



Title: A changing landscape of *Neisseria gonorrhoeae* genotypes in Queensland

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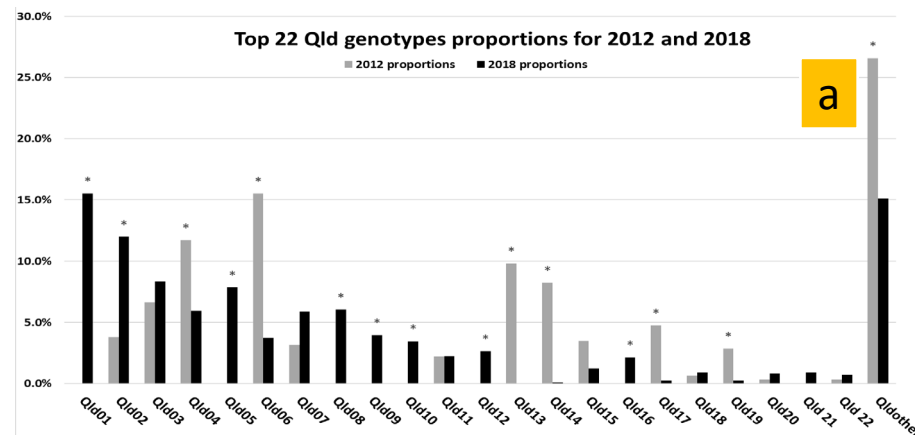
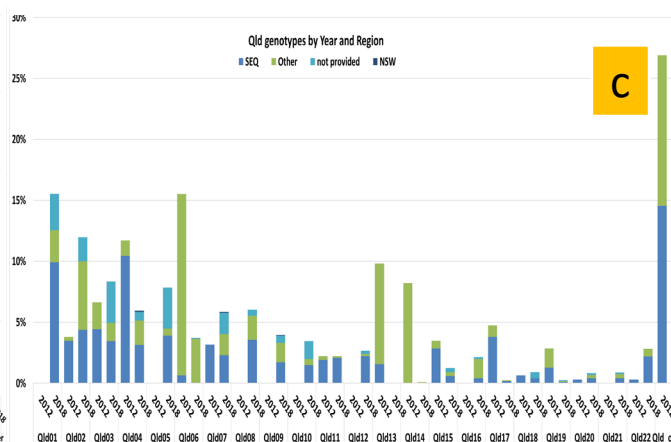
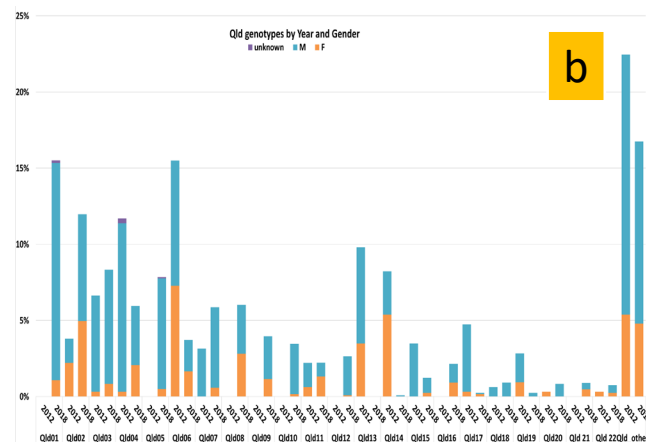


Figure 1 Distribution of the top 22 genotypes in Qld by proportion for 2012 and 2018 (a), gender (b) and region (c)



Results. Overall, n=139 Qld genotypes were observed; **Fig1a** represent the proportion of the most common genotypes Qld01-Qld022 comprising 82.5% of the tested isolates (genotypes comprising ≥ 10 isolates; n=1,260), and all others comprising the remainder 17.5% (n=267). An expansion in genotypes associated with heterosexual cases was observed, specifically Qld02, which comprises near equal male/female ratios (**Fig1b**) significantly expanded between 2012 and 2018 into 'Other' regions (**Fig1c**; $p < 0.05$; 95% CI). Further Qld04 primarily found in SEQ in 2012 (89%), comprising n=1 female and n=35 males, had significantly expanded to 'other' regions by 2018 (**Fig1c**; $p < 0.05$; 95% CI), with females comprising a third of the genotype (**Fig1b**). The most common genotype, Qld01, was not present in our 2012 isolate population, and had spiked to 188 isolates by 2018 (**Fig1a**; $p < 0.05$; 95% CI), with SEQ male majority.

Conclusion. These data reinforce the changing landscape in NG transmission dynamics and the need for enhanced surveillance throughout the state to capture important epidemiological shifts. This is particularly crucial in urban (SEQ) women and remote/regional Qld where 70% of the state's notification arise, yet bacterial culture isolation rates are low.

Methods. Qld NG Isolates from the years 2012 (first 6 months; n=327) and 2018 (n=1,211) were genotyped to inform multi locus sequence type (MLST) and AMR determinants. The results of the above were combined to define a Qld genotype, and its changes in distribution were assessed throughout South East Queensland (SEQ) in comparison to 'Other' Qld regions (North/Far North/Regional).