
The tonsillar microbiome of *Streptococcus suis* diseased piglets

Simen Fredriksen¹, Carlos Neila², Isabela Fernandes de Oliveira¹, Gemma Murray³, Xiaonan Guan⁴, Laura Ferrando¹, Florencia Correa-Fiz², Peter van Baarlen¹, Virginia Aragon², Jerry Wells¹

¹ Host-Microbe Interactomics Group, Wageningen University & Research, The Netherlands

² IRTA, Centre de Recerca en Sanitat Animal, Spain

³ Department of Veterinary Medicine, University of Cambridge, UK

⁴ Schothorst Feed Research B.V., The Netherlands

* Corresponding author. E-mail: simen.fredriksen@wur.nl

The microbiome is important in shaping the host immune system as well as providing direct protection against pathogens by colonization resistance. *Streptococcus suis* is one of the most abundant bacteria in the oral cavity of pigs, but also a zoonotic pathogen of increasing importance. *S. suis* is a complex pathogen with a large diversity of pathogenic and commensal strains, and there is no cross protective vaccine. Pathogenic strains are hypothesized to enter the host via the palatine tonsils, a lymphoid organ colonized by *S. suis* in virtually all pigs. In order to enter the host bloodstream via the tonsils, pathogenic *S. suis* strains first need to colonize the tonsillar biofilm. It is possible that this is facilitated during microbial dysbiosis when there is reduced competition from commensal bacteria. We have utilized both amplicon and shotgun sequencing approaches to quantify the tonsillar microbiome of *S. suis* diseased piglets and healthy controls. We find microbiome composition and diversity to differ between controls and symptomatic animals, even weeks before disease occurrence. The tonsils of symptomatic animals also contain a higher relative abundance of genes that are conserved in disease-associated *S. suis* strains but lacking in commensals. Moreover, we find non-symptomatic littermates of diseased piglets to have an intermediate microbiome profile. We hypothesize that some sows provide piglets with a disease-prone microbiome, possibly due to direct transmission of an unhealthy microbiome or deficient colostrum. Within our consortium we are utilizing the results from this study in vaccine and probiotics development.