In silico assessment of virulence factors in strains of *Streptococcus oralis* and *Streptococcus mitis* isolated from patients with Infective Endocarditis - DTU Orbit (08/04/2018)

**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.

**General information**

**State:** Published

**Organisations:** Department of Bio and Health Informatics, Metagenomics, National Food Institute, Research Group for Genomic Epidemiology, Roskilde University, Slagelse Hospital, University of Copenhagen, Copenhagen University Hospital, Vejle Hospital

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**Pages:** 1316-1323

**Publication date:** 2017

**Main Research Area:** Technical/natural sciences

**Publication information**

**Journal:** Journal of Medical Microbiology

**Volume:** 66

**ISSN (Print):** 0022-2615

**Ratings:**

- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Web of Science (2017): Indexed Yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 2.14 SJR 0.923 SNIP 0.877
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 1.123 SNIP 0.986 CiteScore 2.27
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 1.038 SNIP 1.062 CiteScore 2.26
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 1.021 SNIP 1.047 CiteScore 2.34
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 1.05 SNIP 1.168 CiteScore 2.54
- ISI indexed (2012): ISI indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): SJR 1.118 SNIP 1.117 CiteScore 2.47
- ISI indexed (2011): ISI indexed yes