1248. Genomic Sequencing and Clinical Data Integration for Next-Generation Infection Prevention

Donald Chen, MD[1]; Liyi Xu, PhD[2]; Mary Fortunato-Habib, DNP, MS, RN[3]; Andrew Hoss, PhD[2]; Melissa Chanza, BA[4]; Changhong Yin, MD[4]; Raivo Kolde, PhD[2]; Abhay Dhand, MD[5]; Rita Sussner, BSN, RN, CIC[5]; Juan Carmona, PhD, MPH, MBE[3]; Guiqing Wang, MD, PhD[6]; Weihua Huang, PhD[4]; Brian Gross, MSc, BSEE, RRT, SMIEEE[3] and John Fallon, MD[4]; [1]Infection Prevention and Control, Westchester Medical Center, Valhalla, New York, [2]Philips Research North America, Cambridge, Massachusetts, [3]Philips Innovation Laboratory, Philips Healthcare, Cambridge, Massachusetts, [4]Pathology, New York Medical College, Valhalla, New York, [5]Medicine, Westchester Medical Center/New York Medical College, Valhalla, New York, [6]Pathology and Clinical Laboratories, Westchester Medical Center, Valhalla, New York

Session: 139. Healthcare Epidemiology: Outbreaks
Friday, October 5, 2018: 12:30 PM

Background. Typical Infection Prevention to detect pathogen transmission in hospitals has relied on observation of (1) uncommon pathogen phenotypes or (2) greater than expected number of pathogen phenotypes in a given timeframe and/or location. Genome sequencing of targeted organisms in conjunction with routine patient geo-temporal information and antibiotic susceptibility data holds promise in identifying transmissions with greater sensitivity and specificity, saving time and effort in reviewing for transmission events.

Methods. In an on-going genomic sequencing surveillance effort in a tertiary care hospital, drug-resistant clinical isolates from the "ESKAPE" pathogens were routinely sequenced in 2017. In parallel, potential clusters were identified for 2017 through conventional Infection Prevention approaches. Groups identified by their genetic distances along with visualizations on antimicrobial susceptibilities, and patient location histories and dates were displayed in an interactive interface, Philips IntelliSpace Epidemiology (PIE), and reviewed by Infection Prevention.

Results. Among 656 patients, 1,239 drug-resistant ESKAPE samples were sequenced. Thirty-eight genetically related groups involving 196 patients were identified. Groups ranged in size from two to 44 patients, primarily consisting of VRE and MRSA. Notably, a review of the 38 groups identified 20 groups where the information at hand suggested a concern for transmission. 16 of the 20 were not previously identified by Infection Prevention. Using PIE to review all 38 groups identified from 1 year's worth of data required 3 hours of time by an Infection Prevention professional, averaging less than 5 minutes per cluster, less than 1 minute per patient, and 11 minutes of review time per actionable opportunity. By conventional means, approximately 23 hours would have been required to review the genomic groups without the aid of the PIE tool.

Conclusion. The use of PIE's genomic-defined groups, along with the integrated clinical data platform, allows for a greater ability, certainty, and speed to detect clusters of organisms representing transmission in the hospital setting. Applied prospectively, PIE can detect transmissions sooner than by conventional means for potential patient safety gains and cost savings.

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1249. Emergence of Diverse Carbapenem-Resistant Enterobacteriaceae (CRE) in the Dominican Republic

Rita Rojas Fermin, MD[1]; Nenad Macesic, MBBS[2]; Gilda Tolari, MD[3]; Anel Guzman, PhD[3]; Medini Annavajhala, PhD[2] and Anne-Catrin Uhlemann, MD, PhD[2]; [1]Infectious Diseases, Hospital General Plaza de la Salud (HGPS), Santo Domingo, Dominican Republic, [2]Columbia University Medical Center, New York, New York, [3]Department of Microbiology, Hospital General Plaza de la Salud (HGPS), Santo Domingo, Dominican Republic

Session: 139. Healthcare Epidemiology: Outbreaks
Friday, October 5, 2018: 12:30 PM

Background. Despite the global threat of CRE, data from resource-limited regions such as the Dominican Republic (DR) are limited. A lack of novel antibiotics and molecular diagnostic tools for outbreak detection, coupled with the role of travel in circulating CRE to and from the DR represent significant challenges to limiting their spread. Here, we report the first molecular characterization of DR CRE isolates and compared them to geographically diverse CRE.

Methods. Isolates from DR (one *Citrobacter freundii*, three *Klebsiella pneumoniae),* obtained from patients with bacteremia (one) and pneumonia (three), were compared with CRE from a New York City hospital in a Dominican neighborhood, including isolates (two *Enterobacter cloacae*, one *K. pneumoniae)* from a patient transferred to NYC from another DR institution. Whole genome sequencing was used to determine multi-locus sequence type (MLST) and resistance gene profiles. Phylogenetic analyses of isolates with same ST were performed.

Results. Isolates from the DR and the Dominican patient were of unique genomic backgrounds including pandemic (*K. pneumoniae* ST11) and novel sequence types, and harbored either bla_{KPC-2} or bla_{KPC-3} (Table 1). Replicon typing suggested that these carbapenemase genes were located on distinct plasmids. Phylogenetic analyses using the NYC collection of ~400 sequenced CRE isolates indicated that DR and NYC *K. pneumoniae* ST307 isolates were related (33 SNPs). Further review showed that both patients had recent admissions in Puerto Rico (PR), highlighting the role of regional spread. *K. pneumoniae* ST11 isolates from DR and NYC, on the other hand, were not found to be closely related (1,418–1,440 SNPs).

Conclusion. Genotyping of DR CRE isolates revealed a high genomic diversity, suggesting multiple introductions. Phylogenetics of *K pneumoniae* ST307 place these within a global context, demonstrating links across the Caribbean and North America. International surveillance studies integrating genomics are needed to track and limit the spread of CRE in resource-limited settings such as DR.

Table 1: Comparison of DR Isolates

Organism	MLST	KPC Gene	Origin
K. pneumoniae	ST11	bla_{KPC-2}	DR
	ST1040	bla_{KPC-3}	NYC, DR patient
	ST307	bla_{KPC-2}	DR, travel to PR
	Novel ST	bla_{KPC-3}	DR
C. freundii	ST95	bla_{KPC-2}	DR
E. cloacae	ST456	bla_{KPC-3}	NYC, DR patient

Disclosures. **A. C. Uhlemann**, Merck: Investigator, Grant recipient.

1250. Prevalence and Risk Factors for Acquiring Carbapenem-Resistant *Enterobacteriaceae* in an Intensive Care Unit at a Tertiary Hospital

Jin Suk Kang, MD[1]; Soon Ok Lee, MD[2]; Jeong Eun Lee, MD[2]; So Ra Kim, RN[3]; Han Wool Kim, MT[3]; Seung Hyun Hong, RN[3]; Hye Won Kim, RN[3]; Mi Jin Jang, RN[3]; Sun Hea Shin, RN[3]; Hyun Jung Ha, RN[3]; Nam Jeong Park, RN[3]; Mee Kyung Ko, BS[4]; Jongyoun Yi, MD[4] and Kye-Hyung Kim, MD[2]; [1]Internal Medicine, Inje University Busan Paik Hospital, Busan, Korea, Republic of (South), [2]Internal Medicine, Pusan National University Hospital, Busan, Korea, Republic of (South), [3]Infection Control, Pusan National University Hospital, Busan, Korea, Republic of (South), [4]Laboratory Medicine, Pusan National University Hospital, Busan, Korea, Republic of (South)

Session: 139. Healthcare Epidemiology: Outbreaks
Friday, October 5, 2018: 12:30 PM

Background. Active surveillance testing of carbapenem-resistant *Enterobacteriaceae* (AST-CRE) is recommended in high-risk settings, such as intensive care units (ICUs), to prevent CRE outbreaks or invasive infections. This study aimed to investigate the effects of AST-CRE by analyzing the prevalence and risk factors for acquiring CRE during the ICU care.

Methods. We conducted AST-CRE on rectal swabs of patients admitted to the ICU in the emergency room at a tertiary hospital in South Korea for 12.5 months. AST-CRE was performed upon admission and weekly thereafter. To assess the risk factors of acquiring AST-CRE during the admission period in adult patients, those colonized with CRE upon admission and aged <18 years were excluded. AST-CRE was performed using Centers for Disease Control and Prevention methods. A polymerase chain reaction assay was performed to detect five carbapenemase genes (NDM, KPC, VIM, IMP, and OXA).

Results. A total of 810 patients were admitted during the study period. The acquisition rate and carbapenemase-producing CRE were 2.6% (21/810) and 42.9% (9/21), respectively. No invasive infection due to CRE was found. The most common species were *Klebsiella pneumoniae* (71.4%, 15/21), and eight KPC and one NDM genes were detected. In CRE-positive patients, in-hospital mortality and length of hospitalization were higher ($P = 0.003$) and longer ($P < 0.001$), respectively. Multivariate analyses showed that male gender (adjusted odds ratio [aOR] 8.0; 95% confidence interval [CI] 1.7–36.8), previous hospitalization in the last year (aOR 5.1; 95% CI 1.6–16.4), co-colonization with multidrug-resistant *Acinetobacter* species (aOR 18.3; 95% CI, 4.2–79.2) and extended-spectrum β-lactamase-producing bacteria (aOR 3.4; 95% CI, 1.1–10.9), and length of ICU admission until CRE detection for ≥10 days (aOR 6.5; 95% CI 2.2–19.2) were independently associated with CRE acquisition.

Conclusion. To prevent CRE outbreak or invasive infections, patients admitted in the ICU should be screened using AST-CRE.

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1251. Contaminated Sinks May be an Environmental Source for Serial Transmission of Carbapenem-Resistant *Enterobacteriaceae* (CRE) to ICU Patients

Sarah S. Lewis, MD MPH[1]; Jessica Seidelman, MD[2]; Kirk Huslage, MSPH, BSN, RN, CIC[2]; Charlene Carriker, RN BSN CIC[3]; Amy Hnat, BSN, RN[1]; Erica Lobaugh-Jin, BSN, RN, CIC[1]; Christopher Sova, RN, BSN[1]; Bonnie Taylor, RN, BSN, MPH[1]; Nancy Strittholt, RN, BSN, CIC[3]; Sheila Vereen, RN BSN CIC[3]; Robbie Willis, BA, RN[4]; Christy Campbell, RN[3]; Rachel Addison, MT (ASCP), MPH[5]; Kevin Hazen, PhD, D(ABMM), FIDSA, FAAM[6]; Amy Mathers, MD[7]; Kasi Vegesana, BS[8]; Joanne Carroll, MT[9]; Shireen Kotay, PhD[9]; Arthur W. Baker, MD, MPH[10]; Daniel Sexton, MD, FIDSA, FSHEA[11]; Deverick J. Anderson, MD, MPH, FIDSA, FSHEA[12] and Becky Smith, MD[1,2]; [1]Infection Prevention and Hospital Epidemiology, Duke University Medical Center, Durham, North Carolina, [2]Duke Center for Antimicrobial Stewardship and Infection Prevention, Durham, North Carolina, [3]Duke University Medical Center, Durham, North Carolina, [4]Infection Prevention Hospital Epidemiology, Duke University Medical Center, Durham, North Carolina, [5]Duke Infection Control Outreach Network, Durham, North Carolina, [6]Pathology, Duke University Health System, Durham, North Carolina, [7]University of Virginia