Molecular typing of *Streptococcus pyogenes* isolates collected at a Mongolian Hospital (Ulanbaatar, Mongolia)

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*Streptococcus pyogenes* is a significant cause of morbidity and mortality worldwide, causing an estimated 1.8 million cases and 517,000 deaths each year. *S. pyogenes* infection disproportionately affects low-income countries where routine surveillance is not available. The objective of this study was to investigate the molecular epidemiology and antibiotic resistance patterns of clinically relevant *S. pyogenes* isolates to better understand the burden in this underserved population.

A convenience sample of 41 *S. pyogenes* isolates collected between 2007 and 2016 by the Bacteriological Reference Laboratory, National Center for Communicable Diseases, Ulanbaatar, Mongolia, and sent to our lab for molecular typing. The *emm* gene was sequenced and *emm* type was assigned. We also carried out multi-locus sequence typing (MLST); antibiotic susceptibility testing was carried out via the Vitek-2 system.

We observed 18 distinct *emm* types among the 41 *S. pyogenes* isolates. stG6792.0 was the most common *emm* type, accounting for almost one-third of the isolates followed by *emm*2.0 and *emm* 82.0. 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. Additional MLST analysis is in progress. Most of the isolates were susceptible to all tested drugs.

The findings of this study provided some insights regarding the molecular characteristics of *S. pyogenes* in Mongolia that will be crucial for future surveillance studies. The information about antibiotic susceptibility patterns and molecular types can help to devise better treatment strategies for *S. pyogenes* infections, and inform vaccine development.

Key words: *Streptococcus pyogenes*, Mongolia, *emm* typing, multi-locus sequence typing, drug resistant