most disease occurs. The GAVI Alliance provides co-financing for Hib vaccine to the 72 poorest countries in the world and in 2005 created the Hib Initiative (HI) to accelerate evidence-based decisions for Hib vaccine.**Methods:** The HI adopted a country-focused strategy to build capacity for decision making, based on enhanced communication, advocacy, and selective research. We compared the number of countries using or approved to use Hib vaccine before (2004) and after (2007) the creation of the HI, by income strata and WHO region. Three income strata based on World Bank indicators were compared: 72 GAVI -eligible countries (low and lower middle income), and 124 non -GAVI eligible countries (43 lower middle income, 81 upper -middle and high income). **Results:** The number

of GAVI eligible countries that have introduced or been approved to introduce Hib vaccine increased from 13/75 (17%) in 2004 to 31/72 (43%) in 2007 with a corresponding increase in the number of infants with access to vaccine from 8 million to 16 million, respectively. The applications of 21 other GAVI-eligible countries are under review. Changes were smaller for non-GAVI eligible lower middle income countries using Hib vaccine, increasing from 13/40 (33%) to 17/43 (40%) while the highest income countries increased from 63/81 (78%) to 69/81 (85%) in 2004 and 2007, respectively. Geographical disparities in GAVI -eligible countries that have applied for Hib vaccine persist, ranging from 32/36 (89%) countries in the African region to 3/8 (38%) in the European region. **Conclusions:** Although income and regional disparities persist, disparities in the use of Hib vaccine between rich and poor countries are decreasing. This success suggests that focused strategies to accelerate introduction of new vaccines in developing countries, such as those of GAVI and the HI, are feasible and effective. The limited increase in use of Hib vaccine among lower middle income countries may result from limited external resources available.

Rotavirus Burden in Central Asia: The Value of New Rotavirus Vaccines

E. Flem[1], K. Kasymbekova[2], E. Musabaev[3], R. Juraev[3], S. Abdikarimov[4], J. Gentsch[5], R. I. Glass[6], J. S. Bresee[5];

[1]Norwegian Institute of Public Health, Oslo, NORWAY, [2]Department of the State Sanitary and Epidemiological Surveil, Bishkek, KYRGYZSTAN, [3]National Institute of Virology, Tashkent, UZBEKISTAN, [4]Ministry of Health, Bishkek, KYRGYZSTAN, [5]National Center for Immunizations and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, [6]Fogarty International Center, National Institutes of Health, Bethesda, MD.

Background: New rotavirus vaccines are currently available at a subsidized price through the Global Alliance for Vaccines and Immunization (GAVI) for eligible low-income countries, including neighboring Uzbekistan and Kyrgyzstan in Central Asia. We sought to estimate rotavirus burden in both countries using hospital surveillance to determine the value of rotavirus vaccination in this region. **Methods:** We surveyed a sample of diarrhea cases in children <5 years of age in two hospitals in Uzbekistan and three hospitals in Kyrgyzstan during January 2005-December 2006. Demographic and clinical information and stool samples were collected. We tested stools for rotavirus using an enzyme immunoassay and characterized selected samples to determine genotypes. **Results:** We included a subset of 3537 (37%) diarrhea cases of 9477 eligible children in Uzbekistan and 3014 (34%) of 8841 eligible cases in Kyrgyzstan. We tested samples from all enrolled children and detected rotavirus in 30% (1046) of stools in Uzbekistan and in 26% (770) in Kyrgyzstan. Detection rates in Uzbekistan were higher (33%) in 2005 vs. 2006 (26%) with little variation between hospitals. Detection rates in Kyrgyzstan did not differ by year but rates in the north were higher than in the south (29% vs. 21%). The median age of rotavirus cases in Kyrgyzstan and Uzbekistan was 11 and 13 months, respectively, and 11% of Kyrgyz children with rotavirus were ≤3 months old, whereas the same proportion in Uzbekistan was only 3%. Rotavirus was detected year-round in both countries but rotavirus incidence sharply increased in autumn in Uzbekistan, where majority of diarrheal hospitalizations occurred in summer. The most prevalent rotavirus type was P[8], G1 detected in 51% of characterized samples in Uzbekistan and in 53% in Kyrgyzstan in 2005. A rare type P[6], G12 was also detected in 2% of samples in both countries in 2005. **Conclusions:** This is a first study to document the rotavirus burden in the GAVI-fund eligible countries of the WHO European region. Our findings demonstrate substantial rotavirus morbidity among young children in Central Asia, preventable by use of rotavirus vaccines. Ongoing surveillance will be critical in the future to monitor the effect of rotavirus vaccination program in this region.

Disease and Economic Burden of Rotavirus Diarrhea in Western Kenya

J. E. Tate[1], B. Obonyo[2], C. O'Reilly[1], D. Burton[1], J. Tornheim[2], K. Adazu[2], B. Ochieng[2], T. Kerin[1], R. Rheingans[3], K. Laserson[2], R. Breiman[4], E. Mintz[1], D. Feikin[2], M. Widdowson[1];

[1]CDC, Atlanta, GA, [2]CDC/KEMRI, Kisumu, KENYA, [3]Emory University, Atlanta, GA, [4]CDC/KEMRI, Nairobi, KENYA.

Background: Globally, rotavirus is the most common cause of severe gastroenteritis in children <5 years. Although two new rotavirus vaccines are available, local data are needed for decisions on introduction. We estimated the disease and economic burden of rotavirus diarrhea in children in western Kenya. **Methods:** To estimate rates of death, hospitalization, and clinic visits for rotavirus diarrhea in children <5 years in western Kenya, we extrapolated data from several sources. The annual number of diarrheal deaths in children <5 years was determined using verbal autopsy data from 2002-2005 in the KEMRI/CDC demographic surveillance system. All hospital admission records in one district from 2001-2003 were used to estimate the annual rate of diarrheal hospitalizations in children <5 years. A health utilization survey in 2005 in the same district was used to determine the rate of clinic visits for diarrhea by children <5 years. Surveillance data from 2005-2007 from 2 hospitals and 6 clinics were used to calculate the prevalence of rotavirus among children with diarrhea. Direct medical costs at 2 hospitals and 3 clinics were estimated using record review and interviews with clinical officers. Indirect costs were collected via interviews with parents of children presenting with diarrhea for medical care. **Results:** Rotavirus accounts for 20% of hospitalizations and 15% of clinic visits due to diarrhea in children <5 years. Annually, rotavirus causes >75 deaths, >100 hospitalizations, and >16,900 clinic visits per 100,000 children <5 years in western Kenya. By 5 years, 1 in 264 children will die from rotavirus diarrhea, 1 in 187 will be hospitalized, and every child will have sought care for rotavirus diarrhea. Hospitals and clinics spend approximately 4% of their time and resources treating rotavirus diarrhea in children. Median out-of-pocket cost of a diarrheal hospitalization was 19% of a family's median monthly income which ranged from 33 to 81 USD. Median cost of a clinic visit for diarrhea is 1% of the monthly income. **Conclusions:** Rotavirus diarrhea causes a substantial disease and economic burden to healthcare facilities and families in western Kenya. Rotavirus vaccination could offer an effective strategy to reduce this burden.

Etiologies of Bacterial Meningitis in Bangladesh

E. S. Gurley[1], M. Hossain[1], S. Montgomery[2], L. Petersen[2], J. Sejvar[3], L. Mayer[3], A. Whitney[3], P. Dull[3], L. Davis[2], N. Nahar[4], A. Uddin[4], M. Rahman[5], A. Ekram[6], S. P. Luby[1], R. F. Breiman[1];

[1]ICDDR,B, Dhaka, BANGLADESH, [2]CDC, Ft. Collins, CO, [3]CDC, Atlanta, GA, [4]Dhaka Medical College Hospital, Dhaka, BANGLADESH, [5]Mymensingh and Sylhet Medical College Hospitals, Mymensingh and Sylhet, BANGLADESH, [6]Rajshahi Medical College Hospital, Rajshahi, BANGLADESH.

Background: Rates of bacterial meningitis vary geographically, as do the proportion of cases caused by various pathogens. Anecdotal reports suggest that meningo-encephalitis syndrome is a common cause of hospitalization in Bangladesh. We conducted a study in four public tertiary care hospitals across Bangladesh to identify etiologies of meningo-encephalitis in June 2003- July 2005 and report here the bacterial meningitis findings. **Methods:** Every fourth patient meeting a clinical case definition of meningo-encephalitis syndrome, including fever, evidence of acute brain pathology, and indication for lumbar puncture, was eligible for enrollment. Illness histories and clinical evaluations were conducted and cerebrospinal fluid (CSF) tested for bacterial infection by culture, polymerase chain reaction, latex agglutination, and gene amplification and sequencing. **Results:** A total of 576 patients had

CSF collected and tested for bacterial infection; 32% had evidence of a bacterial etiology by >1 diagnostic method: *Neisseria meningitidis* infections occurred in 23%, 4% had *Streptococcus pneumoniae*, and 4% had *Haemophilius influenzae* type B (Hib). Patients diagnosed with bacterial meningitis had severe disease which included altered consciousness (77-89%) and convulsions (77-92%). Patients with meningococcal meningitis (case fatality ratio (CFR) 11%) were identified year-round and were primarily adult males (mean age 23 years). Patients with pneumococcal meningitis (CFR=25%) were identified in all months except December and January and represented all age groups (41% were children <5 years old, 37% were >15 years old). Patients with Hib meningitis (CFR=25%) were identified year-round and were primarily young children (50% were <1 year old), although 21% were >15 years old. **Conclusions:** Patients presenting to hospital with meningo-encephalitis syndrome frequently suffered from bacterial maningitis, specifically *N. meningitidis*, *S. pneumoniae*, and Hib, which produced severe disease and high mortality. Bacterial meningitis patients represented all age groups, even those with pneumococcal and Hib infections. Introduction of conjugate vaccines against these pathogens in Bangladesh would prevent substantial morbidity and mortality and should be considered.

L4. Tuberculosis

Wednesday, March 19
3:00 PM – 4:30 PM
Centennial III

Evaluation of Microscopic Observation Drug Susceptibility Assay for the Concurrent Detection of Tuberculosis/Multidrug-Resistant Tuberculosis

G. S. Ejigu[1], Y. Woldeamanuel[2], M. Gebeyehu[3], E. Lemma[3];

[1]Medical Faculty, College of Health Sciences, Hawassa Universty, Awassa, ETHIOPIA, [2]Medical Faculty, Addis Ababa University, Addis Ababa, ETHIOPIA, [3]Ethiopian Health and Nutrition Research Institute, Addis Ababa, ETHIOPIA.

Background: Early detection of multidrug-resistant *Mycobacterium tuberculosis* (MDR-TB) is of primary importance for both patient management and infection control. Optimal methods for identifying drug-resistant *Mycobacterium tuberculosis* in a timely and affordable way in resource-limited settings are not yet available. **Methods:** This study prospectively evaluated a low-technology but rapid drug susceptibility testing method, the microscopic observation drug susceptibility assay (MODS), in the concurrent detection of *M. tuberculosis* and its susceptibilities to isoniazid and rifampin (two drugs defining multidrug-resistant *M. tuberculosis*) directly from sputum specimens. Sputum samples were collected from 262 smear-positive TB patients in Addis Ababa, Ethiopia. To undertake MODS, 100 µl of decontaminated samples was inoculated into a 24-well plate containing 1 ml of 7H9 broth with and without appropriate drugs. The assay uses an inverted-light microscope to detect characteristic mycobacterial growth in liquid culture. **Results:** Of 262 smear-positive patients, MODS detected 254 (96.9%) and culture in Lowenstein-Jensen medium detected 247 (94.3%) ($P = 0.016$). For the 247 cultures, the sensitivity, specificity, and accuracy of MODS for detecting MDR-TB were 92.0, 99.5, and 98.8%, respectively, using the method of proportion as a reference (concordance, 98.8%; kappa value, 0.932). Results for MODS were obtained in a median time of 9 days. **Conclusions:** MODS is an optimal alternative method for identifying MDR-TB in a timely and affordable way in resource-limited settings.

Differences in Tuberculosis Knowledge between U.S.-Born and Foreign-Born Adults

H. Free, K. Heyman;

National Center for Health Statistics, Hyattsville, MD.

Background: There is growing evidence showing that tuberculosis (TB) has resurfaced as a public health problem in the United States; therefore it is important to understand current knowledge about TB among the general population. Using National Health Interview Survey (NHIS) data, we examined self-reported knowledge about TB among adults 18 years of age or older by selected socio-demographic characteristics. **Methods:** This study uses the 2004, 2005 and 2006 NHIS. The NHIS uses a multistage probability sample that is representative of the civilian noninstitutionalized population of the U.S. The survey is conducted annually by the U. S. Census Bureau for the National Center for Health Statistics, Centers for Disease Control and Prevention. This study is based upon 53,982 adults who provided information about their knowledge of TB and its method of transmission, by answering the questions "How much do you know about TB?" and "How is TB spread?" Respondents could choose more than one mode of TB transmission from a list of choices made available via handheld flashcard, which include breathing air around sick persons; sharing eating/drinking utensils; semen/vaginal secretions; smoking; mosquitoes/other insect bites; or other. Crude and age-adjusted percent distributions are presented to compare U.S.- and foreign-born adults' knowledge about TB transmission. **Results:** Preliminary results show that more than half of all adults claimed to know "a little" about TB (56.7% U.S.-born; 51.6% foreign-born). A larger percentage of foreign-born adults (17.9%) said they knew "a lot" about TB compared with U.S.-born adults (13.2%). Among adults who said they knew "a lot" about TB, comparable percentages of U.S.-born (91.6%) and foreign-born adults (90.7%) correctly stated that TB is transmitted through "breathing air around persons sick with TB." Foreign-born adults were more likely than U.S.-born adults to provide more than one answer for this question, suggesting more uncertainty within the foreign-born group about how TB is transmitted. **Conclusions:** In general, self-reported knowledge about TB transmission does not correspond well with the facts about modes of transmission. Furthermore, TB knowledge varies between U.S.-born and foreign-born adults, and also varies by selected socio-demographic characteristics.

Overseas Screening for Tuberculosis (TB) in U.S.-bound Immigrants and Refugees, 1999-2004

Y. Liu, M. Weinberg, L. Ortega, S. A. Maloney; Centers for Disease Control and Prevention, Atlanta, GA.

Background: In 2006, 57% of new U.S. TB cases were among foreign-born persons, and the foreign-born TB rate was 9.5 times that among U.S.-born persons. Approximately 380,000 immigrants and 70,000 refugees arrive in the United States annually, and these populations likely contribute substantially to the future foreign-born TB burden in the United States. **Methods:** Based on chest radiograph (CXR) and sputum acid-fast bacilli (AFB) examination results, overseas medical screening classifies U.S.-bound immigrants and refugees into 1) class A TB (infectious, active), 2) class B1 TB (noninfectious, active), 3) class B2 TB (inactive), and 4) no TB. CDC's Division of Global Migration and Quarantine (DGMQ) notifies state and local health departments of arriving immigrants and refugees with TB classifications, and health departments conduct post-arrival follow-up. Demographic, overseas medical screening and post-arrival evaluation data are collected in DGMQ's Information on Migrant Population (IMP) database. We calculated prevalence of class B1 and B2 TB among U.S.-bound immigrants and refugees, examined time trends for prevalence of these conditions, and analyzed results of post-arrival follow-up. **Results:** During 1999-2004, 23,017 class B1 TB conditions

and 20,002 class B2 TB conditions were identified by overseas medical screening among 2,330,891 U.S.-bound immigrants, for a prevalence of 987 and 858 conditions per 100,000 persons, respectively. Among 327,986 U.S.-bound refugees screened during the same period, 2,826 were diagnosed with class B1 TB and 9,561 with class B2 TB, for a prevalence of 862 and 2915 conditions per 100,000 persons, respectively. Prevalence of class B1 TB increased 16% in immigrants and 158% in refugees during 2002-2004 versus 1999-2001. On post-arrival evaluation in the United States, active pulmonary TB was diagnosed in 6.9% of immigrants and 8.6% of refugees with class B1 TB, and in 1.4% of immigrants and 1.7% of refugees with class B2 TB, respectively. **Conclusions:** Immigrants and refugees contribute substantially to the foreign-born TB burden in the United States; enhanced overseas screening and increased investment in global TB control are needed to address this challenge.

Investigation of a Multidrug-resistant *Mycobacterium tuberculosis* Outbreak in a Foreign-born Community _ Tennessee, 2007

R. Miramontes[1], L. Lambert[1], M. Haddad[1], L. Hausman[1], M. Zylstra[2], V. Boaz[2], S. Hawkins[2], E. Holt[3], S. Cox[2], J. Warkentin[3];

[1]CDC, Atlanta, GA, [2]CHCHD, Chattanooga, TN, [3]Tennessee Department of Health, Nashville, TN.

Background: In 2006, less than 1% of reported tuberculosis (TB) cases in the United States were multidrug-resistant (MDR); however, the proportion of MDR TB occurring in foreign-born persons increased from 26% in 1993 to 80% in 2006. In June 2007, the Tennessee Department of Health notified CDC of four MDR TB cases in a Guatemalan community. An investigation was conducted to determine the source of the outbreak and guide contact investigation activities. **Methods:** Medical records were reviewed, and interviews with patients and contacts were completed. Tuberculin skin test (TST) records for TB contacts and other persons served by the local health department were reviewed. A case was defined as culture-confirmed TB with a genotype that matched the index case, or a clinical diagnosis of TB and confirmed contact to an MDR TB case. **Results:** Five TB cases were associated with this outbreak, including one in a 22-month-old child: three were culture-confirmed MDR TB, and two were clinically diagnosed. Secondary cases were identified in the patient's home, place of worship, and workplace. The index patient had TB symptoms starting in September 2005 but did not seek care until September 2006; his TB was diagnosed in January 2007. Interviews with the index patient identified distrust of the healthcare system, lack of financial resources, and delay in diagnosis when the patient did seek care as the main reasons for the extended length of time the patient had infectious TB. Additionally, TST records indicated that among 671 Guatemalan-born persons served by the local health department in the previous 18-month period, 317 (47%) had positive TST results. Of 408 contacts of the index case, 294 (72%) had been screened, with 122 (41%) having positive TST results. **Conclusions:** This investigation highlights the factors that led to an outbreak of MDR TB in Tennessee, which included a prolonged infectious period and delayed diagnosis resulting in a large resource-intensive contact investigation. Additionally, the high baseline prevalence of TB infection in this Guatemalan community made it difficult to differentiate between recently acquired MDR TB infection and previously acquired latent TB infection. Clinicians and public health practitioners should be aware of the continued threat of MDR TB and the potential for additional outbreaks.

Rapid Multidrug-Resistance Profiling of *Mycobacterium tuberculosis*

C. Massire[1], C. Agasino Ivy[1], M. A. Tobar-Mosquera[1], N. E. Kurepina[2], D. Fallows[2], B. N. Kreiswirth[2], G. Kaplan[2], L. B. Blyn[1], S. A. Hofstadler[1], R. Sampath[1], D. J. Ecker[1];

[1]Ibis Biosciences, Inc., Carlsbad, CA, [2]Public Health Research Institute, Newark, NJ.

Background: Recent outbreaks of multidrug-resistant tuberculosis underline the urgent need for new resistance-profiling methods that would allow for timely determination of proper treatment. To rapidly analyze large numbers of samples and obtain resolving power approximating sequence-based methods, we have developed the Ibis T5000 technology, where PCR amplicons are analyzed by electrospray ionization mass spectrometry (ESI-MS) and base composition determination. **Methods**: Using PCR/ESI-MS, we developed a *Mycobacterium tuberculosis* assay that analyzes mutations known to be associated with resistance to Rifampin (RIF), Isoniazid (INH), Ethambutol, Pyrazinamide, Streptomycin, Fluoroquinolone, Amikacin, Kanamycin and Capreomycin. The assay was tested using 127 diverse clinical isolates from the Public Health Research Institute (UMDNJ) collection, including 25 multidrug resistant strains from South Africa. Mutational profiles were identified from the mass spectra analysis, confirmed by direct DNA sequencing and compared to the previously determined phenotypes. **Results:** The PCR/ESI-MS data were overall in excellent agreement with sequencing and phenotypic data, most notably with a 98% correlation for Isoniazid resistance. Twenty-one of the South African strains were confirmed as MDR (RIF^R, INH^R), with only one of these strains showing no additional resistance-conferring mutations. At least three strains were further characterized as XDR, pending a more extensive coverage of Capreomycin resistance. The remaining MDR strains displayed various mutational profiles indicating resistance to up to three other drugs. **Conclusions:** PCR/ESI-MS primer pairs can each cover up to 150 nucleotides, enabling simultaneous identification of multiple mutations in a single reaction. We found that a 24-primer pair scheme, which can be multiplexed into 8 PCR reactions, can provide the essential mutational profiling for rapid characterization of drug resistance in *M. tuberculosis* clinical isolates.

Descriptive Analysis of Tuberculosis Patients Treated in a Binational Setting

M. A. Escobedo[1], M. Sandoval[2], L. G. Escobedo[3], S. Rivas[3];

[1]Centers for Disease Control and Prevention, El Paso, TX, [2]CSTE-Centers for Disease Control and Prevention, El Paso, TX, [3]Texas Department of State Health Services, El Paso, TX.

Background: Yearly rates of reported tuberculosis (TB) in El Paso, Texas, USA, and in Juarez, Chihuahua, Mexico, are respectively twice and three times as high as the overall U.S. rates. In El Paso, 75% of yearly reported cases are among foreign-born individuals from Mexico. Nearly a third (30%) of El Paso health department patients reported pretreatment travel to Juarez, and a similar number of Juarez health department patients reported travel to El Paso. Cross-border movement of infectious TB patients leads to binational disease transmission and the development of drug resistance. Binational "Project Juntos" was established in 1991 to improve cross-border TB control in the El Paso-Juarez border area. **Methods:** We analyzed data from an ongoing database for El Paso and Juarez patients enrolled in Project Juntos during 1997-2007. We obtained frequencies for the following variables: sociodemographics, co-morbidities, sputum conversions, patterns of primary and secondary drug resistance, cure rates, and treatment relapses or failure for both drug-susceptible and multi-drug-resistant TB (MDR TB). **Results:** The largest percentage (41%) of the 703 patients enrolled in Project Juntos during 1997-2007 was Middle aged men (25 to 44 years) and 39% were born in a city other then

Juarez. Of the total patients, 97% received directly observed therapy (DOT), 12% of the isolates were resistant to one or more drugs, 9.7% were resistant to at least isoniazid, and 7.9% were resistant to at least isoniazid and rifampicin (MDR TB). The cure rate was 80% for uncomplicated patients and 54% for MDR TB patients **Conclusions:** The Juntos model has been successfully integrated and supported by U.S. and Mexican health authorities. Despite limited resources, the cure rate for Project Juntos drug-susceptible and for MDR TB patients compares favorably with specialized treatment centers in Mexico and the United States. Project Juntos has contributed significantly to cross-border TB management and control during a time when the border population continues to increase and resources are diminishing.

L5. Sexually Transmitted Diseases

Wednesday, March 19
3:00 PM – 4:30 PM
Centennial IV

High Incidence of HIV-1 infection among Pregnant Youth in Four Provinces of Cameroon

M. M. Soe[1], P. M. Tih[2], M. Bulterys[3], K. M. Sullivan[1], G. Nkuoh[2], G. Ndikintum[2], E. R. Welty[2], T. K. Welty[2];

[1]Emory University, Decatur, GA, [2]Cameroon Baptist Convention Health Board, Nso, CAMEROON, [3]CDC Global AIDS Program, Lusaka, ZAMBIA.

Background: Little intervention research on HIV transmission among sexually active young women has been conducted in sub-Saharan Africa. In Cameroon, we examined factors associated with prevalent HIV-1 infection in pregnant youth who participated in the Cameroon Baptist Convention Health Board (CBCHB) program for prevention of mother-to-child transmission (PMTCT), and indirectly measured annual HIV-1 incidence among pregnant adolescents aged 15-19 years. **Methods:** We analyzed PMTCT program HIV test and risk factor data for 13-22 year old women (n=3257) registered at 23 CBCHB-supported antenatal clinics in four provinces of Cameroon (Central, Northwest, West, Adaouma) during 2000-2002. Logistic regression analyses were performed on data collected from standardized interviews and serologic tests for HIV-1 and syphilis. A validated mathematical formula was applied to estimate age-specific annual HIV-1 incidence among pregnant adolescents after controlling for differential mortality rates among HIV-positive and HIV-negative persons. **Results:** Overall HIV-1 seroprevalence was 10.2% (332/3257). The median age was 20 years (interquartile range IQR: 18-21) and the median age at sexual debut was 16 years (IQR: 15-18). Four percent (126/2951) of participants had positive syphilis serology and 37% (1149/3110) reported ≥2 sexual partners in the past 3 years. In multivariate logistic regression, HIV-1 infection was associated with a history of ≥2 sexual partners, positive VDRL test, and being older ($p<0.001$). When differential mortality rates were taken into account, the model-based annual HIV-1 incidence among pregnant adolescents was estimated at 1.4 per 100 person-years (95% confidence interval 0.9 - 1.9 person-years). **Conclusion:** Monitoring annual HIV incidence rates estimated from cross-sectional surveys in the case of stable HIV prevalence may be less costly, innovative and beneficial to a surveillance system in a developing country. Despite national HIV control efforts focusing on youth, pregnant Cameroonian women in study provinces continue to be at high risk for HIV-1 infection. HIV prevention strategies among female adolescents should include reduction in partners, delaying sexual debut, and culturally appropriate 'safer sex' messages.

Cost-Effectiveness of Chlamydia Screening Policies Among Male Military Recruits

R. L. Nevin[1], E. E. Shuping[2], K. D. Frick[3], J. C. Gaydos[4], C. A. Gaydos[5];

[1]Army Medical Surveillance Activity, Silver Spring, MD, [2]Ireland Army Community Hospital, Ft. Knox, KY, [3]Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, [4]Department of Defense Global Emerging Infections Surveillance & Response System, Silver Spring, MD, [5]Johns Hopkins Medical Institutions, Baltimore, MD.

Background: Despite rising rates of female screening, a high economic burden remains associated with Chlamydia infection from high rates of undetected asymptomatic disease and its associated sequelae of pelvic inflammatory disease (PID) and chronic pelvic pain (CP). Males comprise the majority of U.S. military recruits and represent an ideal population in which to achieve identification and interruption of sexually transmitted infection among infected female partners through mass tandem screening linked to partner notification. **Methods:** We developed a static decision tree incorporating a calibrated Markov model to predict the differences in single-payer direct healthcare costs, cases of PID and chronic CP averted among female partners of male recruits through implementation of either selective (aged 24 and younger) or universal recruit screening policies incorporating partner notification. **Results:** A policy of selective male screening added $10.30 in direct costs per recruit above a policy of no male screening; while universal male screening added an additional $1.60. A policy of selective male screening yielded an incremental cost-effectiveness ratio (ICER) of $3.7K per case of PID averted, and $7.3K per case of CP averted, while universal screening yielded an ICER of $8.2K per additional case of PID and $16.4K per additional case of CP averted beyond selective screening. Neither policy was dominant, and results were qualitatively robust to single-variable and probabilistic sensitivity analysis. **Conclusions:** In agreement with other studies examining mass tandem male screening, we found both selective and universal male recruit screening to be cost-effective as compared to other interventions. Our results argue in favor of screening all male recruits for Chlamydia infection, and performing partner notification of those found positive.

Evaluation of Congenital Syphilis Surveillance in Brazil: High Prevalence, Low Treatment Rates, and Substantial Underreporting

A. Siqueira[1], G. H. Moraes[1], L. Paz[2], D. Hatch[3], J. Sobel[3];

[1]Field Epidemiology Training Program, Secretariat of Health Surveillance, Ministry of Health, Brasilia, BRAZIL, [2]Departament of Epidemiologic Surveillance, STD/AIDS, Secretariat of Health Surveillance, Ministry of Health, Brasilia, BRAZIL, [3]Office of Global Health, CDC, Atlanta, GA.

Background: Congenital syphilis (CS) results from hematogenous transplacental infection of a fetus by *Treponema Pallidum* at any phase of pregnancy. CS is a substantial public health problem in Brazil. **Methods:** We reviewed data of the National Reportable Health Events Information System (SINAN) for 2004, analyzed rates and evaluated the effectiveness of the system in accordance with the CDC Guidelines for Evaluation of Surveillance Systems, and compared prevalence from surveillance data to a contemporaneous point-prevalence study. **Results:** : In 2004, 4,855 cases of CS were reported, of which 3,548 (73%) were in asymptomatic newborns. The incidence was 1.6/1,000 live births. Early congenital syphilis was the diagnosis in 4,547 (94%) cases. Of 3,809 infected pregnant women who received prenatal care, 2,292 (47%) were not tested by VDRL in the first semester, 2,413 (50%) were not tested in the third trimester, and only 707 (14%) completed the three recommended prenatal VDRL tests. Adequate treatment was administered to only 167 (3.4%) of syphilis-infected

pregnant women; 3,215 (66%) of partners were not treated. Of 1,614 infected pregnant women who were VDRL tested in the first trimester, 1,494 (92%) positive and of the 4,289 who were tested at delivery, 4,103 (96%) were positive. The Positive Predictive Value (PPV) of laboratory confirmation in cases varied from 70%-96% for those tested by VDRL. Comparing surveillance system data to a contemporaneous point-prevalence study showed that CS cases reported to the national surveillance system constituted only 40% of actual cases. For reported CS cases, the median time from symptom onset to notification was 2 days, and from notification to investigation, 0 days. In surveillance reports, required fields were blank in 6%-23% of cases. **Conclusions:** Congenital syphilis prevalence in Brazil is high. Over half of infected pregnant women were not adequately treated, increasing the risk of vertical transmission, and recommended prenatal VDRL tests were applied in a minority of pregnancies. For cases in the national surveillance system, reporting is timely and investigation is prompt, but there is substantial underreporting. Improvements in screening and treatment for CS and in surveillance are urgently needed in Brazil.

Host Genetic Determinants Predispose to Complications of *Chlamydia trachomatis* Infections

S. Ouburg[1], J. M. Lyons[2], J. E. den Hartog[3], J. A. Land[4], H. S. Fennema[5], H. J. de Vries[5], J. I. Ito[2], S. Peña[1], S. A. Morré[1];

[1]VU University Medical Center, Amsterdam, THE NETHERLANDS, [2]City of Hope National Medical Center and Beckman Research Institute, Duarte, CA, [3]Academic Hospital Maastricht, Maastricht, THE NETHERLANDS, [4]Academic Medical Centre Groningen, Groningen, THE NETHERLANDS, [5]STD Outpatient Clinic, Public Health Services, Amsterdam, THE NETHERLANDS.

Background: *Chlamydia trachomatis* (CT) is the most prevalent sexually transmitted bacterium around the world. Approximately 70-80% of infected women undergo an asymptomatic course of infection, leading to increased chances of transmission to sexual partners, and increased risk of persistent infection and subsequent late complications, including PID, ectopic pregnancy, and tubal infertility. Clear differences in the clinical course of CT infections have been observed. However studies into bacterial factors, such as serovars, have not explained these differences. It is clear that other factors are involved, including genetic variation in the host immune system. The TLR family is an important group of pathogen recognition receptors involved in the innate immune system. The family members recognise pathogen associated molecular patterns, such as LPS (TLR4) and CpG DNA (TLR9). SNPs in these receptors may alter their expression or function. The *TLR4* +896A>G SNP has been shown to result in LPS hyporesponsiveness, while a *TLR9* haplotype has been associated with asthma. **Methods:** We have used a translational model to study CT infections. **Results**: In a mouse model of primary CT infections, we observed no differences in Chlamydial shedding or mean duration of infection between the *TLR4* KO mice and control mice. A similar result was obtained for *TLR9* KO mice. These results were corroborated by our study into the susceptibility to CT infections in women. We then studied the effect of the *TLR4* and *TLR9* polymorphisms on the severity of CT infections. In *TLR4* and *TLR9* KO mice we observed an increased duration of infection. These results were corroborated by the increased frequency of *TLR4* and *TLR9* SNPs in CT infected women who developed tubal pathology. We also tested *CARD15/NOD2* and *CD14* SNPs in subfertile women. Women carrying two or more SNPs in these four genes have an increased risk to develop tubal pathology following CT infection. **Conclusions:** These results show that combined carriage of SNPs in pathogen recognition receptors increased the risk of late complications. Current study into the effect of other genes encoding pathogen receptors and immune regulatory proteins are currently in progress using the translational model. The studies in mice will help identify clinically relevant genes for studies in human CT infections.

Three-fold Increase in the Rate of Syphilis Among U.S. Air Force Personnel, 2000-2006

N. M. Peduzzi, S. A. Fujimoto;

Air Force Institute for Operational Health, Brooks City-Base, TX.

Background: Anecdotally, sexually transmitted diseases, including syphilis, have been associated with the military. This perception is often due to the fact that military populations are largely composed of young males. Studies have been done investigating syphilis trends and risk factors for the Navy and the Army, but not in the Air Force. This study serves to characterize the epidemiology of syphilis among active duty Air Force (ADAF) personnel from 2000 to 2006 to identify demographic groups at high risk and hypothesize reasons for the trends. **Methods:** ADAF syphilis cases were identified from the Air Force Reportable Event Surveillance System (AFRESS) and the clinical chemistry module of the Composite Health Care System (CHCS). Confirmed syphilis cases identified in CHCS were matched to the ADAF personnel data in order to obtain demographic information, such as sex, race, date of birth and rank. Patient demographics from AFRESS and CHCS were aggregated and tabulated and prevalence rates were calculated to identify trends and potential risk factors for syphilis. **Results:** A total of 227 cases of syphilis were identified during the study time frame (average 32 per year; range 15 to 52). Syphilis rates rose dramatically during this time, from 4.3 persons per 100,000 to 15.1 persons per 100,000. The prevalence of syphilis among African-Americans increased 64% from 8.8 cases per 100,000 in 2000 to 64.1 cases per 100,000 in 2006. Syphilis cases were reported most frequently from bases in the West South Central and South Atlantic regions of the United States. Cumulatively, most syphilis cases were males (173, 75%), enlisted (204, 90%), younger than 35 (141, 62%) and African-American (113, 50%). **Conclusions:** When compared to the civilian population, syphilis trends among ADAF members are similar in terms of age, gender, race and geographic location. Targeted education may help prevent sexually transmitted diseases and should be increased in an attempt to suppress the recent growing trend. Future studies should evaluate the current etiologies of the observed trends and investigate the differences in prevalence of syphilis among ADAF racial groups.

Herpes simplex Virus (HSV) Infection in New York State Excluding New York City (NYS), 1994-2003

P. F. Smith, H. H. Chang, B. Tserenpuntsag, J. K. Schaffzin;

New York State Department of Health, Albany, NY.

Background: HSV infection occurs in 11-33 per 100,000 births in the US. Newborn infection is a potentially life-threatening disease, although antiviral therapy can be effective when given early. We assessed HSV infection rates in hospitalized NYS infants and possible HSV transmission via ritual circumcision. **Methods:** Hospital charts were requested on infants aged less than 42 days, hospitalized from 1994 through 2003 with a discharge diagnosis of herpes or other congenital infection as reported to a statewide hospital discharge database. A laboratory confirmed HSV case was defined as an infant with a positive HSV culture, serum IgM, polymerase chain reaction or Tzank smear. Clinical HSV cases were defined as infants having physician diagnosed HSV without laboratory confirmation, receiving > 6 days acyclovir and having no alternative diagnosis for illness. **Results:** 359 charts met the selection criteria, and 301 (84%) were available for review, resulting in 280 patients for analysis. Eighty- seven patients (31%) were lab-confirmed, and 43 (15%) were clinical cases. The incidence per 100,000 births was 9.7 cases (6.5 for lab-confirmed only). Of the 130 HSV cases, 73 (56%) were male, 80 (62%) white, and 5 cases (lab-confirmed) died. Apparently localized skin infections occurred in 76 (58%) cases. Sixty-five patients (50%) received antibiotic treatment, and 123 received antivirals. Of the 87 lab-confirmed

cases, 51(59%) were males, and 33 were typed: 19 were type-1 and 14 type-2 HSV. Two lab-confirmed cases occurring after possible ritual circumcision are under investigation. **Conclusions:** Neonatal herpes infections are relatively rare but can cause severe disease and death. Ritual circumcision should be considered a potential, though unusual, route of HSV transmission to newborns.

Author Index

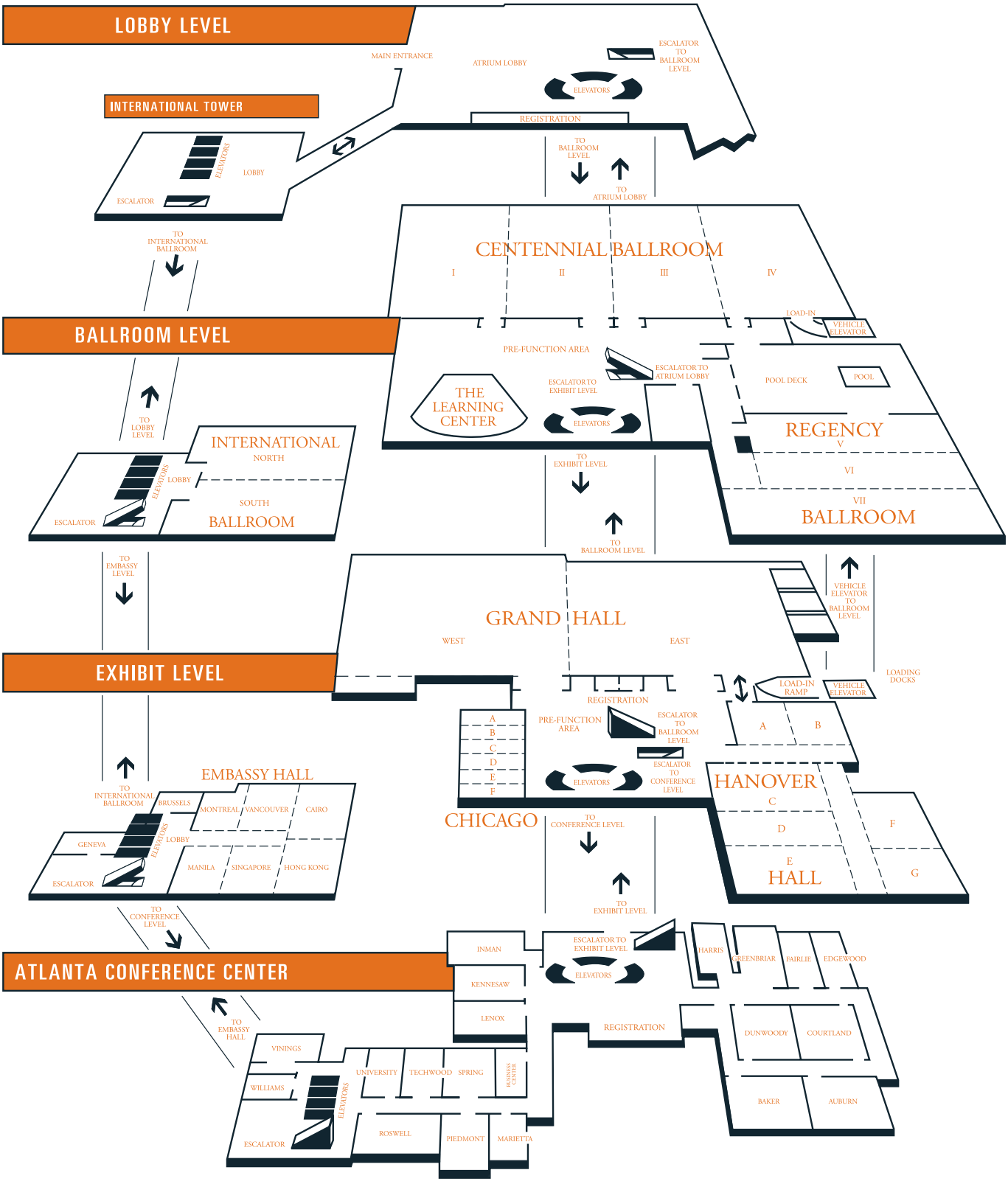
AUTHOR INDEX

Notes

Notes

Notes

Hyatt Regency Atlanta



AMERICAN
SOCIETY FOR
MICROBIOLOGY

ISBN # 978-1-55581-385-7
American Society for Microbiology
1752 N Street, NW
Washington, DC 20036

ICEID 2008
International Conference on Emerging Infectious Diseases

Final Program and Exhibit Guide Addendum

Addendum Highlights

Conference Goals and Objectives

Goal and Prerequisite Skills and Knowledge

Goal

State the goal of the educational activity.

The goal of the conference is to bring together public health professionals to encourage the exchange of scientific and public health information on global emerging infectious disease issues. The conference will provide important new information regarding emerging infectious diseases to public health professionals.

1. Exchange scientific information on emerging and re-emerging infectious disease issues in the United States and other countries.

2. Exchange scientific information on vaccine preventable diseases and their relationship to emerging and re-emerging infectious diseases in the United States and other countries.

3. Exchange scientific information on animal disease issues and their relationship to emerging and re-emerging infectious diseases in the United States and other countries

4. Exchange scientific information on chronic disease issues and their relationship to emerging and re-emerging infectious diseases in the United States and other countries

5. Exchange scientific information on opportunistic disease issues and their relationship to emerging and re-emerging infectious diseases in the United States and other countries.
6. Discuss programs and activities that have been implemented to address emerging and re-emerging infectious disease threats.

7. Identify program gaps with respect to emerging and re-emerging infectious diseases.

8. Increase awareness in the public health and scientific communities of issues related to emerging and re-emerging infectious diseases.

9. Encourage and enhance partnerships to address emerging and re-emerging infectious diseases.

Prerequisite Skills and Knowledge

List any special background, skills, or knowledge the participant must have in order to attend this educational activity.

Participants should have a medical/science background. Participants may be researchers, clinicians, epidemiologists, laboratorians, veterinarians, nurses, or other health professionals.

Exhibits

Prodesse has moved from booth #615 to #405

Career Epidemiology Field Officer Program
Booth #415
Office of Science and Public Health Practice
Coord. of for Terrorism Preparedness & Emergency Response
Centers for Disease Control and Prevention
1600 Clifton Rd, MS: D-29
Atlanta, GA 30333

Quest Diagnostics Booth #514
1777 Montreal Circle
Tucker, GA 30084
www.questdiagnostics.com

Saunders/Mosby/Elsevier Booth #615
4605 Berkeley Walk PT.
Duluth, GA 30096

Veterinary Laboratories Agency Booth #714
VLA, Weybridge New Haw, Addlestone
Surrey, England KT153NB
United Kingdom
www.vla.gov.uk

Additional Affiliated Events

The National Healthcare Safety Network (NHSN)
Monday, March 17
6:00 pm – 7:30 pm
Hanover E

National Association of State Public Health Veterinarians
Monday, March 17
6:00 pm – 9:00 pm
Hanover F & G

CDC/DOD Influenza Working Group
Tuesday, March 18
6:00 pm – 9:00 pm
Hanover E

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 educational activity for a maximum of 18 AMA PRA Category 1 Credits. Physicians should only claim credit commensurate with the extent of their participation in the activity.

This activity for 18 contact hours is provided by the Centers for Disease Control and Prevention, which is accredited as a provider of continuing education in nursing by the American Nurses Credentialing Center's Commission on Accreditations.

The CDC has been approved as an Authorized Provider by the International Association for Continuing Education and Training (IACET), 8405 Greensboro Drive, Suite 800, McLean, VA 22102. The CDC is authorized by IACET to offer 1.8 CEU's for this program.

This program has been submitted (but not yet approved) for 22 hours of continuing education credit in jurisdictions which recognize AAVSB RACE approval; however, participants should be aware that some boards have limitations on the number of hours accepted in certain categories and/or restrictions on certain methods of delivery of continuing education. Call Valerie Curry at 404-498-6393 for further information.

International Conference on Emerging Infectious Diseases (ICEID)
March 16-19, 2008

Course Evaluation

Continuing education credit for this conference is available through the *CDC Training and Continuing Education Online* system only. Please follow the instructions provided below. You must complete the online evaluation by **April 21, 2008** to receive your continuing education credits or your certificate of completion.

To complete online evaluation:

- Go to the *CDC Training and Continuing Education Online* at http://www.cdc.gov/tceonline/. If you have not registered as a participant, click on **New Participant** to create a user ID and password; otherwise click on **Participant Login** and login.
- Once logged on to the *CDC/ATSDR Training and Continuing Education Online* website, you will be on the **Participant Services** page. Click on **Search and Register**. Use either search method to locate the conference and click on **View**.
- Click on the course. The course information page will come up. Scroll down to **Register Here**. Click on the type of CE credit that you would like to receive and then **Submit**. Three demographic questions will come up. Complete the questions and then **Submit**.
- A message will come up thanking you for registering for the conference. You will then be prompted to select the sessions that you would like to attend.
- After attending your selected conference sessions return to the *CDC Training and Continuing Education Online.* Click on **Participant Login** and login. Click on **Evaluations and Tests**. Click on **Conferences**. The conference will be listed with the sessions you selected. You may **Add/Edit Sessions** until you have completed the evaluation for a particular session. After completing all of the session evaluations you will be prompted to complete the overall conference evaluation. A record of your conference completion will be located in the **Transcript and Certificate** section of your record.

If you have any questions or problems contact:

CDC/ATSDR Training and Continuing Education Online
1-800-41TRAIN or 404-639-1292
Email at ce@cdc.gov

Attention Veterinarians:
If you desire AASVB/RACE credit, select CME for non-physicians to take the online test and evaluation. Print out the certificate and fax to:
ATTN: Dr. Sharon Hall
(fax) 404-498-6045
(voicemail) 404-498-6537
You will be faxed back a correct AAVSB/RACE certificate.

Changes to the Program
**Please note changes are italicized*

Monday, March 17, 2008

A1 Concurrent Plenary Sessions
8:30 AM – 10:10 AM Centennial I

One Medicine/One Health
8:30 AM – 9:15 AM

Moderator:
NINA MARANO, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:
One World, One Health, One Medicine
THOMAS MONATH, Pandemic and Bio Defense Fund, Kleiner Perkins Caufield & Byers, Menlo Park, CA
ROGER MAHR, American Veterinary Medical Association, St. Charles, IL

A3 Concurrent Plenary Sessions
8:30 AM – 10:10 AM Centennial III

Global Infectious Disease Disparities & Poverty
8:30 – 9:15 AM

Moderator:
HAZEL DEAN, Centers for Disease Control and Prevention, Atlanta, GA

Speaker:
Global Infectious Diseases and Poverty
DAVID SATCHER, Center of Excellence on Health Disparities, Atlanta, GA

B3 Concurrent Panel Sessions
Regency VI

HIV
10:30 AM – 12:00 PM

Conveners:
ROBERT CHEN, Centers for Disease Control and Prevention, Atlanta, GA
MARY LOU LINDEGREN, Centers for Disease Control and Prevention, Atlanta, GA

Moderators:
DAWN SMITH, Centers for Disease Control and Prevention, Atlanta, GA

THOMAS SPIRA, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:
Emerging Biomedical Modalities for the Prevention of HIV Transmission
PETER KILMARX, Centers for Disease Control and Prevention, Atlanta, GA
Strategies for National HIV Incidence Surveillance
THOMAS REHLE, Human Sciences Research Council, Cape Town, South Africa
Global Monitoring of HIV Resistance
DIANE BENNETT, World Health Organization, Geneva, Switzerland

B4 Concurrent Panel Sessions
Regency VII

Globally Mobile Populations & EIDs
10:30 AM – 12:00 PM

Conveners:
LIN CHEN, Harvard University, Boston, MA
NINA MARANO, Centers for Disease Control and Prevention, Atlanta, GA

Moderators:
LIN CHEN, Harvard University, Boston, MA
NINA MARANO, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:
Vaccine-Preventable Diseases and Mobile Populations
MARTY CETRON, Centers for Disease Control and Prevention, Atlanta, GA
Health Screening of Refugees to Detect Emerging Diseases
PATRICIA WALKER, University of Minnesota, St. Paul, MN
Travelers Visiting Friends and Relatives
ELIZABETH BARNETT, Boston Medical Center, Boston, MA

Tuesday, March 18, 2008

G3 Concurrent Panel Sessions
Centennial II

Antimicrobial Resistance 2008: Use and Consequences
1:15 PM – 2:45 PM

Conveners:
PATRICK MCDERMOTT, US Food and Drug Administration, Laurel, MD
FRED TENOVER, Centers for Disease Control and Prevention, Atlanta, GA

Moderators:
FRED TENOVER, Centers for Disease Control and Prevention, Atlanta, GA

Speakers:
Antimicrobial Resistance in Foodborne Bacteria: What NARMS is Telling Us
DAVID WHITE, US Food and Drug Administration, Rockville, MD
The Impact of Antimicrobial Resistance on Treating Sexually Transmitted Diseases
KIMBERLY WORKOWSKI, Centers for Disease Control and Prevention, Atlanta, GA
Changes in Antimicrobial Agent Prescribing Patterns in the Outpatient Setting
LINDA MCCAIG, Centers for Disease Control and Prevention, Hyattsville, MD

Wednesday, March 19, 2008

I1 Concurrent Plenary Sessions
Centennial I
Role of Political/Social Disruption
9:25 AM – 10:10 AM

Moderator:
J. TODD WEBER, Centers for Disease Control and Prevention
Speaker:
The Impact of War and Terrorism on Emerging Infectious Diseases

BARRY LEVY, Tufts University School of Medicine, Boston, MA

Emerging Infections & Animals
Moderator:
THOMAS GOMEZ, US Department of Agriculture, Atlanta, GA

Speaker:
Emerging Virus Infections: a Continuing Threat from the Animal World
ALBERT OSTERHAUS, Erasmus MC, Rotterdam, The Netherlands

I3 Concurrent Plenary Sessions
Centennial III

Outbreaks of Emerging Infections
9:25 AM – 10:10 AM

Moderator:
NANCY COX, Centers for Disease Control and Prevention, Atlanta, GA

Speaker:
Profile of the Emerging Infectious Disease in India During the Last Five Years
NIRMAL GANGULY, Indian Council of Medical Research, New Delhi, India

Moderators for Slide Sessions

Monday, March 17, 2008
1:15 PM – 2:45 PM

1. Foodborne and Waterborne Diseases I
   Moderator: HENRIK WEGENER, National Food Institute Denmark, Copenhagen, Denmark
2. Influenza I
   Moderator: BRIAN MAHY, Centers for Disease Control and Prevention, Atlanta, GA
3. Surveillance: International
   Moderator: SONJA OLSEN, Centers for Disease Control and Prevention, Atlanta, GA
4. Zoonotic and Animal Diseases I
   Moderator: TRACEE TREADWELL, Centers for Disease Control and Prevention, Atlanta, GA
5. Methicillin Resistant *Staphylococcal* Infections
   Moderator: RACHEL GORWITZ, Centers for Disease Control and Prevention, Atlanta, GA
6. Vectorborne Diseases
   Moderator: RON ROSENBERG, Centers for Disease Control and Prevention, Fort Collins, CO

Moderators for Slide Sessions con't

Monday, March 17, 2008
3:00 PM – 4:30 PM

1. Foodborne and Waterborne Diseases II
   Moderator: ROBERT TAUXE, Centers for Disease Control and Prevention, Atlanta, GA
2. Influenza II
   Moderator: DAVID BELL, Centers for Disease Control and Prevention, Atlanta, GA
3. Surveillance: Domestic
   Moderator: KEVIN GRIFFITH, Centers for Disease Control and Prevention, Atlanta, GA
4. Zoonotic and Animal Diseases II
   Moderator: THERESA SMITH, Centers for Disease Control and Prevention, Atlanta, GA
5. Nosocomial Infections
   Moderator: TBA
6. Late Breakers I
   Moderator: CAROLYN BLACK, Centers for Disease Control and Prevention, Atlanta, GA

Tuesday, March 18, 2008
3:00 PM – 4:30 PM

1. Respiratory Diseases
   Moderator: CHARLES CALISHER, Colorado State University, Fort Collins, CO
2. Health Communications
   Moderator: PETER DROTMAN, Centers for Disease Control and Prevention, Atlanta, GA
3. Blood, Organ, and Tissue Safety
   Moderator: MARY BRANDT, Centers for Disease Control and Prevention, Atlanta, GA
4. Tropical Diseases
   Moderator: J.GLENN MORRIS, University of Florida, Gainseville, FL
5. Late Breakers II
   Moderator: TBA

Wednesday, March 19, 2008
3:00 PM – 4:30 PM

1. New Rapid Diagnostics
   Moderator: J. MICHAEL MILLER, PhD, Centers for Disease Control and Prevention, Atlanta, GA
2. Mobile Populations
   Moderator: NINA MARANO, DVM, Centers for Disease Control and Prevention, Atlanta, GA
3. Vaccine Preventable Diseases
   Moderator: MARTIN MELTZER, Centers for Disease Control and Prevention, Atlanta, GA
4. Tuberculosis
   Moderator: TBA
5. Sexually Transmitted Diseases
   Moderator: MARY KAMB, Centers for Disease Control and Prevention, Atlanta, GA

D6 Slide Session - Late Breakers I

Monday, March 17, 2008
3:00 PM – 4:15 PM
Regency VII

3:00 – 3:15 PM
Multistate Investigation of *Escherichia coli* O157:H7 Infections Associated with Frozen Pizza

J. MacFarquhar[1], J. Dunn[1], D. Swerdlow[2], K. Jackson[2], W. Schaffner[3], S. Stroika[2], T. Jones[1]; [1]Tennessee Department of Health, Nashville, TN, [2]Centers for Disease Control and Prevention, Atlanta, GA, [3]Vanderbilt University Medical Center, Nashville, TN

Background: *Escherichia coli* O157:H7 (O157) is an important cause of hemorrhagic colitis and hemolytic uremic syndrome (HUS). As recognition of multistate outbreaks has increased, so has the identification of unique vehicles as the source of infection. We investigated a multistate cluster of O157 cases to identify the vehicle and prevent additional cases. **Methods:** We defined a case as culture-confirmed O157 infection, demonstrating the outbreak pulsed-field gel electrophoresis (PFGE) pattern with a two enzyme match, occurring during July 20-October 19, 2007. In Tennessee (TN), we performed a 3:1 case-control study, frequency matched on age and geography, using sequential digit-dialing. Fisher's exact 95% confidence intervals (CI) and odds ratios (OR) were computed by using SAS®. **Results:** In TN, eight cases of O157 were identified (median age: 14.5 years; range: 2-65 years). Illness onset ranged from August 16 to September 19. Five patients were hospitalized and three experienced HUS. Six (75%) case-patients reported having eaten Brand X or Y frozen pizza (manufactured at the same plant), compared with one (4.0%) control subject (OR: 144; CI, 5.8-22,000). Of these, five (63%) had eaten pepperoni-containing pizza (OR: undefined) ≤7 days before experiencing illness. In total, 26 PFGE-matched O157 infections were identified in 13 states; onset dates ranged from July 20 to October 19, and median patient age was 8 years (range: 1-65 years). Ten case-patients were hospitalized; four experienced HUS. Nine non-TN case-patients were interviewed; three reported having consumed pepperoni-containing Brand X or Y pizza. **Conclusions:** This outbreak likely resulted from consumption of pepperoni-containing Brand X and Y pizza. The investigation is ongoing. Rapid epidemiologic investigation and prompt multiagency and industry collaboration resulted in voluntary recall of the implicated products, possibly preventing additional cases.

3:15 – 3:30 PM
Immunization Screening Among Newly Arrived Refugees Versus Asylum Recipients _ District of Columbia, 2003-2007

S. J. Chai[1], S. T. Cookson[1], T. Vu[2]; [1]Centers for Disease Control and Prevention, Atlanta, GA, [2]District of Columbia Department of Health, Washington, DC

Background: Refugees are screened for immunizations soon after U.S. arrival, which decreases their risk for vaccine-preventable diseases. Asylum recipients, or asylees, who are granted asylum while residing in the United States are infrequently screened in many jurisdictions; consequently, their vaccination needs are largely unknown. Uniquely, the District of Columbia (DC) Department of Health (DOH) screens a substantial number of asylees through local agency collaborations. We compared need for immunization and time elapsed before vaccine administration among DC refugees versus asylees. **Methods:** We used data from refugee and asylee medical screening examinations administered by the DC DOH during September 2003-August 2007. Recommendations from the U.S. Advisory Committee on Immunization Practices were used to determine the need for diphtheria-tetanus-acellular-pertussis (DTaP), measles-mumps-rubella (MMR), and polio vaccinations among children and adolescents and diphtheria-tetanus (Td) and MMR vaccinations among adults. U.S. entry and DOH screening dates were used to calculate time elapsed before vaccination administration. **Results:** Of 781 persons who completed the DOH screening, 151 (19%) were refugees and 630 (81%) were asylees. Refugee and asylee children had similar need for DTaP (49% versus 52%), MMR (62% versus 66%), and polio (44% versus 44%) vaccinations. Refugee and asylee adults had similar need for MMR (64% versus 67%) and Td (61% versus 64%) vaccinations. However, asylees were screened much later after U.S. entry than refugees (54 weeks versus 1 week; $P<0.001$), even after adjusting for demographic characteristics. **Conclusions:** Asylees in DC are similar to refugees in their need for immunizations but receive screening much later. Because delays in immunizations place asylees and the public at risk, asylees in DC and possibly in jurisdictions where asylee screening is infrequent should be assessed for immunization needs with the same urgency as refugees.
Note: The findings and conclusions in this presentation have not been formally disseminated by the Centers for Disease Control and Prevention and should not be construed to represent any agency determination or policy.

3:30 – 3:45 PM

Risk Factors Associated with Methicillin-Resistant *Staphylococcus aureus* Skin and Soft Tissue Infections and Colonization in a Rural Community -- Northern Plains, United States, 2005-2006

C. Dubray[1], A. L. Cohen[2], D. A. Mark[3], R. G. Byron[3], P. T. Troel[4], E. G. Olson[4], L. J. Layne[5], S. K. McAllister[2], G. Fosheim[2], R. J. Gorwitz[2], J. T. Redd[5], J. E. Cheek[5]; [1]Centers for Disease Control and Prevention, Albuquerque, NM, [2]Centers for Disease Control and Prevention, Atlanta, GA, [3]Indian Health Service, Crow Agency, MT, [4]Johns Hopkins School of Public Health, Baltimore, MD, [5]Indian Health Service, Albuquerque, NM.

Background: Our recent hospital-based investigation found that methicillin-resistant *Staphylococcus aureus* (MRSA) has emerged as a community pathogen among a rural Northern Plains population. The annual incidence of MRSA skin and soft tissue infection (SSTI) in that community was 1%. We describe risk factors for confirmed MRSA infection and evaluate prevalence of and risk factors for MRSA colonization among patients with MRSA infections and their household members (HMs). **Methods:** Patients had ≥1 culture-confirmed MRSA SSTIs during April 1, 2005-March 31, 2006. We conducted an in person community-based patient household (HH) survey during December, 2006-June, 2007. Of the 137 patients with MRSA SSTIs included in our initial retrospective, hospital-based cohort study, we interviewed 48 (35%) randomly selected patients in 42 HHs and 116 (59%) of their 195 HMs. We collected 135 nasal swabs from 41 (85%) patients and from 94 (48%) HMs. Using univariate analysis, we calculated risk factor odds ratios (OR) and 95% confidence intervals (CI) for MRSA SSTIs and for MRSA colonization. We calculated the prevalence of *Staphylococcus aureus* (SA) and MRSA colonization among patients and HMs swabbed. **Results:** Patients with confirmed MRSA SSTIs were more likely than HMs to have diabetes (OR=4.1, 95% CI=1.3-12.5), to have a dermatologic condition (OR=2.4, 95% CI=1.2-4.6), to have snorted any substance in the previous 2 years (OR=16.7, 95% CI=1.8-156.9), or to have used sauna-like facilities (OR=2.8, 95% CI=1.3-6.1). The overall prevalence of SA and MRSA colonization was 54.1% (73/135) and 9.6% (13/135), respectively. MRSA colonization was detected among 14.6% (6/41) of patients and 7.4% (7/94) of HMs (p = 0.195). Nasal MRSA colonization in ≥1 HM or patients occurred among 23.8% (10/42) of HHs. Patients or HMs colonized with MRSA were more likely than those not colonized with MRSA to take <5 showers per week (OR=4.0, 95% CI=1.2-13.1) or to share soap with someone with a skin infection (OR=9.7, 95% CI=1.2-82.1). **Conclusions:** Prevalence of MRSA nasal colonization was high among patients with recent MRSA infection and their HMs. Individual characteristics and modifiable behaviors related to medical history, hygiene, and social activities might be contributing to transmission and might provide opportunities for prevention.

3:45 – 4:00 PM

Incidence and Epidemiology of Influenza and Influenza-like Illness in a Nicaraguan Pediatric Cohort

A. Gordon[1], G. Kuan[2], O. Ortega[3], S. Saborio[4], A. Balmaseda[4], E. Harris[1]; [1]University of California, Berkeley, Berkeley, CA, [2]Socrates Flores Vivas Health Center, Managua, NICARAGUA, [3]Sustainable Sciences Institute, Managua, NICARAGUA, [4]National Center for Diagnosis and Reference, Managua, NICARAGUA.

Background: The epidemiology and burden of influenza in the tropics is poorly understood, yet this knowledge is critical not only from a public health standpoint but also for pandemic models and planning worldwide.
Methods: To characterize the burden and epidemiology of influenza and influenza-like illness (ILI) in a tropical developing country, we are conducting a community-based cohort study examining the incidence of laboratory-confirmed influenza and ILI in ~3,700 children 2-11 years in Managua, Nicaragua. Clinical information on ILI was collected since April of 2005, and in June of 2007 we began collecting nasal and throat swab specimens from a random 25% of all participants that presented with fever or a history of fever, and sore throat or cough. RT-PCR for influenza A and B was performed, followed by PCR typing and viral isolation of RT-PCR-positive swab samples. Weekly influenza incidence in the cohort was estimated by applying the percentage of samples positive for influenza in the calendar week to the total number of children that presented with the testing criteria, divided by the total person-years for that week. Risk factor analysis for ILI was performed using general estimating equations with a Poisson model
Results: Seasonal variation of influenza activity was observed, with a peak occurring in June/July of 2007. The estimated incidence of influenza in the cohort from June 2007 to January 2007 was 23.4 cases per 100 person-years. Seasonal peaks of ILI were observed, with peaks in June 2005 and July and November of 2006. In multivariate models, age was the most significant risk factor for ILI, with the risk decreasing sharply with each 1-year increase in age. In household risk factor models, asthma and person density greater than 5 people per room were both significant risk factors when adjusted for age and sex, with incidence rate ratios of 1.51 (95% CI 1.32, 1.75) and 1.18 (1.04, 1.34), respectively. Mother literacy and presence of a dirt floor were protective for ILI, with IRRs of 0.79 (0.64, 0.98) and 0.88 (0.78, 1.00), respectively.
Conclusions: Our results suggest that the Nicaragua has a high influenza burden and has at least one peak of influenza activity in June/July. This is the first large-scale prospective study to provide data on the incidence and risk factors for influenza in Central America.

4:00 – 4:15 PM

Risk of avian influenza virus exposure at the human-wildlife interface

J. L. Siembieda; University of California, Davis, CA

INTRODUCTION: In North America and other parts of the developed world, people are in direct or indirect contact with wild animals during a variety of daily and seasonal activities. Contacts happen through human activity and the type (duration and route) of exposure and its amount (infectious virus titer) varies depending on the activity. This study assesses the risk of human exposure to influenza A viruses at common points of contact between humans and wild animals. The general public primarily has indirect contact with the feces and secretions of birds through outdoor activities and backyard bird feeders. During hunting and bird cleaning activities, waterfowl hunters have direct contact with the waterfowl they harvest over a short period of time. Wildlife biologists frequently trap and sample free-ranging wild birds and marine mammals and occasionally perform field necropsies. Workers at wildlife rehabilitation centers handle sick and injured wild animals daily and routinely perform necropsies. We apply a unique approach to understand influenza A virus infection in wild birds and marine mammals so that we can inform public health professionals on the risks associated with specific casual, recreational and occupational activities. We determined the prevalence of influenza A in wild birds and marine mammals in California from 2005-2007 to evaluate the risk of human exposure. **METHODS:** Birds and marine mammals were categorized based on sampling location into a human exposure risk group: 1) casual contact by the general public during outdoor activities, 2) short and intense contact by hunters who handle and dress waterfowl, and 3) prolonged and repeated contact by occupational workers (wildlife biologists, rehabilitation workers, and veterinarians). **RESULTS:** The prevalence of influenza A viruses was extremely low < 1 % in all three groups and was highest among waterfowl. **CONCLUSIONS:** We found the risk was negligible to the general public but with hunters and occupational workers the risk increased slightly. Infection control and appropriate use of personal protective equipment could prevent influenza virus introductions at critical human-wildlife interfaces. We recommend continued surveillance of wild birds and marine mammals where human-wildlife interaction is likely as well as expanded human surveillance.

H5 Slide Session - Late Breakers II
Tuesday, March 18, 2008
3:00 PM – 4:30 PM
Regency VII

3:00 -3:15 PM

Modified Vaccinia Virus Ankara Vaccine Protects Nonhuman Primates from Aerosolized Monkeypox

V. Livingston, N. Garza, A. Nalca; U.S. Army Medical Research Institute of Infectious Diseases (USAMRIID), Fort Detrick, MD

Background: Monkeypox virus, when aerosolized, causes severe respiratory disease in cynomolgus monkeys (*Macaca fascicularis*). The aerosolized monkeypox primate model is a valuable and informative model to test medical countermeasures against smallpox because the disease progression is similar to smallpox in humans. Dryvax, the original smallpox vaccine has many potential side effects including postvaccinial encephalitis, encephalomyelitis, and serious skin infections, including progressive vaccinia (vaccinia necrosum). The potential for the smallpox virus to be used as an agent of bioterrorism has accelerated the effort to develop new vaccines with fever side effects such as Modified vaccinia virus Ankara (MVA), a highly attenuated, replication-deficient, strain of vaccinia virus. Developed in the 1960s, MVA was administered as a smallpox vaccine to more than 100,000 people in Germany but has never been evaluated in an area where smallpox was endemic. Its protective efficacy in humans remains unknown. **Methods:** In this study, we tested the efficacy of MVA vaccine to protect cynomolgus monkeys against aerosolized monkeypox virus. Four groups of six monkeys were vaccinated with PBS, Dryvax, single dose of MVA, or two doses of MVA (28 days apart). An aerosol challenge of 10 LD_{50} was given 28 days after vaccination. **Results:** Clinical signs of monkeypox disease and classical pock lesions were present in all animals in the PBS group with two succumbing to the disease by day 11 and two becoming severely ill. None of the animals in the Dryvax group showed any signs of the disease. The single-dose MVA group included two animals that showed a mild outbreak of pock lesions and no deaths. All of the animals that were vaccinated with the MVA twice were fully protected from clinical disease.
Conclusion: This study shows that MVA is a very effective vaccine against aerosolized monkeypox virus.

3:15 – 3:30 PM

Adenovirus Serotype 14 Infection at a Military Training Installation in South Texas, 2007

J. R. Su[1], V. P. Fonseca[2], J. E. Tate[3], M. Widdowson[3], M. L. Bunning[4]; [1]CDC EIS Officer at Texas Department of State Health Services, Austin, TX, [2]Texas Department of State Health Services, Austin, TX, [3]Centers for Disease Control and Prevention, Atlanta, GA, [4]United States Air Force, Kelly USA, TX

Background: Acute respiratory disease (ARD) (defined as fever ≥100.5°F plus one or more respiratory symptoms) associated with adenovirus serotypes 4 and 7 is common among basic military trainees (BMTs). ARD delays training and deployment of personnel, despite usually being self-limiting. In June 2007, we investigated a cluster of unusually severe ARD cases (including 27 hospitalizations and one death associated with adenovirus serotype 14 (Ad14)) at a military training installation in Texas. **Methods:** BMTs are organized into single-sex groups of 45-60 persons ("flights"). We reviewed personnel and laboratory databases for BMTs on the installation during January 1-June 25, including BMTs segregated to an isolation flight to reduce spread and morbidity of ARD. Testing for respiratory pathogens included polymerase chain reaction and viral culture of throat swabs and nasal washes. **Results:** We identified 689 cases of ARD among 11,234 BMTs during January-June 2007. Among the 193 male and 67 female flights on the installation, 61% (298/488) of ARD cases tested positive for adenovirus: 52% (150/298) of adenoviruses typed as Ad14. Median attack rate of adenoviral ARD was 2% (range: 0%-45%) among male flights and 0% (range: 0%-6%) among female flights: 47% (91/193) of male flights compared with 28% (19/67) of female flights had attack rates exceeding 2% (relative risk [RR] =1.66, 95% confidence interval [95%CI] =1.10-2.50). Twenty-seven male flights exceeded the highest female flight attack rate of 6%. Of BMTs in the isolation flight, 61% (150/244) had laboratory data available: 71% (94/133) of male BMTs and 12% (2/17) of female BMTs had adenovirus (RR=6.01, 95%CI=1.63-22.19), with 42 male BMTs and one female BMT having Ad14. **Conclusions:** Male BMTs were at elevated risk for ARD associated with Ad14, a previously rarely reported adenovirus. Identifying risk factors (e.g., biologic or behavioral factors) that might predispose male BMTs to infection with Ad14 might allow targeted interventions to reduce ARD.

3:30 – 3:45 PM

Clinical Features of Inflammatory Neuropathy in an Outbreak among Swine Slaughter Plant Workers - Minnesota, 2007

A. DeVries[1], S. Holzbauer[2], J. Sejvar[2], D. Lachance[3], C. Lees[1], R. Danila[1], R. Lynfield[1]; [1]Minnesota Department of Health, St. Paul, MN, [2]Centers for Disease Control and Prevention, Atlanta, GA, [3]Mayo Clinic, Rochester, MN

Background: Many inflammatory neuropathies, including Acute (AIDP) and Chronic Inflammatory Demyelinating Polyneuropathy (CIDP), are associated with chronic diseases, immunizations, and antecedent infections. MDH was notified of inflammatory neuropathy cases in workers at swine slaughter Plant A. An investigation was initiated to characterize the illness and confirm an outbreak. **Methods:** Case finding included worker interviews, physician health alerts, and press releases. Clinicians near swine slaughter plants were personally contacted, ICD-9 code searches performed, and plant occupational records reviewed. Standardized questionnaires and medical records were obtained from persons with symptoms of inflammatory neuropathy. A case was defined as a person participating in swine slaughtering developing inflammatory neuropathy. **Results:** Twelve persons, all Plant A workers, were identified with onset from 11/06-11/07. Median age was 31 years (range, 21-51), 6 were female. All had been previously healthy. Symptoms ranged from acute paralysis to gradually progressive symmetric weakness over 8-213 days. Eleven had evidence of axonal and/or demyelinating peripheral neuropathy by electrodiagnostic testing (EDT), 7/7 had elevated cerebrospinal fluid (CSF) protein (median 125 mg/dL, range 75-231), and 5 had inflammation on magnetic resonance imaging (MRI): 4 in peripheral nerve roots, and 1 in multi-level central gray matter of the spinal cord and third cranial nerve. We classified cases as follows: confirmed (progressive symmetric weakness, decreased deep tendon reflexes (DTR), and axonal and/or demyelinating peripheral neuropathy by EDT; probable (weakness or decreased DTR, and nerve or spinal cord inflammation on MRI or elevated CSF protein); and possible (weakness or decreased DTR only). To date 8 confirmed, 2 probable, and 2 possible cases have been identified. All cases either worked at or had exposure to swine head processing. **Discussion:** This investigation describes a unique outbreak of an illness which has been termed Progressive Inflammatory Neuropathy (PIN). Features of this illness include symptoms of inflammatory neuropathy, variable temporal progression, and a distinctive epidemiology. Additional case finding and an in-depth investigation to identify an etiology are ongoing.

3:45 – 4:00 PM

Isolation of methicillin-resistant *Staphylococcus aureus* (MRSA) from swine in the midwestern United States

T. C. Smith, M. J. Male, A. L. Harper, E. Moritz-Korolev, J. S. Kroeger, D. J. Diekema, L. A. Herwaldt; University of Iowa, Iowa City, IA

Background: Over the past decade, the epidemiology of methicillin-resistant *Staphylococcus aureus* (MRSA) has undergone significant changes. Once primarily a hospital-based pathogen, MRSA is now found increasingly in the community, and this bacterium has caused serious infections in individuals with no history of hospitalization. Additionally, MRSA infections have been documented in horses, dogs, cats, and cattle, among other animals. Recent research has also shown that swine and swine farmers are colonized with MRSA at high levels in the Netherlands and Canada. However, to date no studies had investigated carriage of MRSA in swine and swine farmers in the United States. **Methods:** We collected samples from swine on 7 different farms in Iowa and Illinois. These farms are part of a single closed production system consisting of approximately 60,000 live animals at any given time. Nasal swabs were taken from 209 swine representing 7 different age groups. Isolates were typed by pulsed field gel electrophoresis (PFGE) using *SmaI* and *EagI* restriction enzymes. **Results:** Overall MRSA prevalence was found to be 70% (147/209). Prevalence varied by age group and farm, ranging from 36% (11/30) in adult swine, to 100% (60/60) of all animals aged 9 and 12 weeks. Isolates were not typeable by PFGE using the *SmaI* enzyme, but were found to be clonal using *EagI*, and were not related to common human types isolated in Iowa (USA100, USA300, and USA400). **Conclusions:**.These results show that colonization of swine by MRSA is very common on the farm system we examined in the midwestern U.S., adding to the concern about domestic animal species as a reservoir of this bacterium. Additional studies are ongoing to examine carriage rates on additional farms, to further investigate the molecular epidemiology of these isolates, and to determine carriage rates of MRSA among workers in contact with these colonized pigs.

4:00 – 4:15 PM

Outbreak of Escherichia coli O157:H7 Infection Associated with Various Beef Products in Canada and US

R. McCormick1, D. MacDonald1, C. Nadon2, C. Misfeldt3, M. Leblanc4, C. Gaulin4, H. Akwar5, M. Anderson6, Outbreak Investigation Team, A. Ellis1; 1Public Health Agency of Canada, Guelph, ON, CANADA, 2Public Health Agency of Canada, Winnipeg, BC, CANADA, 3Public Health Agency of Canada, Winnipeg, MB, CANADA, 4Ministère de la santé et des services sociaux du Québec, Quebec City, QC, CANADA, 5New Brunswick Department of Health and Wellness, Fredericton, NB, CANADA, 6BC Centre for Disease Control, Vancouver, BC, CANADA

Background: : The Public Health Agency of Canada identified an interprovincial outbreak of *Escherichia coli* O157:H7 infection in September 2007 following identification of a rare Pulsed Field Gel Electrophoresis (PFGE) pattern associated with an ongoing outbreak and recall of frozen hamburgers in the US. **Methods:** The case definition included all cases in Canada on or after 30 June 2007 with confirmed *E.coli* O157 infection with PFGE patterns matching the outbreak strains in the US. Detailed information, particularly related to beef consumption was collected for all cases. Traceback investigation of the beef products was conducted to determine the source of the outbreak and implement prevention and control measures. **Results:** A total of 47 laboratory confirmed *E.coli* O157 cases with one of 11 implicated PFGE patterns were identified in Canada with symptom onsets between 30 June and 30 September 2007. Cases were identified in 6 provinces. *E.coli* O157 with the predominant PFGE pattern was identified in meat isolates from producer A, a suspect source for the US outbreak. Between 27 October and 15 November 2007, the Canadian Food Inspection Agency (CFIA) issued 2 Health Hazard Alerts of meat products associated with production dates related to positive meat isolates. While frozen beef patties were the vehicle for the US outbreak, cases in Canada reported consumption of fresh and frozen ground beef as well as whole cuts of beef. **Conclusions:** This international outbreak was associated with the consumption of various beef products and highlighted the integration of the meat supply between Canada and US. The variety of products consumed added to the complexity of source identification and highlighted the importance of seeking timely detailed food histories. USDA traceback allowed for identification of meat producer A (suspect source) in Canada. This outbreak was also unique due the number of PFGE patterns involved. The PulseNet Canada discussion board allowed identification of related PFGE patterns across Canada and a rapid response to this international outbreak.

4:15 – 4:30 PM

Rare Usage of Oseltamivir in Norway Prior to Emergence of Oseltamivir Resistant Influenza A/H1N1 Virus in the 2007-2008 Season

P. Aavitsland, S. H. Hauge, K. Borgen; Norwegian Institute of Public Health, Oslo, NORWAY

Background: On January 25, 2008, we notified WHO under the International Health Regulations of an unusually high proportion (12 of 16) of oseltamivir resistant influenza A/H1N1 strains among strains collected as part of the seasonal routine surveillance. Sequence analysis of the viral neuraminidase gene showed that the strains carried a mutation resulting in a substitution of histidine by tyrosine at residue 274 (H274Y) of the neuraminidase. Did these strains emerge and persist as a consequence of widespread oseltamivir use in Norway? **Methods:** The Norwegian Prescription Database is a national health register that since 2004 has received electronic data on all prescriptions filled in any of the five hundred pharmacies in Norway. From this register, we extracted data on all prescriptions for oseltamivir since 2004. Using population statistics, we calculated the number and prevalence per 1000 inhabitants who had filled an oseltamivir prescription. These drugs are not available over the counter in Norway. **Results:** In 2004, 692 individuals (0.15 per 1000) filled a prescription for oseltamivir in Norway. In 2005, the figure was 22119 (4.78 per 1000), and in 2006, 4584 (0.98 per 1000). The highest prevalence was among 50 to 79 year olds. The prevalence varied somewhat from county to county. Preliminary data from the start of the 2007-2008 season show the same pattern (final data will be presented). **Conclusions:** Oseltamivir is rarely used in Norway. (The higher rates in 2005 were probably caused by families stockpiling the drug for fear of a pandemic.) Still, oseltamivir resistant influenza virus has spread in the community. This independence from an antiviral selection pressure means that the H274Y mutant influenza A/H1N1 viruses may not have lower fitness than wild type viruses

Additional Abstract

Viet Nam National Influenza Sentinel Surveillance: Organization and Findings, 2006-2007

N. T. Hien1, B. T. Chien2, N. T. Dat3, N. T. Tien4, D. T. Dannis5; 1National Institute of Hygiene and Epidemiology, Hanoi, VIET NAM, 2Pasteur Institute in Nha Trang, Nha Trang, VIET NAM, 3Institute of Hygiene and Epidemiology in Tay Nguyen, Buon Ma Thuot, VIET NAM, 4Pasreur Institute in Ho Chi Minh city, Ho Chi Minh city, VIET NAM, 5US Centers for Disease Control and Prevention, Hanoi, VIET NAM.

Background: In Vietnam, Influenza Like Illness (ILI) is the single most common cause of patient visits to health care facilities (HCF), routinely accounting for more than a million visits a year. General objectives of the program are to obtain epidemiological and virological information to guide influenza prevention and control policies and activities. **Methods:** This system became functional on 01/01/2006 with 4 participating regional public health institutes supporting 7 sentinel HCF, growing to 12 sentinel sites in Jul 2006. First 2 ILI patients each day are sampled for investigation. Throat swabs collected from sampled patients were tested for influenza viruses by RT-PCR using WHO primers and procedures. The percentage of the total visits for ILI and the percentage of sampled patients positive for influenza by RT-PCR were calculated weekly. Patients admitted to hospital with illnesses defined as severe viral pneumonia (SVP) were tested for influenza virus infection and epidemiological and clinical features were evaluated. Standard PCR and viral isolation techniques were used to detect influenza, including testing for H5N1 virus. **Results:** For the first 18 months, there were 861,607 total patient visits; of these, 149,106 (17.3%) were for ILI. Of 7398 ILI patients tested for influenza by RT-PCR, 1450 (19.6%) tested positive (A/H1N1, 7.8%; A/H3N2, 6.3%; B, 5.5%). Nationally, there were 3 peaks in influenza activity: a B peak in Feb-Mar 2006; a H1N1 peak in Jun-Jul 2006; and a broader H3N2 peak in Jan-Apr 2007. From Jan 2006 through Jul 2007, 179 SVP patients were enrolled; Among these, 17.3% were aged <15 years, 15.1% were 15-24 years, 37.5% were 25-64 years, and 10.1% were 65+ years. SVP patients were from 44 of the 64 provinces. 14 (8%) of 179 SVP patients were infected with influenza, among those, 8 were infected with seasonal influenza viruses (H1N1, H3N2 and B), and 6 with H5N1 viruses. **Conclusions:** The data demonstrate the burden of ILI at sentinel sites and permit spatiotemporal evaluations of influenza activity by virus type/subtype. The viral circulation data collected can be used to make estimates of morbidity and mortality associated with influenza activity in Viet Nam. It also has identified that seasonal influenza is a cause of severe pneumonia in Viet Nam, and has permitted rapid detection and confirmation of H5N1 cases.

International Conference on Emerging Infectious Diseases (ICEID) - March 16-19, 2008
Conference No: EV1271

Start Date: 3/16/2008 5:00 PM ET
End Date: 3/19/2008 4:30 PM ET

The International Conference on Emerging Infectious Diseases brings together public health professionals to encourage the exchange of scientific and public health information on global emerging infectious disease issues. The program will include plenary and panel sessions with invited speakers as well as oral and poster presentations on emerging infections. Major topics to be included are current work on surveillance, epidemiology, research, communication and training, bioterrorism, and preventions and control of emerging infectious diseases, both in the United States and abroad.

Program Information

TARGET AUDIENCE: The audience includes physicians, nurses, veterinarians, laboratorians, epidemiologists, program managers, and other interested individuals.

PREREQUISITES: Participants should have a medical/science background. Participants may be researchers, clinicians, epidemiologists, laboratorians, veterinarians, nurses, or other health professionals.

ADDITIONAL INFO: Early registration is $400, on-site registration is $450.

DEVELOPED BY: American

CE Expiration Date: 4/21/2008

Credit Statements

Register Here	
Credits Available Select the appropriate continuing education credit. Select audit for courses without credit or if you do not want credit.	☐ **CME (for physicians)** ☐ **CME (attendance for non-physicians)** ☐ **CNE (for nurses)** ☐ **CEU (for other professionals)** ☐ **Audit**
Click submit to ***Register*** for your selection and obtain event information.	

Disclosure Statements

All faculty members participating in continuing medical education programs sponsored by CDC are expected to disclose any real or perceived conflict of interest related to the content of their presentation, as well as any off-label uses of a product or drug. A listing of faculty disclosures will be available in the program addendum.

Elizabeth Barnett, MD would like to disclose that she receives honoraria as a member of the Speakers' Bureau for Merck.

Maria Brandl, PhD would like to disclose that she performs contracted research as a researcher for DSM Foods, Inc.

Lin Chen, MD would like to disclose that she receives an honorarium as the Associate Editor for the Travel Medicine Advisor.

Tai-Ho Chen, MD would like to disclose that his spouse receives a salary for employment by Maxim Healthcare Services.

Sarah Cleaveland, PhD would like to disclose that she receives an honorarium and lecture fee as a speaker for Intervet.

Nancy Cox, PhD would like to disclose that she receives an honorarium as the Outstanding Federal Government Employee of the Year from the Partnership for Public Service.

Ron Dagan, MD would like to disclose that he receives honorariums & grants as a speaker and consultant and for research from Wyeth and GSK. He also would like to disclose that he receives grants for research from Medimmune and MSD as well as an honorarium as a speaker and consultant for Novartis.

David Fredricks, MD would like to disclose that he receives a consulting fee for consulting for Oxonica, Inc.

Joel Gaydos, MD would like to disclose that his spouse receives an honorarium and grant support as an investigator for Becton Dickson and laboratory kits as an investigator for GenProbe. He would also like to disclose that his spouse receives honorariums as an Advisory Committee member from both Genocea and Trinity Unigold.

Gregory Gray, MD, MPH would like to disclose that he receives research contracts as a principal investigator for GlxoSmithKline Biologicals, ThermoFisher/Remel, Quidel, Inc., and ViroStat, Inc.

Sharon Hillier, PhD would like to disclose that she receives honorariums as a consultant for Ther-Rx Corportation, Enzybiolics, and Tibotec/J&J.

Jay Keystone, MD, MSc would like to disclose that he receives honorariums as a speaker from GlaxoSmithKline, Sanofi Pasteur, and Merck Frosst.

Jeffrey Klausner, MD, MPH would like to disclose that he receives an educator grant for an educational program from King Pharmaceutical.

Keith Klugman, PhD would like to disclose that he receives honorariums as a consultant/speaker from Wyeth, GSK, and Bayer.
Ian Lipkin, MD would like to disclose that he receives stock options as a member of the Scientific Advisory Board for 454 Life Sciences and Tetragenetics.

Roger Mahr, DVM would like to disclose that he receives dividends as a stockholder from Monsanto Co. and Pfizer Inc.

Christian Massire, PhD would like to disclose that he receives salary as an employee of Ibis BioSciences, Inc.

Mark Miller, MD would like to disclose that his spouse receives a consulting fee as a consultant for Roche and Merck.

Thomas Monath, MD would like to disclose that he receives consulting fees for consultaion on smallpox vaccine from Acambis.

Janet Nicholson, PhD would like to disclose that she receives book royalties from Wiley-Liss Publishing.

Walter Orenstein, MD would like to disclose his relationship in studies with Novartis on influenza vaccine coverage in health care, with Merck on HIV vaccine studies (Hope Clinic MUMPS research study; Uganda MVNA Immunization Project), with sanofi pastier on Yellow Fever Vaccine and IG –Hope Clinic, with Encorium, DSMB on VEE, Plague, and other potential BT vaccines, and with GSK, DSMB on pneumococcal vaccine development. He would also like to disclose that he receives honorariums as a member of the Board of Directors for the Sabin Vaccine Institute, Every Child by Two, and the National Foundation for Infectious Diseases. He would like to disclose his relationship as a member of 317 Coalition for Vaccine Finance, present Advocates for immunization funding at CDC.

David Relman, MD would like to disclose that he receives consultant fees as a member of the Scientific Advisory Board for NanBio, Cepheid, Novartis, and Applied BioSystems. He would also like to disclose that he receives an honorarium as a course lecturer from Bristol-Myers Squibb.

Louis Rice, MD would like to disclose that he receives honorariums as a consultant for Wyeth, Cadence, Novexel, Johnson & Johnson, Advanced Life Sciences, and Pfizer. He would like to disclose that he receives honorariums as a speaker from Arpida and Targanta. He would also like to disclose that he receives an honorarium as a member of the Data Safety Monitoring Board for Paratek.

Lynette Sawyer, DPH would like to disclose that she receives a salary as an employee of Cerus Corporation.

Sam Telford, MS, ScD would like to disclose that he receives honorariums as a consulting scientific expert for Imugen, Inc. and Fuller Laboratories.

James Versalovic, MD, PhD would like to disclose that he receives an honorarium as an advisor for Roche Diagnostics.

Patricia Walker, MD, DTM&H would like to disclose that she receives royalties as a co-editor for Immigrant Medicine textbook from Elsevier Publishing.

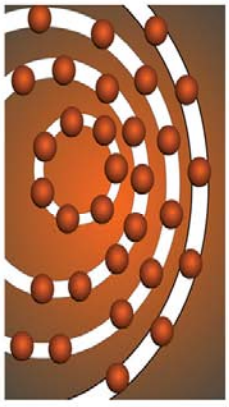
Angela Weaver, MPH would like to disclose that she receives a salary from the Public Health Institute, employment (contracted to USAID).

Samuel Yang, MD would like to disclose that he receives a royalty for patent licensing from Cambrex.

Presentations will not include any discussion of the unlabeled use of a product or a product under investigational use with the exception of the presentation on Major Global Disease Initiatives: Malaria, Tuberculosis, HIV-AIDS. Regina Rabinovich, MD, MPH will present the research and development pipeline for products for these diseases.

CE Session Credits

No.	Session Title	Date	Time	CME1	CME2	CNE	CEU
A1	One Medicine/One Health and Foodborne Illness and Plants/Produce	3/17/2008	8:30 AM - 10:10 AM	1.5	1.5	1.5	0.15
A2	Antimicrobial Resistance and XDR TB	3/17/2008	8:30 AM - 10:10 AM	1.5	1.5	1.5	0.15
B1	Respiratory Disease Outbreaks	3/17/2008	10:30 AM - 12:00 PM	1.5	1.5	1.5	0.15
B3	HIV	3/17/2008	10:30 AM - 12:00 PM	1.5	1.5	1.5	0.15
B4	Globally Mobile Populations & EIDs	3/17/2008	10:30 AM - 12:00 PM	1.5	1.5	1.5	0.15
B5	Health & Risk Communication	3/17/2008	10:30 AM - 12:00 PM	1.5	1.5	1.5	0.15
B6	Surveillance Role in Detection & Control	3/17/2008	10:30 AM - 12:00 PM	1.5	1.5	1.5	0.15
C1	Foodborne and Waterborne Diseases I	3/17/2008	1:15 PM - 2:45 PM	1.5	1.5	1.5	0.15
C2	Influenza I	3/17/2008	1:15 PM - 2:45 PM	1.5	1.5	1.5	0.15
C3	Surveillance: International	3/17/2008	1:15 PM - 2:45 PM	1.5	1.5	1.5	0.15
C4	Zoonotic and Animal Diseases I	3/17/2008	1:15 PM - 2:45 PM	1.5	1.5	1.5	0.15
C5	Methicillin Resistant *Staphylococcal* Infections	3/17/2008	1:15 PM - 2:45 PM	1.5	1.5	1.5	0.15
C6	Vectorborne Diseases	3/17/2008	1:15 PM - 2:45 PM	1.5	1.5	1.5	0.15
D1	Foodborne and Waterborne Diseases II	3/17/2008	3:00 PM - 4:30 PM	1.5	1.5	1.5	0.15
D3	Surveillance: Domestic	3/17/2008	3:00 PM - 4:30 PM	1.5	1.5	1.5	0.15
D5	Nosocomial Infections	3/17/2008	3:00 PM - 4:30 PM	1.5	1.5	1.5	0.15
E1	Travel Globalization and Major Global Disease Initiatives: Malaria, Tuberculosis, HIV-AIDS	3/18/2008	8:30 AM - 10:10 AM	1.5	1.5	1.5	0.15
E2	Dengue Control/Mosquito-borne Illness and Rift Valley Fever	3/18/2008	8:30 AM - 10:10 AM	1.5	1.5	1.5	0.15
E3	Avian Influenza Prevention in Poultry and Influenza & Emerging Influenza Viruses	3/18/2008	8:30 AM - 10:10 AM	1.5	1.5	1.5	0.15
F2	Arboviral Disease Risk in a Changing World	3/18/2008	10:30 AM - 12:00 PM	1.5	1.5	1.5	0.15
F3	Tuberculosis	3/18/2008	10:30 AM - 12:00 PM	1.5	1.5	1.5	0.15
G1	Novel Vaccine Strategies in Preventing EIDs in Humans & Protecting Animal Health	3/18/2008	1:15 PM - 2:45 PM	1.5	1.5	1.5	0.15
G3	Antimicrobial Resistance 2008: Use and Consequences	3/18/2008	1:15 PM - 2:45 PM	1.5	1.5	1.5	0.15
G4	Emerging & Re-emerging Vaccine-Preventable Diseases	3/18/2008	1:15 PM - 2:45 PM	1.5	1.5	1.5	0.15
G6	Zoonotic Infectious Disease: Perspectives from CDC's International Emerging Infections Program Kenya and Thailand	3/18/2008	1:15 PM - 2:45 PM	1.5	1.5	1.5	0.15
H4	Tropical Diseases	3/18/2008	3:00 PM - 4:30 PM	1.5	1.5	1.5	0.15
I1	Climate Change and Role of Political/Social Disruption	3/19/2006	8:30 AM - 10:10 AM	1.5	1.5	1.5	0.15
I3	Vaccine Emerging Issues and Outbreaks of Emerging Infections	3/19/2006	8:30 AM - 10:10 AM	1.5	1.5	1.5	0.15
J1	Issues in Vaccination & Vaccine-Preventable Diseases	3/19/2008	10:30 AM - 12:00 PM	1.5	1.5	1.5	0.15
J2	Pathogen Discovery	3/19/2008	10:30 AM - 12:00 PM	1.5	1.5	1.5	0.15
J4	International Networks that Work	3/19/2008	10:30 AM - 12:00 PM	1.5	1.5	1.5	0.15
J5	Public Health Genomics	3/19/2008	10:30 AM - 12:00 PM	1.5	1.5	1.5	0.15
J6	MRSA	3/19/2008	10:30 AM - 12:00 PM	1.5	1.5	1.5	0.15



ICEID 2008
International Conference on Emerging Infectious Diseases

Final Program and Exhibit Guide Addendum

Educational Documentation Forms

1 - 59

2008 International Conference on Emerging Infectious Diseases
Atlanta Georgia – March 16 – 19, 2008 – ADDENDUM