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TITLE

ANALYSES OF TONSILLAR MICROBIOME IN PRRSV VACCINATED VS. NON-VACCINATED GILTS AFTER EXPERIMENTAL INFECTION WITH TWO DIFFERENT PRRSV-1 FIELD ISOLATES

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CONTENT

Background and Objectives:
Tonsils are a reservoir for host-specific pathogens and commensal organisms, mostly bacteria and viruses. The resident tonsillar microbiome is assumed to interact with incoming pathogens by preventing colonization via competitive exclusion. The present study aimed to investigate alterations of the tonsillar microbiome in PRRSV vaccinated vs. non-vaccinated gilts after experimental infection with two different PRRSV-1 field isolates and a potential association with tonsillar viral load.

Material and Methods:
Twentyfour gilts, divided into 6 groups, one non-vaccinated and one vaccinated control group, one non-vaccinated and one vaccinated group infected with one of two PRRSV field isolates. Vaccination was done twice prior to insemination and once in mid gestation with ReproCyc®PRRS EU. Experimental PRRSV infections with either the virulent PRRSV-1 AUT15-33 (syn. Acro, Austria 2015) or PRRSV-1 720789 (Germany 2012) were done on gestation day 84. Three weeks post infection gilts were euthanized and tonsillar tissues were collected. DNA was extracted and 16S rRNA gene sequencing using Illumina MiSeq was performed. Bioinformatics were done using QIIME pipeline and data were analysed using SAS and mixOmics in R.

Results:
The bacterial community in the tonsils across all sow groups was dominated by Proteobacteria, Bacteroidetes, Fusobacteria, Firmicutes and Actinobacteria. Non-infected gilts comprised more Flavobacteriaceae than infected gilts and the genera Haemophilus and Mycoplasma showed differences between PRRS-1 isolates and vaccinated groups. All but two infected gilts were PRRSV positive in tonsillar tissues. Relevance networks showed positive correlations between Sphingomonaceae, Sediminibacterium and Pasteurella and viral load in the tonsils. Moreover, Microbacterium and Clostridium were negatively associated with weight gain during gestation.

Discussion and Conclusion:
Results showed that an experimental PRRSV infection with two different PRRSV-1 isolates altered the abundance of pathogenic bacterial phylotypes in vaccinated and non-vaccinated gilts. Results further indicated that virus load may influence bacterial community in tonsils.