Salmonella is a leading bacterial cause of foodborne illness in the United States. It is a remarkably diverse species that can be separated into over 2500 serovars, many of which exhibit different phenotypes, including virulence, antimicrobial resistance, and host restriction. Poultry is a major *Salmonella* reservoir, but current culture-based detection methodology is limited to identifying the most abundant serovars while those at lower frequencies remain undetected.

The CRISPR arrays in *Salmonella* are highly conserved, and the spacer content and organization are well correlated with serovar identity. CRISPR-SeroSeq is an amplicon based next generation sequencing tool that exploits this characteristic to be able to map frequencies of *Salmonella* serovars within a single population. This allows us to directly address dynamic changes at the serovar level in mixed populations and is particularly important when trying to detect serovars commonly associated with foodborne illness.

Initial studies using CRISPR-SeroSeq in both poultry environments and a large watershed in the Northeast have allowed us to analyze *Salmonella* populations for the first time.