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Project Overview: Infections caused by multidrug-resistant bacteria (MDRB), a critical problem in healthcare settings, are an increasing concern in the community (1). Methicillin resistant staphylococci are now responsible for the majority of community-acquired skin and soft tissue infections (2). Extended spectrum beta-lactamase producing Enterobacteriaceae are found in our meats and fluoroquinolone-resistant *Clostridium difficile* is now a community-based pathogen (3,4). Strategies to track this trend and identify risk factors that contribute to the emergence of these MDRB in the community are needed. Traditional surveillance methods, designed to document the emergence and spread of specific bacterial pathogens, have been unable to provide insight into the overall patterns of antimicrobial resistance that have emerged in different regions.

The overall goal of this study is to pilot a new approach to infectious disease surveillance. Rather than focusing on selected MDRB, we will map the distribution of antimicrobial resistance genes across New York City (NYC). We will then use this map to identify individual and neighborhood level factors that contribute to regional differences in the distribution of these genes. The result will be an “antibiotic resistome” map for NYC.

This approach builds on recent studies that have used next generation sequencing to map the prevalence of antibiotic resistance genes in such diverse environmental settings as farms, waterways and healthcare facilities (5-7). The result, based on the presence of antimicrobial resistance genes identified from a diversity of bacterial species, is expressed as an antibiotic resistance profile or an “antibiotic resistome” for the particular environment being studied.

We hypothesize that this approach will allow us to provide a more comprehensive picture of the diversity of antimicrobial resistance than is currently possible. It will also allow us to identify variables such as antibiotic use, socioeconomic status or disease frequency (e.g., diabetes, obesity) in different neighborhoods that are associated with an increased risk of antimicrobial resistance. By identifying these risks we will be able to develop new intervention strategies to reduce the spread of MDRB.