Effect of Killed PRRSV Vaccine on Gut Microbiota Diversity in Pigs

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Background
Non-infectious PRRSV vaccines, including killed virus vaccines, are safer to use but the vaccine efficacy needs to be improved. New strategies are needed to develop innovative non-infectious PRRSV vaccines. Microbiota — the collection of trillions of bacteria, viruses, and other microorganisms that inhabit the various body sites of the animal — are proposed to play key roles in the development and modulation of immune systems, which could contribute to the host responses to vaccination. The interaction between PRRSV infection/vaccination and microbiota could provide novel insights into microbiota-targeted intervention strategies and vaccine development.

Objective
To evaluate the effectiveness of a killed PRRSV vaccine and explore potential interactions between gut microbiota and improved outcomes and vaccine-induced immunity in a nursery pig model.

Materials and Methods
Fecal microbial communities were longitudinally assessed in three groups of pigs (vaccinated/challenged with PRRSV, unvaccinated/challenged with PRRSV, and unvaccinated/unchallenged) before and after vaccination and after viral challenge. Composition of the fecal microbiome in all groups of pigs was determined by 16s rRNA gene amplification and next-generation sequencing on fecal swab samples. Microbial community diversity and composition were analyzed using DADA2 and R statistical software.

Results
1. Significant effects of viral challenge and vaccination on both taxonomic richness and community diversity of the gut microbiota were observed.
2. Vaccination with killed PRRSV vaccine incompletely protects pigs against viral impacts on the microbiome.
3. The abundances of several microbial taxa correlated with the level of viral load and the host T-cell immune response.

Conclusions and Implications
This study highlights the potential roles of gut microbiota in the response of pigs to vaccination, which may pave the road for the development of novel strategies to enhance vaccine efficacy.

Figure 1. Relative microbial abundance of fecal microbiota in genus level. Genus level fecal microbial composition of all piglets at 0 dpv, 35 dpv, and 45 dpv was calculated. The legend on the right represents each individual microbial genus in different colors. The top two genera include Clostridium in light blue and Lactobacillus in dark blue.

Figure 2. Alpha diversity of fecal microbiota. Boxplot depicting species richness (a) and Shannon diversity index (b) were graphed using all group pig samples from 0 dpv, 35 dpv, and 45 dpv (10 dpc). Legend on the right shows four factors including control, vaccine, virus, and virus + vaccine. Black dot in panel b indicates a statistical outlier (i.e., Quartile 3 + 1.5 × Interquartile range).

The full paper can be found at: https://www.mdpi.com/1999-4915/14/5/1081
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