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TITLE

VARIATIONS IN THE ASSOCIATION OF NASAL MICROBIOTA WITH VIRULENT AND NON-VIRULENT STRAINS OF HAEMOPHILUS PARASUIS IN WEANING PIGLETS

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CONTENT

Background and Objectives

Haemophilus parasuis causes Glässer's disease, which results in high economic losses in the swine industry. To understand the polymicrobial interactions of H. parasuis and the nasal microbiota, the statistical association patterns of nasal colonizing bacteria with virulent and non-virulent strains of H. parasuis, were studied accounting for the farm management practices as potential risk factors for the occurrence of Glässer's disease in weaning piglets.

Material & Methods

The bacterial communities inhabiting the nares were characterized from 51 weaned-piglets (3–4 weeks of age) randomly selected from seven farms from Spain; four of them with Glässer's disease (A-B-C-D) and three with no respiratory diseases, as control (E-F-G). Production system was either multi-sites (A-C-D-F-G) or farrow to finish (B-E). Presence of virulent and/or non-virulent H. parasuis strains in the nasal cavities was determined by PCR. Multivariate logistic regression models were performed with "glm" function in R, between the various members of nasal microbiota based on the relative abundance values of operational taxonomic units (family and genus levels), and H. parasuis strains (virulent and non-virulent).

Results

Several families such as Ruminococcaceae, Clostridiaceae¹, and Peptostreptococcaceae together with some genera i.e. Clostridium, XI, Oscillibacter and Escherichia/Shigella, were significantly associated with H. parasuis virulent strains. Whereas, Ruminococcaceae, Bacteroidaceae, Porphyromonadaceae, Enterococcaceae families and Corynebacterium, Bacteroides, Barnesiella, Odoribacter, Leuconostoc, Flavonifractor, Bordetella, Neisseria and Acinetobacter genera were significantly associated with H. parasuis non-virulent strains.

Discussion & Conclusion

Our findings showed a wide variation in the association of nasal microbiota communities with virulent and non-virulent strains of H. parasuis in weaning piglets. The multi-site production system and disease status of the farm were both significantly associated with virulent strain at the explored taxa levels. The findings of this study boost our understanding of Glässer's disease development and could be a base for innovative non-antimicrobial alternatives for Glässer's disease control.