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Project Summary/Abstract
There has been a dramatic increase in infections caused by methicillin-resistant *Staphylococcus aureus* (MRSA) that originate in the community. In the United States, a single *S. aureus* epidemic clone, USA300, has been responsible for the vast majority of these infections. Although USA300's rapid spread is well documented, few studies have investigated the basis for its remarkable transmissibility. Overcoming this gap in knowledge is critical to the design of interventions that can effectively prevent dissemination of these epidemic clones at the population level. We recently conducted an NIH funded, case-control study of MRSA transmission in Northern Manhattan. A major limitation of this study was our inability to trace transmission pathways within infectious networks in the community. This was in part due to the poor resolution of current molecular typing techniques. Recent studies suggest that more detailed sequence analysis, such as that provided by whole genome sequencing, by documenting the phylogenetic relationship of different strains, can provide far greater information on paths of transmission in the community. The goal of this study is to test the utility of whole genome sequencing as a tool to trace the spread of *S. aureus* in the community. To accomplish this goal we will utilize our well-characterized collection of USA300 isolates from the MRSA transmission study. These isolates are linked to the detailed study subject database that contains sociodemographic, medical and *S. aureus* risk factor information. The ability of whole genome sequencing to discriminate among strains and as a result to help identify how these strains spread will be compared with the currently available techniques. Based on the genome sequence, a phylogenetic tree will be assembled of the USA300 isolates and will serve as the basis for a number of different comparisons. The primary outcome measure will be the proximity of isolates on the phylogenetic tree. The comparisons will include the source of the isolates (e.g. colonization, infection, environment), the spatial location of the strain isolation and whether previously undetected transmission pathways can be identified. Whole genome sequencing has the potential to provide unique insight into the basis for the dramatic emergence of this highly successful clone, and perhaps become the standard approach for these types of investigations. The availability of the USA300 collection coupled with the extensive study subject data provides a unique opportunity to address this question.
