Whole genome sequencing as a tool for phylogenetic analysis of clinical strains of Mitis group streptococci

Identification of Mitis group streptococci (MGS) to the species level is challenging for routine microbiology laboratories. Correct identification is crucial for the diagnosis of infective endocarditis, identification of treatment failure, and/or infection relapse. Eighty MGS from Danish patients with infective endocarditis were whole genome sequenced. We compared the phylogenetic analyses based on single genes (recA, sodA, gdh), multigene (MLSA), SNPs, and core-genome sequences. The six phylogenetic analyses generally showed a similar pattern of six monophyletic clusters, though a few differences were observed in single gene analyses. Species identification based on single gene analysis showed their limitations when more strains were included. In contrast, analyses incorporating more sequence data, like MLSA, SNPs and core-genome analyses, provided more distinct clustering. The core-genome tree showed the most distinct clustering.

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