

THE MOLECULAR EPIDEMIOLOGY OF NEISSERIA GONORRHOEAE IN NEW SOUTH WALES, 2012-2014

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Introduction: Molecular tools can enable us to better understand *Neisseria gonorrhoeae* (NG) epidemiology. In this study, we used genotyping technology to examine diversity and temporal differences in NG genotypes in New South Wales (NSW) over a 2-year period.

Methods: All clinical isolates of NG were acquired from NSW during the first six months of 2012 (n = 767) and 2014 (n = 864). These were genotyped using the Sequenom MassARRAY iPLEX technology to distinguish 14 informative single nucleotide polymorphisms on NG house-keeping genes, commonly used in multilocus sequencing typing investigations, and 12 mutations associated with resistance to azithromycin, ciprofloxacin, penicillin and ceftriaxone.

Results: A total of 162 distinct genotypes were identified over the two year period: 90 in 2012 and 108 in 2014. Only 36 genotypes were present in both years, 54 were observed in 2012 only and 72 in 2014 only. The 10 most common genotypes accounted for 69% of all infections, of which 7 were present in both years.

The majority of genotypes (94%) were presumed to be among men who have sex with men according to the male to female ratio (> 95% of samples from men). The most prevalent genotype in 2012, which comprised 22% of isolates and had the second highest prevalence of 13% in 2014, was presumed to be from heterosexuals (33% of samples from women). The most common genotype in 2014 (14% of isolates), was also presumed to be from heterosexuals (26% of samples from women), yet only comprised 3% of isolates in 2012.

Conclusion: Overall, considerable NG genotype diversity was observed. A small number of NG genotypes accounted for a large proportion of infections. Considerable temporal changes were observed, and likely reflect increasing infection rates in certain sexual networks, including amongst heterosexuals, as well as ongoing importation of new genotypes.

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