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 guideline. 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 emm82.0 (ST314) (2/41). A total of seven sequence types (STs) were detected among 15 tested isolates. The most common ST type was ST35 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. The 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 evidence of an alternative diagnostic evaluation. Subjects were excluded if there was a history of treatment before enrollment. Plasma samples from each patient were drawn at baseline and before antibiotics were administered, then 1–3 weeks and 1–3 months later. The microbiologic samples were tested for Lyme disease using the enzyme-linked immunosorbent assay (ELISA) and capture enzyme-linked immunosorbent assay (cELISA) tests. McDNA was subsequently extracted and tested for Borrelia burgdorferi DNA using a real-time PCR assay. McDNA testing was performed at follow-up visits.

Results. We enrolled 5 subjects (ages 4–15 years old, median age 4). Four subjects had a single EM and negative Lyme serology. One subject had approximately 20 EMs and negative Lyme serology. One subject had approximately 20 EMs and negative Lyme serology. One subject had approximately 20 EMs and negative Lyme serology. One subject had approximately 20 EMs and negative Lyme serology. One subject had approximately 20 EMs and negative Lyme serology. One subject had approximately 20 EMs and negative Lyme serology.

Conclusion. NGS of mcDNA did not identify B. burgdorferi DNA in the plasma of pediatric patients with active EM rash. This approach is unlikely to be helpful in diagnosing early localized Lyme disease.

Disclosures. All authors: No reported disclosures.

231. Microbial cell-free DNA Sequencing to Detect Borrelia burgdorferi DNA in the Plasma of Pediatric Patients with Lyme Disease

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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 evidence of an alternative diagnostic evaluation. Subjects were excluded if there was a history of treatment before enrollment. Plasma samples from each patient were drawn at baseline and before antibiotics were administered, then 1–3 weeks and 1–3 months later. The microbiologic samples were tested for Lyme disease using the enzyme-linked immunosorbent assay (ELISA) and capture enzyme-linked immunosorbent assay (cELISA) tests. McDNA was subsequently extracted and tested for Borrelia burgdorferi DNA using a real-time PCR assay. McDNA testing was performed at follow-up visits.

Results. We enrolled 5 subjects (ages 4–15 years old, median age 4). Four subjects had a single EM and negative Lyme serology. One subject had approximately 20 EMs and negative Lyme serology. One subject had approximately 20 EMs and negative Lyme serology. One subject had approximately 20 EMs and negative Lyme serology. One subject had approximately 20 EMs and negative Lyme serology. One subject had approximately 20 EMs and negative Lyme serology.

Conclusion. NGS of mcDNA did not identify B. burgdorferi DNA in the plasma of pediatric patients with active EM rash. This approach is unlikely to be helpful in diagnosing early localized Lyme disease.

Disclosures. All authors: No reported disclosures.

233. The Epidemiology, Genomics, and Evolution of Staphylococcus aureus in Northeast Ohio

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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 results were 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 034 (6/129, 4.7%). In comparison, the most frequently detected spa types from the environmental isolates were 018 (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 42 008 type (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.