year. S. pyogenes infections disproportionately affect low-income countries where routine surveillance is not available. The objective of this study was to investigate the molecular epidemiology and antibiotic resistance of clinically relevant S. pyogenes isolates in Ulaanbaatar, Mongolia, to better understand the burden in this under-served population.

Methods. Clinical S. pyogenes isolates (n = 41) collected at the Bacteriological Reference Laboratory, National Center for Communicable Diseases, Ulaanbaatar, Mongolia, were cultured and characterized using PCR techniques. The emm gene was sequenced and emm type was assigned as per Center for Disease Control and Prevention (CDC) methods and guidelines. Multi-locus sequence typing (MLST) was carried out on selected isolates (n = 15). Antibiotic susceptibility testing (AST) was done via the Vitek-2 system as per manufacturer's instructions.

Results. We observed 18 distinct emm types among the 41 S. pyogenes isolates, stG6792.0 was the most common emm type, accounting for more than one-third of the isolates (15/41) followed by emm2.0 (ST55) (5/41) and emm 82.0 (ST314) (2/41). A total of seven sequence types (STs) were detected among 15 tested isolates. The most common ST type was ST55 accounting for one-third of the isolates (5/15). Most of the isolates were susceptible to all tested drugs.

Conclusion. The findings of this study provided some insights regarding the molecular characteristics of S. pyogenes in Mongolia that will be crucial for future surveillance. The high prevalence of ST55 suggests the potential for dissemination of a clonal strain in this population. The SNVs included a frameshift mutation in the putT gene, which encodes a formate-dependent phosphoribosylglycinamidine formyltransferase involved in de novo purine synthesis, and missense mutations in dnaA and the DNA methylation hsdM genes. The emm gene was sequenced and emm type was assigned as per manufacturer's instructions. Only one (6.2%) was PVL-positive. The clinical spa types were compared with ones from our data base of S. aureus strains previously collected and sequenced from the community and environment in Northeast Ohio.

Results. A total of 51 spa types were detected from 129 S. aureus clinical isolates (discriminatory index, 0.876; 95% confidence interval [CI], 0.827–0.925; Table 1). The most common spa types were 008 (42/129, 32.6%), 002 (16/129, 12.4%), and c334 (6/129, 4.7%). In conclusion, the most frequently detected spa types from the environmental samples were t189 (40/257, 15.6%), t002 (16/257, 6.2%), and t008 (11/257, 4.3%). Among the S. aureus isolates (n = 145), 45 were PVL-positive (30.8%) and 94 (66.7%) carried mecA. Of the 42 t008 (ST8/USA300; a common community-associated strain) isolates, 35 (83.3%) were methicillin-resistant S. aureus (MRSA) (based on the presence of the mecA gene) and 35 (59.5%) were PVL-positive. Thirteen of the sixteen (81.2%) 002 (ST5/USA100; a common hospital-associated strain) were MRSA and only one (6.2%) was PVL-positive.

Conclusion. There is considerable overlap of S. aureus strains present in clinical samples with those found in the environment. This finding should draw attention to the need for more effective prevention strategies to reduce the risk of transmission of S. aureus, including MRSA, in the environment to humans.
Strain: if of isolates with valid value: 129
# of different values: 1

| Strain | # of isolates | % of isolates with valid value |
|--------|---------------|--------------------------------|
| 0      | 1             | 32.4                           |
| 1      | 4             | 32.4                           |
| 2      | 2             | 32.4                           |
| 3      | 1             | 32.4                           |
| 4      | 1             | 32.4                           |

Table 1. Spa Types

Disclosures. All authors: No reported disclosures.

234. Reversal of Carbapenem and Amikacin Susceptibilities in Isogenic Klebsiella pneumoniae From a Patient with Persistent Bacteriuria
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Session: 39. Diagnostics: Sequencing and Typing
Thursday, October 3, 2019: 12:15 PM

Background. Carbapenem-resistant Enterobacteriaceae constitute an urgent public health problem worldwide. In 2018, carbapenem-resistant Klebsiella pneumoniae (CR-KP) caused outbreaks of infection in 4 intensive-care units (ICUs) in a tertiary-care hospital in Egypt. We aimed to identify the clonal relatedness of isolates by whole genome sequencing (WGS).

Methods. Identification and antibiotic susceptibility testing was done by VITEK-2. Eleven isolates showed identical resistance pattern (resistant to Amikacin, gentamicin, imipenem, meropenem, levofloxacin, and Piperacillin/Tazobactam) and were susceptible only to colistin. Caba-NP test was positive for carbapenemase production. The 11 isolates were studied by WGS by illumina MiSeq in a reference lab in Cairo University Hospital.

Results. In only one ICU, WGS identified 4 outbreak isolates of CR-KP that group together as a tight clonal cluster, suggestive of intra-ward transmission event. The outbreak isolates belonged to MLST 147. All isolates carried blaKPC, blactB, and blaOXA, encoding ESBL and carbapenemase activity. One identified resistance genes were Str, AAD/1, MsrE, Tet, and DfrA, encoding resistance to aminoglycosides, macrolides–lincomamide–streptogramin, tetracycline and trimethoprim/sulphonamides. Virulence genes included Yersiniabactin, aerobactin, and wzi64.

Disclosures. All authors: No reported disclosures.

235. Next-Generation Sequencing for Investigation of Hospital Outbreak of Carbapenem-Resistant Klebsiella pneumoniae
Amani Kholy, MD, PhD1; May Mohamed Sherif. Soliman, MD, PhD2; Arwa Ramadan, Pharm D1 and Jehan El-Kholy, MD, PhD3; 1Cairo University, Egypt; 2Dar Al Fouad Hospital, Cairo, AI Qahirah, Egypt
Session: 39. Diagnostics: Sequencing and Typing
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Background. Carbapenem-resistant Enterobacteriaceae cause outbreaks of infection in 4 intensive-care units (ICUs) in a tertiary-care hospital in Egypt. We aimed to identify the clonal relatedness of isolates by whole genome sequencing (WGS).

Methods. Identification and antibiotic susceptibility testing was done by VITEK-2. Eleven isolates showed identical resistance pattern (resistant to Amikacin, gentamicin, imipenem, meropenem, levofloxacin, and Piperacillin/Tazobactam) and were susceptible only to colistin. Caba-NP test was positive for carbapenemase production. The 11 isolates were studied by WGS by illumina MiSeq in a reference lab in Cairo University Hospital.

Results. In only one ICU, WGS identified 4 outbreak isolates of CR-KP that group together as a tight clonal cluster, suggestive of intra-ward transmission event. The outbreak isolates belonged to MLST 147. All isolates carried blaKPC, blactB, and blactA, encoding ESBL and carbapenemase activity. One identified resistance genes were Str, AAD/1, MsrE, Tet, and DfrA, encoding resistance to aminoglycosides, macrolide–lincomamide–streptogramin, tetracycline and trimethoprim/sulphonamides. Virulence genes included Yersiniabactin, aerobactin, and wzi64.

Disclosures. All authors: No reported disclosures.

236. The Comparative Utility Of Metagenomic Next-Generation Sequencing and Universal PCR for Pathogen Detection on Cerebrospinal Fluid: A Retrospective Analysis From A Tertiary Care Center
Andrew D. Kerkhoff, MD, PhD1; Michelle Mattzko, MD, PhD2; Charles Chiu, MD, PhD3; Steve Miller, MD, PhD and Jennifer M. Babik, MD, PhD4; 1UCSF, San Francisco, California
Session: 39. Diagnostics: Sequencing and Typing
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Background. Carbapenem resistance in the initial KP is likely explained by overexpression of cephalosporinases in combination with changes in membrane permeability, while amikacin resistance is likely due to AMEs. Since no significant gene variation was observed in the susceptible KP, reversal of resistance was likely due to decreased expression of cephalosporinases and AMEs after antibiotics were stopped. Incorporation of antibiotic history and host factors can explain clinically important changes in antibiotic resistance.