

WHOLE GENOME SEQUENCING OF BACTERIA, HOW IT IS ROUTINELY USED IN PUBLIC HEALTH / HOSPITAL SETTINGS, AND APPLICATIONS IN THE STUDY OF GONORRHOEA AND ASSOCIATED ANTIMICROBIAL RESISTANCE

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Background:

Whole genome sequencing (WGS) has streamlined microbiology testing particularly in public health surveillance, source tracking and outbreak investigations. The Public Health Microbiology (PHM) laboratory is the reference laboratory for all notifiable bacterial infections in Queensland, including *N. gonorrhoeae*. The laboratory has been employing genomics for disease surveillance for over five years and is now exploring the integration of WGS into gonococcal source tracking, antimicrobial resistance gene extrapolation and direct clinical sequencing on PCR positive specimens.

Methods:

The use of WGS for public health surveillance and outbreak investigations will be discussed. All Queensland *N. gonorrhoeae* isolates are referred to the PHM laboratory for antibiotic resistance phenotypic testing. The PHM laboratory are establishing enhanced gonococcal surveillance through in house genomic sequencing using a NATA accredited workflow, in order to generate genotyping information including sequence type, NG-MAST and NG-STAR profiles, extrapolate resistance genes and mutations and perform cluster analysis based on cgMLST and/or core SNP detection for determine phylogenetic relationships. Additionally, the PHM laboratory has been exploring the application of deep sequencing directly on clinical samples to generate genotyping information in the absence of a culture.

Results:

Queensland *N. gonorrhoeae* epidemiological understanding is currently limited in the absence of molecular typing. Genomics offers the ability to not only efficiently generate extensive genotyping information useful for distinguishing endemic circulating strains from sporadic strains but to also visualise genetic relatedness and assist in understanding why some strains are endemic. Direct deep sequencing on PCR positive clinical extracts has demonstrated that genotype and resistance genes consistent with the predicted strain type can be extrapolated.

Conclusion:

WGS is already providing efficient enhanced surveillance in microbiology reference laboratories. Studies such as this are establishing the feasibility of whole genome sequencing for not only population based surveillance of gonococcal disease but the possibility for near real time management of disease clusters. Furthermore, deep sequencing may be of assistance in providing molecular epidemiological information for the approximately 75% of *N. gonorrhoeae* notifications generated by PCR diagnosis, which do not have a respective culture available for typing.

Disclosure of Interest Statement:

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