

## Two *Treponema pallidum* strains account for the majority of syphilis infections in Queensland, Australia.

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### Background:

An ongoing outbreak of syphilis in Australia, first reported in Queensland in 2011, has led to increasing cases of congenital syphilis, including several deaths.

### Methods:

Here, we applied a multi-locus sequence typing (MLST) approach on available *Treponema pallidum* PCR-positive samples from Queensland, from the beginning of the outbreak to July 2020.

### Results:

A total of 393 samples from 337 males and 56 females were genotyped. Of 36 different *Treponema pallidum* sequence types (STs) observed, the two most common STs, ST1 and ST100 comprised 69% (271/393) of all samples, including the majority of samples in females (44/56; 79%). ST1 was prevalent throughout the entire study period and both ST1 and ST100 remained the most common strains during the year 2020, even where social distancing and other measures were in place. Both STs had high male-to-female ratios, including male rectal samples. This suggests that syphilis infections are primarily among MSM but that bridging from MSM into heterosexual networks may potentially contribute to infectious syphilis among females; however, further studies are required to confirm this.

### Conclusion:

Overall, there was considerable diversity among syphilis STs throughout the study period. The fact that two key STs accounted for the majority of infections locally stresses the need for further investigations into the transmission of these strains, and may inform targeted public health interventions to better control the spread of syphilis in Queensland.

### Disclosure of Interest Statement:

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