

Genomic epidemiology of syphilis in Victoria, Australia

Authors: Tairaoa, G¹, Taouk, ML¹, Pasricha, S¹, Azzato, F², Williamson, DA^{1,3,4}

¹ Department of Microbiology and Immunology at the Peter Doherty Institute for Infection and Immunity, The University of Melbourne, Melbourne, Australia

² Victorian Infectious Diseases Reference Laboratory, Melbourne Health at the Peter Doherty Institute for Infection and Immunity, Melbourne, Australia

³ Microbiological Diagnostic Unit Public Health Laboratory, The University of Melbourne at The Peter Doherty Institute for Infection and Immunity, Melbourne, Australia

⁴ Royal Melbourne Hospital, Melbourne, Victoria, Australia

Background:

The resurgence of syphilis in Australia is of clear public health concern, reaching 5793 notifications (23.1 per 100,000) in 2019. In the state of Victoria, this includes increasing rates in men and women, and an increase in congenital syphilis. Although molecular approaches have previously shown the genetically monomorphic nature of *T. pallidum*, the causative microbe of syphilis, it remains possible that genetic diversity within this species may provide insight into the evolution and transmission of this pathogen.

Methods:

Here we use sequence-based approaches to describe the genetic epidemiology of the Victorian syphilis epidemic (2015-2020), including trends in antibiotic resistance status conferred by changes at ribosomal 23S RNA genes, and place these isolates in a global context through comparison to publicly available data. State-of-the-art capture sequencing approaches are being applied to recreate *T. pallidum* genomes directly from patient samples.

Results:

Here we show that both SS14 and Nichols-lineages continue to circulate in clinically relevant populations and contribute to the current syphilis epidemic. Of characterised cases, the majority belonged to the SS14 lineage subgroup G (62.9%, 410/652); this subgroup being observed frequently in the global dataset (41.5%, 833/2006).

Although penicillin resistance has not been described in *T. pallidum*, resistance to macrolide-class antibiotics such as azithromycin is notable in contemporary isolates from Victoria (95.3%, 201/211 of 2018-2019 isolates carrying variants conferring macrolide resistance). Capture-based sequencing and genomic epidemiology may support the inference of transmission patterns and dynamics of *T. pallidum* in Victoria going forward.

Conclusion:

These findings inform our understanding of the current syphilis epidemic in the state of Victoria by describing the underlying population structure and genetic features of the causative pathogen, *T. pallidum*.

Disclosure of Interest Statement:

None.