Multivariate regression analyses were used to adjust for demographic variables and Charlson Comorbidity Index.

**Results.** A total of 26,415 patients underwent LT in the study period, of which 180 had MSSA and 160 had MRSA infection reported. The mean age was 51.5 years and 35.6% were female. Patients with MSSA and MRSA displayed significantly higher inpatient mortality rates (11.1% and 9.4%, respectively) compared with non-MSSA/MRSA patients (3.4%) who underwent LT (P < 0.001). After adjusting for confounders, patients with MSSA infection displayed higher mortality odds (aOR: 4.45, P < 0.01), while patients with MRSA infection had non-statistically significant higher inpatient mortality odds (aOR: 3.10, P = 0.12) compared with patients without MSSA/MRSA infection. Both MSSA and MRSA cohorts displayed higher mortality odds if the infection resulted in sepsis (aOR: 9.92 and 5.70, respectively; P < 0.01).

**Conclusion.** There is a direct correlation between *S. aureus* bacteremia and increased mortality rates and incidence of sepsis and shock in LT recipients. Patients with *S. aureus* bacteremia spent more days in hospital and had higher cost of healthcare. Preventing and aggressively treating *S. aureus* infections in the immediate post-LT setting is key to reducing mortality, morbidity and resource utilization in patients undergoing LT.

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

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**228. Early Recurrent Postoperative Bloodstream infections in Living-Donor Liver Transplant Recipients**

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**Session:** 38. Transplant ID: Bloodsteam Infections

**Thursday, October 3, 2019: 12:15 PM**

**Background.** Bloodstream infections (BSIs) represent a poor prognosis in living-donor liver transplant recipients (LDLT Rs). Some patients develop recurrent BSIs. We evaluated the impacts of ER-BSIs on outcomes in LDLT-Rs.

**Methods.** All LDLT-Rs with follow-up data between January 2008 and December 2016 were included. Early BSIs (E-BSIs) defined as BSI events within 2 months after LDLT. ER-BSI was defined as new-onset BSI within 2 months due to another pathogen besides the previous (post-LT) pathogen. Both MSSA and MRSA cohorts displayed higher mortality odds if the infection resulted in sepsis (aOR: 9.92 and 5.70, respectively; P < 0.01). Enterococcus faecalis was the most relevant risk factor for 1-year mortality (adjusted OR = 8.26; 95% CI = 4.30–15.88).

**Conclusion.** There is a direct correlation between *S. aureus* bacteremia and increased mortality rates and incidence of sepsis and shock in LT recipients. Patients with *S. aureus* bacteremia spent more days in hospital and had higher cost of healthcare. Preventing and aggressively treating *S. aureus* infections in the immediate post-LT setting is key to reducing mortality, morbidity and resource utilization in patients undergoing LT.

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

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**229. Molecular Typing by RAPD, Characterization and Antibiotic Resistance Profile of ESBL Producing and Non-ESBL Producing Klebsiella Species Isolated From Diarrheal Stool and Environmental Samples**

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**Session:** 39. Diagnostics: Sequencing and Typing

**Thursday, October 3, 2019: 12:15 PM**

**Background.** Extended-spectrum β-lactamase is a major public health problem in hospitals and community that mediate resistance to Penicillins, Cephalosporins, and Monobactams. Data regarding the detection of TEM, CTX-M, and SHV genes by molecular techniques and typing by RAPD in ESBL producing bacteria can be useful in epidemiology and risk factors associated with infections.

**Methods.** Total of 140 samples were collected. Well water (n = 50), Fish effluents (n = 40), and Diarrheal stool samples (n = 50). Antibiotic susceptibility test was done using the Kirby-Bauer disc diffusion method. Phenotypic detection of ESBL enzyme was done by Double disk diffusion test. PCR analysis was carried out for β-lactamase (blaTEM, SHV, and CTX-M). Molecular Typing was done by RAPD.

**Results.** 38 (57.5%) Klebsiella spp. isolated from Fish Effluents,11 (57.8%) from Well water and 15 (18.98%) from Diarrheal stool samples. ESBL producers were 4 (26.66%) from stool and 12 (31.57%) from fish effluents. Stool isolates showed high resistance to Ampicillin (86.7%), Cefuroxime (83.3%), Ceftazidine (76.7%), and Cefazidime (70%). Fish effluents were more resistant to Cefepime sulbactum (95.9%), Ampicillin (81.6%) while well water isolates showed high resistance to Ampicillin (94.7%) and Erythromycin (73.7%). Molecular identification showed the presence of more than 2 genes among the isolates. Prevalence of gene bla-TEM was highest, followed by bla-CTX-M and bla-SHV. Genetic relatedness are expressed as percentage similarity and presented as dendogram.

**Conclusion.** The study shows high prevalence of ESBL among Klebsiella isolates mainly from Fish effluents and diarrheal stool samples. It shows 24% ESBL positive rate. Antibiotic-resistant bacteria from fish effluents highlights the associated human health risk when they enter food chain and become passive carriers. Practice of routine ESBL testing with conventional antibiotic susceptibility testing would be useful for combating multi drug resistance.

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**230. Molecular Typing of Streptococcus pyogenes Isolates Collected at Mongolian Hospital (Ulaanbaatar, Mongolia)**

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**Session:** 39. Diagnostics: Sequencing and Typing

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**Background.** Streptococcus pyogenes is a significant cause of morbidity and mortality worldwide causing an estimated 1.8 million cases and 517,000 deaths each

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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 Centers 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 research. These findings may help to devise better treatment strategies for S. pyogenes infections, and potentially inform vaccine development.

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231. Microbial cell-free DNA Sequencing to Detect Borrelia burgdorferi DNA in the Plasma of Pediatric Patients with Lyme Disease
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Session: 39. Diagnostics: Sequencing and Typing
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Background. Diagnosing Lyme disease often involves laboratory evaluation, yet available tests have limitations. Serology remains negative for weeks after infection occurs, and may then remain positive for years. Borrelia burgdorferi blood PCR testing has low sensitivity, rendering it unhelpful. We sought to determine whether an emerging technology, next-generation sequencing (NGS) of microbial cell-free DNA (mcDNA), can detect B. burgdorferi DNA in the plasma of pediatric patients with erythema migrans (EM).

Methods. Patients aged 1–17 years with a clinically-identified single or multiple EM were enrolled. Two clinical investigators were required to agree on the EM finding, with no evidence of another diagnostic diagnosis. Subjects were excluded if they had Lyme disease, had received antibiotics within 30 days prior to enrollment, or if the rash had resolved before the first blood draw. Three blood samples were taken during the study period: one before antibiotics were administered, then 1–3 weeks and 2–3 months after. At each timepoint, plasma was tested for Lyme disease using C6 antibody with reflex to Western Blot and mcDNA sequencing (Karius, Inc., Redwood City, CA).

Briefly, mcDNA was extracted from plasma and NGS performed. Human reads were removed and remaining sequences were aligned to a curated microbial database. Only mcDNA sequences matching >90% of B. burgdorferi DNA by mcDNA sequencing. No other infections, including other tick-borne infections, were detected.

Conclusion. NGS of mcDNA did not identify B. burgdorferi DNA in the plasma of pediatric patients with active EM rashes. This approach is unlikely to be helpful in diagnosing early localized Lyme disease. This may be because spirochetes are localized to the periphery of the rash in EM and spirochetemia likely occurs at later stages of infection. Follow-up studies are planned to investigate how NGS of mcDNA performs during early and late disseminated Lyme disease.

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232. Genomic Evidence for Dissemination of Mycobacterium marinum in an HIV Patient with Multifocal Cutaneous Disease
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Background. Hematogenous dissemination has been proposed to explain multifocal cutaneous disease caused by Mycobacterium marinum in certain patients. Treatment duration for disseminated disease is often months longer than for skin infection alone. However, distinguishing multiple independent inoculation events from dissemination has relied primarily on clinical judgement. Additionally, whether temperature-sensitive non-tuberculous mycobacteria such as M. marinum are indeed capable of invading the vascular space at core body temperature is debated. Here we used whole-genome sequencing (WGS) of serial isolates from a single patient with multifocal cutaneous M. marinum infection to distinguish dissemination of a clonal strain from multiple inoculation events.

Methods. A 35-year-old male with HIV (CD4 of 66 cells/μL) presented with a two-month history of a non-healing M. marinum wound on his left elbow (isolate MM0). This was followed a month later after initiation of antiretroviral therapy by a second M. marinum lesion on the right heel (MM1) without history of repeat inoculation, and increased swelling and erythema of the wound on the left arm (MM2) consistent with paradoxical immune reconstitution inflammatory syndrome. A PacBio genome was generated for MM0 and short read Illumina genomes were generated for MM1 and MM2.

Results. All isolates were found to be closely related, with MM1 and MM2 distinguished from MM0 by one and five single-nucleotide variants (SNVs), respectively. Given the substantial genetic heterogeneity among environmental M. marinum strains, such close relatedness of these isolates suggests common origin, and provides strong evidence for dissemination of a clonal strain in this patient. The SNVs included a frameshift mutation in the purT gene, which encodes a formate-dependent phosphoribosylpyrimidine formyltransferase involved in de novo purine synthesis, and missense mutations in atsA and the DNA methylase kudM. All isolates grew at 35°C, compared with the optimal growth temperature of 30°C typically observed for M. marinum, suggesting thermotolerance permissive for dissemination.

Conclusion. These results demonstrate the potential role of WGS for providing superior evidence of disseminated infection with M. marinum.

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233. The Epidemiology, Genomics, and Evolution of Staphylococcus aureus in Northeast Ohio
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Session: 39. Diagnostics: Sequencing and Typing
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Background. Infections due to S. aureus result in significant morbidity, mortality, and healthcare expense. We sought to identify the strains of S. aureus causing infections in hospitalized patients in Northeast Ohio and determine whether those strains are reflective of the S. aureus strains present in the surrounding environment.

Methods. The study was approved by the Institutional Review Board at Cleveland Clinic Akron General. Clinical S. aureus isolates (n = 300) were cultured and PCR was used to amplify the staphylococcus protein A (spa), Panton-Valentine Leukocidin (PVL), and mecA genes. 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 comparison, the most frequently detected spa types from the environmental samples were 1189 (40/257, 15.6%), 002 (16/257, 6.2%), and 008 (11/257, 4.3%). Among the S. aureus isolates (n = 146), 45 were PVL-positive (30.8%) and 94 (66.7%) carried mecA. Of the 42 0088 (ST8/USA300), a common community-associated strain, 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.