

(1) Submission ID#1539913

Population Genomics of *Neisseria gonorrhoeae*

Author(s)

Duncan Carruthers-Lay, n/a

PhD Candidate

University of Toronto

Emil Jurga, n/a

MsC

Molecular Genetics

Scott Gray-Owen, PhD

Professor

University of Toronto

John Parkinson, PhD

Professor

University of Toronto

Background

Neisseria gonorrhoeae is an emerging pathogen of global concern due to the emergence of widespread antimicrobial resistance (AMR). A better understanding of underlying population structures and its diverse collection of infection-associated genomic factors will aid in combatting the spread of this rapidly developing public health threat.

Aim/Methods

We began by collecting a set of ~7400 genomic sequences from the NCBI Sequence Read Archive and aligning them to the reference genome of *N. gonorrhoeae* strain FA1090 to identify and define a reference set of maximally diverse isolates. This set encompasses 767 isolates from around the world and forms the basis for the following analyses. Using the population genomics tool PopNet developed by the Parkinson lab, I interrogated population structures using a whole genome approach to compare and contrast with the commonly used MLST scheme for *N. gonorrhoeae* typing. We also sought to compare the pangenome of *N. gonorrhoeae* across the 767 isolates which may include relevant virulence-associated genes or genetic elements absent in the core genome.

Results

We identified a core genome of 1526 genes, and 8105 accessory genes for a total of 9631 unique genes shared among the isolates. We began by identifying mobile genetic elements, prophage genes and phase variable genes. We then used the Comprehensive Antibiotic Resistance Database Resistance Gene Identifier to identify AMR associated genes and the Scoary tool to analyze genes overrepresented in isolates with

multiple determinants of AMR. We found strong associations between the presence or absence of accessory genes and PopNet groups, indicating genomic and evolutionary relationships. We also analyzed connections between mobile elements, AMR and phase variable genes, indicating possible linkage of specific virulence-associated traits.

Conclusions

This analysis will provide a powerful resource for researchers in the gonococcal field and will reveal important insights into gonococcal population structures around the world.