

The Pan-Genome of *Treponema pallidum* Reveals Differences in Genome Plasticity between the subspecies

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Abstract

Spirochetal organisms of the *Treponema* species are responsible for causing Treponematoses. Pathogenic treponemes cause multi-stage infections like endemic syphilis, venereal syphilis, yaws and pinta. Out of these four lethal diseases, venereal syphilis is transmitted by sexual contact; the other three diseases are transmitted by close personal contact. *Treponema pallidum* subspecies *pallidum* is Gram-negative, motile, spirochete pathogen that cause syphilis in human. Syphilis is a multistage infectious disease that can be communicated by sexual contact. The current worldwide prevalence of syphilis emphasizes the need for continued preventive measures and strategies. Unfortunately, effective measures are limited. The genome sequence of all 49 *T. pallidum* strains available from NCBI, isolated from different hosts and countries, were comparatively analysed using pan-genomic strategy. Phylogenomic, pan-genome, core genome and singleton analyses disclosed the close connection among all strains of the pathogen *Treponema pallidum*. The pan-genomic analysis showed that all the strains are highly clonal. Furthermore, the genome plasticity analysis among the subspecies *T. pallidum* subsp *pallidum*, *T. pallidum* subsp *endemicum* and *T. pallidum* subsp *pertenue* revealed differences in the pathogenicity island (PAIs) and genomic island (GIs) repertoire. We found 4 pathogenicity island (PAIs) and 8 genomic island (GIs) in subsp *pallidum*, whereas subsp *endemicum* has 3 PAIs and 7 GIs and subsp *pertenue* harbour 3 PAIs and 8 GIs. The differences observed in genome plasticity among sub species can be useful for further characterization of their epidemic behaviour.

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