
In-depth cultivation and characterisation of the pig tonsil microbiome: towards targeted approaches for microbiome manipulation

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The palatine tonsils function as a secondary lymphoid organ and play an important role in the induction of mucosal antibody responses at mucosal surfaces. The tonsils are colonised by an extensive microbiota, mainly bacteria which interact with each other and the host, through their metabolites, influencing health and physiology. Pigs are very important animals in both biomedical research and agriculture, but knowledge about their tonsil microbiota is very limited despite evidence that perturbation of the tonsil microbiota is associated with infection with pathogens such as *Streptococcus suis*. Here we report novel data on the cultured fraction of porcine tonsil microbiomes opening up avenues for functional studies and targeted approaches to reduce infections in the oral cavity through microbiome manipulation. We established a collection of 420 abundant bacterial species present in the oropharyngeal biofilms of healthy animals using MALDI-TOF and 16S rRNA gene sequencing. Genome mining of 42 genomes, from six different genera revealed biosynthetic gene clusters predicted to produce antibiotic non-ribosomal peptides and other secondary metabolites that may have the potential to modulate microbe-microbe and microbe-host interactions.