**Title:** Molecular epidemiology and phylodynamic and phylogeographic analysis of Community-associated Methicillin-resistant *Staphylococcus aureus* transmission: An Emergency Department Population Sampling Strategy

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**Research Project Description**

Methicillin-resistant *Staphylococcus aureus* (MRSA), a leading cause of healthcare-associated infections, has significantly amplified healthcare costs. While the sub-strains and transmission patterns of this bacterium are yet to be completely understood, Community-associated Methicillin-resistant *Staphylococcus aureus* (CA-MRSA) is rapidly proliferating within healthcare settings. Further, there is scarce literature focusing on the transmission of CA-MRSA within community settings and the impact of this transmission on the increased prevalence of CA-MRSA infections in healthcare settings. Novel uses of molecular tools, such as whole genome sequencing (WGS) and single nucleotide polymorphism analysis, are resulting in more powerful phylogenetic and phylogeographic techniques that can infer origin and transmission of MRSA subtypes over time and through a geographic area, especially when combined with patient level information. Emergency departments have become the entryway for large populations of patients into the healthcare system and represent an extensive frontline when considering an interface for transmission interface between community and hospital settings. A well-planned isolate sampling strategy in emergency department populations may facilitate opportunities to conduct spatiotemporal analyses and hypothesis testing, which could be essential to developing novel strategies for infection control and eradication of this particularly virulent agent.

**Purpose and rationale:**

We propose to integrate *Staphylococcus aureus* protein A molecular typing and whole genome next-generation sequencing with phylodynamic analysis and patient-level epidemiological data to analyze the spatiogeographical transmission of CA-MRSA among patients presenting to the emergency department with skin and soft tissue infections (SSTI).

**Objectives:**

The study objectives include:

1. To characterize the diversity of MRSA isolates from emergency department patients presenting with an acute SSTI using cultures and next-generation WGS and phylogenetic analysis.

2. To determine patient-level characteristics, including social and medical history, associated with a presentation related to SSTIs.

3. Conduct a phylogenetic analysis of MRSA transmission to identify genetic clustering of cases among patient populations, risk groups, or patient geographic location in the community.

4. Compare patient-level characteristics and phylogenetic clustering between pediatric and adult patients presenting with SSTIs.

**ROLE OF MEDICAL STUDENT** – The medical student will be responsible for obtaining informed consent from ED patients eligible and willing to participate. The student will also be responsible for survey administration, data entry, specimen collection and processing. The student will contribute to data analysis, data interpretation and presentation.
REFERENCES


