1248. Genomic Sequencing and Clinical Data Integration for Next-Generation Infection Prevention
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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 genome 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 through genetic distances along with visualization of antimicrobial resistances, and patient location histories and dates were displayed in an interactive interface, Philips Intellispace Epidemiology (PIE), and reviewed by Infection Prevention.
Results. Among 2017 patients, 1,393 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 the spread 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
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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. In total, 14 isolates 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 ST111) and novel sequence types, and harbored either blaKPC or blaOXY1 (Table 1). Replicon typing suggested that these carbapenemase genes were located on distinct plasmids. Phylogenetic analyses using the NYU 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. Whole-genome sequencing of DR CRE isolates revealed a high genomic diversity, suggesting multiple phylogenetic origins. 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       | 1    | blaKPC   | DR              |
| ST1040     | 2    |          | NYC, DR patient |
| ST307      | 4    |          | DR, travel to PR|
| Novel ST   | 6    |          | DR              |
| C. freundii| ST86 |          | NYC, DR patient |
| E. cloacae  | ST456|          |                 |

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1250. Prevalence and Risk Factors for Acquiring Carbapenem-Resistant Enterobacteriaceae in an Intensive Care Unit at a Tertiary Hospital
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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 on mortality 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. The risk factors of acquiring AST-CRE during the admission period in adult patients, those who 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) (p<0.01), 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<0.005) and longer (P<0.001, respectively. Multivariate analyses showed that higher age (adjusted odds ratio [aOR] 8.0; 95% confidence interval [CI] 3.7-16.8), previous hospitalization in the last year (aOR 5.1; 95% CI 1.6-16.4), co-infection 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 ≥210 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 Sink May be an Environmental Source for Serial Transmission of Carbapenem-Resistant Enterobacteriaceae (CRE) to ICU Patients
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