In silico assessment of virulence factors in strains of Streptococcus oralis and Streptococcus mitis isolated from patients with Infective Endocarditis

Streptococcus oralis and Streptococcus mitis belong to the Mitis group, which are mostly commensals in the human oral cavity. Even though S. oralis and S. mitis are oral commensals, they can be opportunistic pathogens causing infective endocarditis. A recent taxonomic re-evaluation of the Mitis group has embedded the species Streptococcus tigurinus and Streptococcus dentisani into the species S. oralis as subspecies. In this study, the distribution of virulence factors that contribute to bacterial immune evasion, colonization and adhesion was assessed in clinical strains of S. oralis (subsp. oralis, subsp. tigurinus and subsp. dentisani) and S. mitis. Forty clinical S. oralis (subsp. oralis, subsp. dentisani and subsp. tigurinus) and S. mitis genomes were annotated with the pipeline PanFunPro and aligned against the VFDB database for assessment of virulence factors.

Results/Key findings. Three homologues of pavA, psaA and lmb, encoding adhesion proteins, were present in all strains. Seven homologues of nanA, nanB, ply, lytA, lytB, lytC and iga, of importance regarding survival in blood and modulation of the human immune system, were variously present in the genomes. Few S. oralis subspecies specific differences were observed. Iga homologues were identified in S. oralis subsp. oralis, whereas lytA homologues were identified in S. oralis subsp. oralis and subsp. tigurinus. Differences in the presence of virulence factors among the three S. oralis subspecies were observed. The virulence gene profiles of the 40 S. mitis and S. oralis (subsp. oralis, subsp. dentisani and subsp. tigurinus) contribute with important new knowledge regarding these species and new subspecies.

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