Genomic characterisation of the *Neisseria gonorrhoeae* population structure in Victoria, Australia from 2017-2020

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Background:

Neisseria gonorrhoeae, the causative agent of gonorrhoea, is a major public health threat due to increasing incidence and antimicrobial resistance. Previously, we demonstrated large transmission clusters and lineages of *N. gonorrhoeae* in Victoria, Australia throughout 2017, with some lineages resistant to one or more antimicrobials, suggestive of a competitive advantage. We hypothesised that these lineages would persist into 2019-2020.

Methods:

Clinical data, susceptibility data and genomic data from all non-redundant *N. gonorrhoeae* isolates in Victoria, Australia from two time periods (i) July 1st to December 31st 2017 and (ii) July 1st 2019 to June 30th 2020 were integrated and the dynamics of lineages and transmission clusters over time was assessed.

Results:

Phylogenetic analysis of these *N. gonorrhoeae* isolates showed emergence, consolidation, and expansion of some lineages over time. Notably, there were distinct separations of isolates from 2017 and 2019-2020, even within individual sequence types (STs) and several dominant, globally disseminated, antimicrobial resistant lineages in 2017 subsequently decreased in proportion. Instead, in 2019-2020 there was a substantial increase in the antimicrobial susceptible lineages ST8156 from 12.55% (n=257/2048) in 2017 to 27.59% in 2019-2020 (n=533/1932) and ST11864 from 1.61% (n=33/2048) in 2017 to 17.34% (n=335/1932) in 2019-2020. Further, the antimicrobial resistant lineage ST7363 increased in proportion from 6.59% (n=135/2048) in 2017 to 14.23% (n=275/1932) in 2019-2020. Notably, greater than 70% of all ST7363 isolates in 2019-2020 were resistant to penicillin, tetracycline, and ciprofloxacin. We also described 28 large transmission clusters of ≥10 individuals in 2019-2020, where the 3 largest clusters consisted of ≥100 individuals each and were associated with the three largest STs: ST8156, ST11864 and ST7363.

Conclusion:
These results demonstrate the transformation of the *N. gonorrhoeae* population structure in Victoria over time. Further research is needed to identify the host, pathogen, behavioural and epidemiological factors that are driving these changes.

Disclosure of Interest Statement: