1249. Genomic Sequencing and Clinical Data Integration for Next-Generation Infection Prevention

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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 "EKAPE" pathogens were routinely sequenced in 2017. In parallel, potential clusters were identified for 2017 through conventional Infection Prevention approaches. Groups identified by both genetic distances along with visualization 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 1248 patients, 1239 drug-resistant EKAPE 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 reviewing 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 PIES-genomic-defined groups, along with the integrated clinical and molecular platform, allows for a greater ability to detect and identify groups 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.

**Disclosures.** D. Chen, Philips: Scientific Advisor, Consulting fee. M. Fortunato-Habib, Philips Healthcare: Consultant and Employee, Salary A. Hoss, Philips: Employee, Salary R. Kolde, Philips: Employee, Salary A. Dhand, Merck: Speaker's Bureau, Speaker honorarium. Astellas: Scientific Advisor, Consulting fee. R. Sussner, Philips: Scientific Advisor, Consulting fee. J. Carmona, Philips Healthcare: Employee, Salary B. Gross, Philips Healthcare: Employee, Investigator, Research Contractor, Scientific Advisor and Shareholder, Salary J. Fallon, Philips Healthcare: Investigator, Research support.

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

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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, drug-resistant CRE isolates and harbor either bla<KPC> or bla<KPC> (Table 1). Replicon typing suggested that these carbapenemase genes were located on distinct plasmids. Phylogenetic analyses using the NYCC collection of ~400 sequenced CRE isolates indicated that DR and NYC K. pneumoniae ST307 isolates were isolated (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).

**Methods.** Genotype typing of CRE isolates revealed a high genomic diversity, suggesting multiple phylogenotypes. Genotypes 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   |      |          |        |
| ST307           |      |          |        |
| ST1040          |      |          |        |
| ST11            |      |          |        |
| Novel ST        |      |          |        |
| C. freundii     |      |          |        |
| ST95            |      |          |        |
| E. cloacae      |      |          |        |
| ST456           |      |          |        |

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

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

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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) (9/21), respectively. No invasive infection due to CRE was found. The most common species found to be closely related (1,418–1,440 SNPs). Replicon typing suggested that these carbapenemase genes were located on distinct plasmids.

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

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

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

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