Session: 260. HAI: Surveillance, International
Saturday, October 5, 2019: 12:15 PM

Background. National surveillance data should be validated to identify data quality issues. This study tested the validity of healthcare-associated infection (HAI) data in the Korean National Healthcare-associated Infections Surveillance System (KONIS), intensive care unit (ICU) module.

Methods. The validation process consisted of external (EV) and internal (IV) validation phases. For the 10 hospitals that were selected based on the HAI rate, among the 193 participating hospitals between July 2016 and June 2017, both EV and IV were performed. For the EV, the validation team reviewed 295 medical records of 60 patients with reported HAIs, including 20 urinary tract infections (UTIs), 27 bloodstream infections (BSIs), and 13 cases of pneumonia (PNEU), and 235 patients with no reported HAI during 1-day visits conducted in November and December 2017. The reviewer's diagnosis of HAI was regarded as the reference standard. IV was conducted by the staff of each hospital and evaluated whether UTI or BSI were present. Primary IV was performed for 279 patients who were subject to EV. Secondary IV was performed on 203 patients in another 11 selected participating hospitals that did not report HAIs to KONIS during the 1-year study period.

Results. In the EV, the diagnosis of UTI in the participating hospitals had a sensitivity of 72.0% and specificity of 99.3%. The sensitivity of BSI and PNEU was 63.2% and 70.6%, respectively, and specificity was 98.8% and 99.6%. The agreement (kappa) between the EV and primary IV was significant, with $\kappa = 0.754$ for UTI and $\kappa = 0.674$ for BSI. The results of the secondary IV showed that the hospitals that had no reports of HAI had few hospital beds and performed few blood or urine culture tests. In the secondary IV, eight UTIs and three BSIs were newly diagnosed in three hospitals, respectively. The reasons for not reporting the HAIs were presumed to be a lack of understanding of the surveillance standards and fear of the disadvantages of disclosing the HAI.

Conclusion. This study shows the need for ongoing validation and continuous training of surveillance personnel to maintain the accuracy of surveillance data. We also confirmed that IV can be used as an alternative monitoring method to examine validity and accuracy.

Disclosures. **All authors:** No reported disclosures.

2477. Antimicrobial Resistance patterns of *Enterobacteriaceae* and *Pseudomonas aeruginosa* from Colombian clinical isolates. 2017–2018

Monica Maria Rojas Rojas, MPH[1]; Catalina López, MSc[1]; Jaime Ruiz, MSc[2]; Jacqueline Pavía, MSc[3]; Jose Oñate, ID [4]; Cristhian Hernández-Gómez, MSc[1]; [1]MSD Colombia, Bogota, Distrito Capital de Bogota, Colombia; [2]MSD, Colombia, Bogotá, Distrito Capital de Bogota, Colombia; [3]MSD Colombia, Bogota, Distrito Capital de Bogota, Colombia; [4]Centro Medico Imbanaco, Cali, Valle del Cauca, Colombia

Session: 260. HAI: Surveillance, International
Saturday, October 5, 2019: 12:15 PM

Background. The Study for Monitoring Antimicrobial Resistance Trends (SMART) is a worldwide initiative to monitor in vitro susceptibility of clinical Gram-negative isolates to several antimicrobial agents. Surveillance initiatives are essential to provide real-world evidence to support local guidelines development. Colombia has participated since 2012 with isolates from complicated intrabdominal infections (cIAI), complicated urinary tract infections (cUTI) and respiratory tract infections (RTI). This study describes resistant patterns of *Escherichia coli* (Eco), *Klebsiella pneumoniae* (Kpn) and *Pseudomonas aeruginosa* (Pae) clinical isolates collected in Colombian hospitals in a 2 years period (2017–2018).

Methods. Isolates from patients with cIAI, cUTI and RTI were collected. Identification confirmation was done in central laboratory. Minimum inhibitory concentrations (MIC) were performed by broth microdilution and interpreted according to 2018 CLSI guidelines, same criteria for Extended-spectrum β-lactamase (ESBL) classification. The antimicrobial activity was evaluated for aztreonam (ATM), ceftolozane/tazobactam (C/T), ceftazidime (CAZ), colistin (COL), ertapenem (ETP), cefepime (FEP), imipenem (IMP), meropenem (MEM) and piperacillin–tazobactam (TZP).

Results. During 2017–2018, 1492 isolates were collected. The main organism was Eco (51%) followed by Kpn (29%) and Pae (20%). In vitro susceptibility activity is presented in Table 1. COL, C/T, ETP, MEM and IPM exhibited over 95% susceptibility in Eco. ESBL prevalence was 18% for Eco (53/314) and 22% for Kpn (36/165). COL and C/T were the most active agents against Pae isolates. For Kpn, $MIC_{50/90}$ values were: MEM (0.12 / 8), C/T (0.5 / 8) and for TZP (8 / > 64), meanwhile for Pae were MEM (0.5 / 32), C/T (0.5 / 32) and for TZP (8 / > 64).

Conclusion. Continued antimicrobial resistance surveillance initiatives are critical to guide the empiric treatments decision in a multidrug resistance era. This study shows that Ceftolozane/Tazobactam, MEM and COL have the best susceptibility profile against Eco, Kpn and Pae of cIAI, cUTI and RTI cases in Colombia. The C/T susceptibility rates and low MIC distribution provide evidence to support its use as a non-carbapenem therapeutic alternative for Gram-negative infections.

Table 1

Escherichia coli, Klebsiella pneumoniae and Pseudomonas aeruginosa in vitro susceptibility (%S), Colombia 2017-2018

Organism	ATM %S	C/T %S	CAZ %S	COL %S	ETP %S	FEP %S	IPM %S	MEM %S	TZP %S
Escherichia coli (767)	81.52	97.77	82.33	98.55	96.52	82.12	96.24	97.44	89.24
Klebsiella pneumoniae (n=428)	62.62	77.12	65.96	98.52	75.90	65.20	77.03	78.17	64.25
Pseudomonas aeruginosa (n=297)	64.59	86.26	76.51	99.05	-	76.51	63.03	66.45	71.39

Aztreonam (ATM), Ceftolozane/Tazobetam (C/T), Ceftazidime (CAZ), Colistin (COL), Ertapenem (ETP), Cefepime (FEP), Imipenem (IPM), Meropenem (MEM), Piperacillin/Tazobactam (TZP)

Disclosures. **All authors:** No reported disclosures.

2478. Surveillance of antibacterial resistance among clinical isolates from hospitals in Shanghai: results of 2018

Yang Yang, Master of Medicine[1]; Yan Guo, Master[2]; Demei Zhu, Bachelor[2]; Fupin Hu, PhD[2]; [1]Institute of Antibiotics, Huashan Hospital, Fudan University, and Key Laboratory of Clinical Pharmacology of Antibiotics, National Health and Family Planning Commission, Shanghai, China, Shanghai, Shanghai, China (People's Republic); [2]Institute of Antibiotics, Huashan Hospital, Fudan University, Shanghai, Shanghai, China (People's Republic)

Session: 260. HAI: Surveillance, International
Saturday, October 5, 2019: 12:15 PM

Background. To investigate the current state of antibacterial resistance of clinical isolates from hospitals in Shanghai, China.

Methods. Antimicrobial susceptibility testing (AST) was carried out for the clinical isolates from 50 hospitals (including 30 grade A tertiary hospitals and 20 grade B tertiary hospitals/grade A secondary hospitals, and there were 3 children hospitals among them) according to a unified protocol using Kirby–Bauer(KB) method or automated AST systems. Results were analyzed according to CLSI 2018 breakpoints.

Results. Of the 144373 clinical isolates, Gram-positive cocci and Gram-negative bacilli accounted for 29.6% and 70.4%, respectively. The overall prevalence of MRSA in *Staphylococcus aureus* was 45.9% and 78.4% for MRCNS in coagulase-negative *Staphylococcus*. No strains were found resistant to vancomycin in *Staphylococcus* spp. 84.1% of the 1204 strains of non-meningitis *S. pneumoniae* isolated from children were penicillin-susceptible (PSSP), 15.9% were penicillin-nonsusceptible, including penicillin-intermediate (PISP, 10.5%) and penicillin-resistant (PRSP, 5.4%) strains. Of the 361 strains isolated from adults, 94.5%, 3.0% and 2.5% were PSSP, PISP, and PRSP, respectively. Vacomycin-resistance *E. feacium* was 0.7% and no vacomycin-resistant *E. feacalis* were identified. According to PCR results, most of these resistant strains were *van*A genotype. The prevalence linezolid-nonsusceptible *E. faecalis* was about 1.6%, few *E. feacium* was resistant to Linezolid. The overall prevalence of ESBL-producing strains was 54.0% in *E. coli*, 35.0% in *Klebsiella pneumoniae* and 47.1% in *Proteus mirabilis*. *Enterobacteriaceae* isolates were still mainly susceptible to carbapenems. Overall, 11.7% and 11.2% of the *Enterobacteriaceae* isolates were resistant to imipenem and meropenem, respectively. The predominant organism of CRE isolates was *K. pneumoniae*. The prevalence of CRAB and CRPA were 62.5% and 28.7%, respectively.

Conclusion. Antimicrobial resistance remains to be a problematic issue in healthcare settings, especially in Gram-negative bacilli, effective infection-control measures should be promoted to tackle this critical threat.

Disclosures. **All authors:** No reported disclosures.

2479. Trends and Regional Differences in Extended Spectrum β-lactamase (ESBL)-producing Enterobacteriaceae, 2012–2017

Hannah Wolford, MSPH[1]; Kelly M. Hatfield, MSPH[1]; Babatunde Olubajo, PhD, MPH[2]; Sujan Reddy, MD, MSc[2]; John A. Jernigan, MD, MS[2]; James Baggs, PhD[3]; [1]Centers for Disease Control and Prevention (CDC), Atlanta, Georgia; [2]Centers for Disease Control and Prevention, Atlanta, Georgia; [3]CDC, Atlanta, Georgia

Session: 261. HAI: Surveillance, Regional
Saturday, October 5, 2019: 12:15 PM

Background. Extended spectrum β-lactamase-producing Enterobacteriaceae (ESBLs) have been identified as a serious antibiotic-resistant threat. Studies have shown that ESBL infection rates were increasing through 2014. Our objective was to examine more recent ESBL trends and to evaluate differences across regions in the United States.

Methods. We measured the incidence of positive clinical cultures from inpatient encounters in a cohort of hospitals submitting data to the Premier Healthcare Database and Cerner Health Facts from 2012 through 2017. We included *Escherichia coli* and *Klebsiella* spp. cultures and defined ESBL as non-susceptibility to cefotaxime, ceftriaxone, ceftazidime, or cefepime. Cultures collected on days 1, 2, or 3 of hospitalization were considered community-onset (CO); cultures from day 4 or later were considered hospital onset (HO). We developed weights using a raking procedure to match the American Hospital Association distribution for acute care hospitals based on US census division, bed size category, teaching status, and urban/rural designation. We used weighted multivariable logistic regression adjusting for hospital characteristics to examine trends and regional differences in ESBL rates.

Results. In 2017, the estimated rate of ESBLs was 40.3 per 10,000 discharges for CO and 6.4 per 10,000 discharges for HO; 86% of all ESBLs were CO. The percent that were ESBLs among all included cultures increased for CO (8.2% in 2012 to 11.6% in 2017) and HO (13.1 to 16.8%) cultures. From 2012 – 2017, adjusted ESBL rates increased for CO (7.9% annually, $P < 0.0001$), while HO rates did not change significantly over time ($P = 0.39$, Figure 1). We found significant regional differences in the rates of ESBL ($P < 0.0001$) across US census divisions in 2017 (Figure 2). Estimated rates for 2017 varied 5-fold from 15.3 ESBLs per 10,000 discharges in the Northwest Central to 82.4 ESBLs in the Mid-Atlantic.

Conclusion. We estimated a 40% increase in the rate of CO-ESBLs among hospitalized patients from 2012 to 2017, but no increase in HO rates. ESBL rates varied greatly by region of the country and are estimated as much as 5× higher in some areas. A better understanding of factors contributing to community transmission and regional variation is necessary in order to inform ESBL prevention efforts.

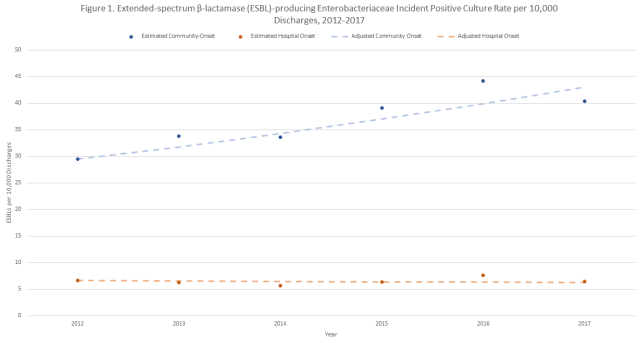
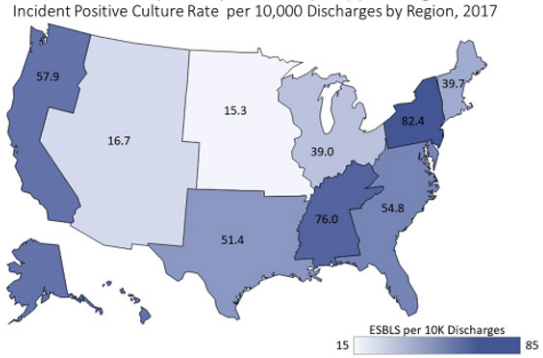


Figure 2. Estimated Extended-spectrum β-lactamase (EBSL)-producing Enterobacteriaceae Incident Positive Culture Rate per 10,000 Discharges by Region, 2017



Disclosures. **All authors:** No reported disclosures.

2480. Communication During Patient Transfers: Describing Gaps in the Infectious Status Information Pipeline

Jeanmarie Mayer, MD[1]; Roberta Horth, PhD, MPH[2]; Madison Todd[3]; Randon Gruninger, MPH[4]; Allyn K. Nakashima, MD[3]; [1]University of Utah School of Medicine, Sandy, Utah; [2]Centers for Disease Control and Prevention, Decatur, Georgia; [3]Utah Department of Health, Salt Lake City, Utah; [4]Utah Department of Health, Kaysville, Utah

Session: 261. HAI: Surveillance, Regional

Saturday, October 5, 2019: 12:15 PM

Background. Fragmented communication of patients' infectious status across healthcare networks impact regional spread of multidrug-resistant organisms (MDRO). This study aimed to quantify gaps in communication of patient MDRO status across Utah healthcare facilities and to identify opportunities to improve.

Methods. This is a cross-sectional retrospective mixed-methods study of patient transfers from three purposively selected healthcare facilities: an acute care (ACF), long-term acute care (LTAC), and skilled-nursing facility (SNF). Patients with known MDRO transferred out of these facilities over the previous week were identified in bi-monthly samples spanning 2 months. Infection preventionists and admission nurses from facilities receiving these patients were interviewed.

Results. Of 293 patients transferred to another facility, 13% (n = 38) had an active infection or colonization with an MDRO. These 38 patients were transferred to 26 healthcare facilities within the state (4 ACF, 3 LTAC, 19 SNF). Gram-negative organisms with resistance to a carbapenem accounted for 15.8% of those transferred with an MDRO. There was no documentation of the state infection control transfer form (ICTF) at the sending facility for 68.5% of MDRO patient transfers. Of 22 admitting nurses interviewed, 19 (86.4%) did not receive an ICTF, 6 (27.3%) received no communication regarding patients' infectious status, and 11 (50%) had to contact the sending facility for additional information. Moreover, 18.2% of patients had not been put on appropriate precautions. Several nurses expressed confusion with MDRO definitions and lack of guidance regarding care of MDRO colonized patients. Among infection preventionists asked about general MDRO transfers (n = 26), 26.9% reported that communication on infectious status of MDRO patients was received in under 40% of incoming transfers. When asked about a planned statewide MDRO registry, 80.8% felt that such a system would be actively searched at their facility, and 96.2% felt that a system that pushes out alerts would be useful.

Conclusion. Given the widespread gaps in communication of infectious status of patients with MDROs transferred across the healthcare facilities sampled, efforts to standardize and improve MDRO communication in the region is warranted.

Disclosures. **All authors:** No reported disclosures.

2481. Comparing inter-hospital patient movement patterns to better understand mechanisms for regional dissemination of carbapenem-resistant Enterobacteriaceae

Hannah Wolford, MSPH[1]; Justin O'Hagan, ScD[2]; Prabasaj Paul, PhD, MPH[2]; Sujan Reddy, MD, MSc[2]; Brandon Attell, MA[2]; John A. Jernigan, MD, MS[2]; Rachel Slayton, PhD, MPH[2]; [1]Centers for Disease Control and Prevention (CDC), Atlanta, Georgia; [2]Centers for Disease Control and Prevention, Atlanta, Georgia

Session: 261. HAI: Surveillance, Regional

Saturday, October 5, 2019: 12:15 PM

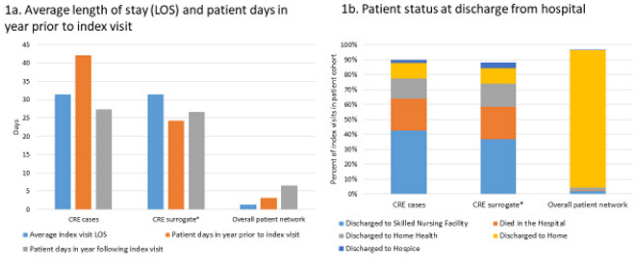
Background. Understanding inter-hospital movement of patients provides insight into regional transmission of multidrug-resistant organisms (MDROs) that can guide containment efforts. Movement of general patient populations are often used for this purpose, but movement of the specific patient population of MDRO carriers may be more useful. We sought to compare movement of CRE patients with that of other patient populations to explore whether CRE carriers move differently, and if so, to determine whether administrative data can be used to identify patient populations with transfer patterns that mimic CRE patients.

Methods. We used New York's Statewide Planning and Research Cooperative System (SPARCS), to create a patient network of all acute care hospital encounters ("overall hospital population") during 2013–2015. We identified the subset of CRE cases in the network by linking the SPARCS data to CRE cases reported to the National Healthcare Safety Network in 2014, matching on admission date, date of birth, gender, and facility. We described patient characteristics and movement patterns across 3 cohorts: (1) CRE cases, (2) overall hospital population, (3) CRE surrogate (patients clinically similar to CRE cases based on length of stay [LOS] ≥14 days and Clinical Classification Software [CCS] category of sepsis plus at least one of the following additional CCS categories: adult respiratory failure, acute renal failure, procedure complication or device complication). Correlations between cohorts were calculated using patient transfer matrices to determine similarities between the networks.

Results. The average LOS for CRE cases was 25× higher than the overall hospital population (31.4 vs. 1.3 days, Figure 1a), and CRE cases were more likely to die or be discharged to a skilled nursing facility (Figure 1b). CRE movement networks were only moderately correlated with the overall hospital population (R^2 = 0.51); there was higher correlation between CRE case and CRE surrogate networks (R^2 = 0.73).

Conclusion. CRE patients have different healthcare experiences in the hospital and between hospitals in New York compared with the overall hospital population. The CRE surrogate cohort transfer patterns were more similar, and could be used to understand CRE patient movement in the absence of CRE culture data.

Figure 1. Patient characteristics of index visits* by cohort



*index visit was defined as the first visit with a CRE culture for CRE patients, the first visit in 2014 meeting the cohort definition for the CRE surrogate and the first hospital visit (inpatient or outpatient) in 2014 for the overall patient network.
*defined as LOS >= 14 days and a Clinical Classification Software (CCS) diagnosis of sepsis with at least one additional CCS category: adult respiratory failure, acute renal failure, procedure complication or device complication

Disclosures. **All authors:** No reported disclosures.

2482. Clinical Outcomes of Once-Daily Darunavir in Treatment-Experienced Patients with Darunavir Resistance Associated Mutations Through 48 Weeks of Treatment

Charlotte-Paige M. Rolle, MD MPH[1]; Omar Marquez, LPN CRC[1]; Vu Nguyen, MS[2]; Federico Hinestrosa, MD[3]; Edwin DeJesus, MD[3]; [1]Orlando Immunology Center, Orlando, Florida; [2]University of Central Florida College of Medicine, Orlando, Florida; [3]Orlando Immunology Center, University of Central Florida College of Medicine, Orlando, Florida

Session: 262. HIV: Antiretroviral Therapy

Saturday, October 5, 2019: 12:15 PM

Background. Darunavir (DRV) is a well-tolerated, potent protease inhibitor used once-daily in patients with no DRV resistance-associated mutations (RAMs) and twice-daily in those with DRV RAMs. Treatment guidelines encourage use of once-daily regimens to optimize patient adherence, convenience and tolerability. Several studies suggest that once-daily DRV retains efficacy in the setting of 1–2 DRV RAMs whereas 3 or more DRV RAMs (with multiple background PI RAMs) is needed for DRV resistance. Currently, there is little clinical data to support the long-term use of once-daily DRV in patients with DRV RAMs.

Methods. This is a retrospective study evaluating the 48-week clinical outcomes of 22 treatment-experienced patients with DRV RAMs switched to once-daily DRV between 2014 and 2017 at the Orlando Immunology Center. The primary endpoint was the proportion with virologic suppression (HIV-1 RNA< 50 copies/mL) at Week 48. Adherence, adverse events (AEs) and laboratory parameters were analyzed throughout the study.

Results. The median age (range) of the sample was 53 (21–77) years, median baseline CD4+ count was 609 cells/mm3, 18 (82%) had baseline HIV-1 RNA <50 copies/mL, 15 (69%) had previously used 1 or more PIs and median number (range) of