Decreased Neisseria gonorrhoeae genotypic diversity following COVID-19 restrictions in Queensland, Australia 2020

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Abstract

We investigated the potential effects of COVID-19 public health restrictions on the prevalence and distribution of Neisseria gonorrhoeae (NG) genotypes in our Queensland isolate population in the first half of the year 2020. A total of 763 NG isolates were genotyped to examine gonococcal strain distribution and prevalence for the first 6 months of 2020, with 1 January 2020 to 31 March 2020 classified as ‘pre’ COVID-19 restrictions (n = 463) and 1 April 2020 to 30 June 2020 classified as ‘post’ COVID-19 restrictions (n = 300). Genotypes most prevalent ‘pre’ restrictions remained proportionally high ‘post’ restrictions, with some significantly increasing ‘post’ restrictions. However, genotype diversity was significantly reduced ‘post’ restrictions. Overall, it seems public health restrictions (9–10 weeks) were not sufficient to affect rates of infection or reduce the prevalence of well-established genotypes in our population, potentially due to reduced access to services or health-seeking behaviours.
were observed (detailed in Supplementary Table S2); 31 genotypes appeared in both pre- and post-restrictions (total = 707 isolates; pre-restrictions n = 413 isolates; post-restrictions n = 294 isolates), 34 genotypes appeared only in the pre-restriction time period (n = 50 isolates), and 6 genotypes were only observed post-restrictions (n = 6 isolates). Figure 1 illustrates the top 25 genotypes circulating in Queensland in the first 6 months of 2020: G1–G25 comprising the most common genotypes (four or more isolates each) and the remaining genotypes G26–G71 comprising three or fewer isolates. There was no significant reduction in the most common NG genotypes after COVID-19 restrictions eased in Queensland, and in fact, some genotypes proportionally increased (using Fisher’s exact test). These included several genotypes (G2, G3, G5, G6, G10, G12, G13, G15, G16, G20, and G24) with G2, G6, and G13 all exhibiting significant increases post-restrictions; p < 0.05. These genotypes were associated with both heterosexual (G2) and MSM networks (G6 and G13), based on male/female proportion (Figure 1a). G2 was observed in both the major metropolitan area of Southeast Queensland (SEQ) and regional areas of North Queensland (NQ); G6 in SEQ, NQ, and Far NQ; and G13 in SEQ (Figure 1b).

In contrast, there was a significant difference in prevalence for the less-common genotypes (G26–G71) between pre- and post-restriction periods (p < 0.05), with a marked reduction in these genotypes (comprising three or fewer isolates) for both males and females (Figure 1a), across both SEQ and non-SEQ regions (Figure 1b). Notably, there were 46 of the lesser common genotypes in total; of these, 7 were observed in both the pre- and post-restriction periods, whereas 33 were detected in the pre-restriction period, and 6 were detected in the post-restriction period only. This suggests, consistent with the border closures, that the diversity of circulating genotypes relies on both interstate and overseas incursions.

These results show that the public health restrictions for the mandated approximately 10-week period in late March 2020 were not sufficient to affect rates of infection or reduce the prevalence of well-established genotypes in our population. In fact, based on these data, the prevalence of certain NG genotypes significantly increased. While the reasons for these increases are unclear, we can postulate that these were due to no change in sexual relationships with a more limited pool of sexual partners enhancing the proportions of already circulating genotype. Alternatively, this may also suggest that condomless sex escalated during this period and/or access to sexual health services decreased. We postulate that health-seeking behaviours may have also changed during this period of increased restrictions, resulting in non-timely diagnosis and treatment of infection. This highlights the need to consider the implications of a pandemic and subsequent restrictions on other infections.

Limitations-wise, a longer-term study may be warranted along with sexual orientation data for increased precision of sexual networks. Yet overall, based on available data, the only obvious positive impact of the restrictions in terms of gonorrhoea was a reduction in the introduction of novel strains into our population, which potentially reduced the incursion of AMR strains. However, this may only be a reprieve. Notably, FC428, previously detected in Australia [8] and not observed in Queensland in 2020, is now known to be circulating widely in Asia [9, 10]. Such new AMR threats highlight that further enhancing surveillance concerning AMR and associated AMR molecular targets in NG will be valuable as restrictions on local and international travel further ease.
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**Data availability statement.** Data will be made available upon request with the corresponding author.

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