Antibiotic resistance and gastroenteritis: Determining host-plasmid associations in the human gut.

Quince group

Bacterial gastroenteritis causes over 525,000 deaths worldwide and is often prevalent in countries with a rapidly expanding population and developing infrastructure. Diarrheagenic *Escherichia coli* are significant causative agents of bacterial gastroenteritis which result in over 300 million illnesses and 200,000 deaths each year, with a disproportionate fatality rate in children under five.

Treatment of gastroenteritis has become more challenging due to the emergence of resistance to primary-use and broad-spectrum antibiotics. Extended spectrum beta lactamases (ESBLs) are often associated with pathogenic *E. coli* and are comprised of a complex and diversifying class of resistance enzymes that are often genetically encoded on mobile plasmids. One of the most common and globally disseminated plasmid mediated ESBL genes that is frequently associated with gastroenteritis caused by *E. coli* is $bla_{\text{CTX-M-15}}$.

What is currently unclear is how gastroenteric infections caused by antibiotic resistant strains of *E. coli* effect the gut resistome following symptomatic recovery. Therefore, understanding the community level dynamics and host associations of $bla_{\text{CTX-M-15}}$ in the gut environment will better elucidate the long-term health impacts of bacterial gastroenteritis infections at the global level.

We have recently begun development of a long-read chromatin conformation sequencing protocol that attempts to provide targeted information on host-plasmid associations in a complex bacterial community down to the species level. This project aims to further develop the sequencing protocol to target $bla_{\text{CTX-M-15}}$ in simplistic whole cell mock communities. The candidate will develop skills in in-silico oligo design, molecular laboratory techniques, long read sequencing and basic bioinformatics approaches.