MOLECULAR EPIDEMIOLOGY: NEISSERIA GONORRHOEAE CIRCULATING AMONGST HETEROSEXUALS IN NEW SOUTH WALES.

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Background:
Molecular methods can enhance our understanding of *Neisseria gonorrhoeae* (NG) epidemiology. Here, we applied NG genotyping and whole genome sequencing to NG isolates from New South Wales.

Methods:
NG isolates collected from NSW in the years 2012 (n = 762) and 2014 (n = 863) were genotyped using MassARRAY iPLEX technology. Whole genome sequencing was selectively applied to isolates from the most common genotype.

Results:
A total of 162 distinct NG genotypes were identified; 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 isolates, with the majority among men who have sex with men. However, the most prevalent genotype in 2012 (22%) and second highest in 2014 (13%), was associated with heterosexuals. Whole genome sequencing analysis was applied to 94 isolates (all females) from this most common genotype; the majority of isolates belonged to one of five clusters, and comprised patients of varying age groups. Several patients had indistinguishable isolates suggesting a common infection source.

Conclusion:
The results provide evidence of sustained transmission of NG amongst heterosexuals in NSW, and highlight the added value of using molecular tools for NG outbreak investigations.