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Prediction of immune response to vaccine against the influenza A virus or *Mycoplasma hyopneumoniae* in pigs based on data from fecal microbiota and blood collected before vaccination

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Background: Understanding why some animals respond better to vaccination than others is important to improve vaccine efficacy. We focused on the immune response of pigs to Influenza A virus (IAV) or *Mycoplasma hyopneumoniae* (*M. hyo*) vaccination.

Aim: We analyzed blood transcriptome and fecal microbiota before vaccination and searched for associations and biomarkers that could differentiate animals with contrasted vaccine responses.

Results: Large White pigs were vaccinated at weaning against IAV (98 pigs) or *M. hyo* (182 pigs) with a booster 21 days post-vaccine (dpv). Vaccine responses were monitored at 21 dpv (early response), 28 or 35 dpv (maximum response intensity) or 118 dpv (long-term persistence). The humoral response was evaluated by measuring seric specific IgGs by ELISA. For IAV vaccine, the immune response was also assessed by hemagglutination inhibition assays. Blood and stools were collected before vaccination (0 dpv). Blood transcriptome was analysed by RNA-Seq and fecal microbiota by 16S rRNA gene sequencing. For each vaccine, we identified blood gene and fecal microbiota profiles associated to high and low vaccine responses at each post-vaccine time points. For both vaccines, we identified that a stronger immune response is linked with operational taxonomic units assigned to the genus *Prevotella*, and sparse partial least squares discriminant analysis identified a shared list of 101 blood genes that efficiently predicted divergent vaccine responders.

Conclusion: Our results highlighted that specific as well as shared biomarkers might predict the intensity of immune response to several vaccines, IAV and M. hyo in this study, which need further investigation.