BACKGROUND:
An ongoing outbreak of syphilis in Australia, first reported in Queensland in 2011 has led to increasing cases of congenital syphilis, including 12 deaths, which disproportionately affect Indigenous Australians.

Between 2013 and 2017, there has been a 135% increase in syphilis notification rates in Australia, seen initially in men-who-have-sex-with-men (MSM) but more recently we have observed the re-emergence of congenital syphilis heterosexual females.

The relationship, if any, between syphilis infections in these infections is currently unknown.

METHODS:
We applied multi-locus sequence typing (MLST) on available Treponema pallidum PCR-positive samples from the beginning of the outbreak (2011) to July 2020.

RESULTS:
A total of 393 samples from 337 males and 56 females were genotyped. A total of 36 different Treponema pallidum sequence types (STs) were identified.

The two most common STs comprised 69% of all samples, including the majority of females (Figure 1). Both strains were common throughout the outbreak and had high male-to-female ratios, using male rectal samples as a proxy for MSM status (Figure 2).

CONCLUSION:
The two predominant syphilis STs had high male-to-female ratios, suggestive of bridging of MSM and heterosexual networks.

Despite enhanced social distancing measures due to the COVID-19 pandemic, we saw very little impact on the prevalence of these major syphilis STs, which stresses the need for targeted public health interventions.

KEY MESSAGES:
• Of 36 STs identified, the two most common STs comprised 69% of all samples
• Bridging of MSM and heterosexual networks may be a key driver of syphilis infections in females in Queensland
• Targeted public health interventions are required to control syphilis in Australia.