The porcine gut microbiota: composition and links with host's genetics and phenotypes

Jordi Estellé, Claire Rogel Gaillard

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J. Estellé and C. Rogel-Gaillard
INRA, UMR1313 Génétique Animale et Biologie Intégrative (GABI), Domaine de Vilvert, Bat. 320, 78350 Jouy-en-Josas, France; jordi.estelle@jouy.inra.fr

Microbiomes and their effects on hosts are emerging as outstanding factors to study in the animal production field. In fact, the microbiome of the intestinal tract may be considered a new host organ that plays a major role in health and well-being. In our laboratory we are developing a research line that targets the pig's gut microbiota with the objective to study the interplay with its host for shaping host's phenotypes. To this end, a cohort of French Large White piglets ranging from 14 to 70 days old was assessed for fecal microbiota composition by pyrosequencing the 16S rRNA gene. All animals were weaned at 28 days and measured for immunity and production traits. Bacteroidetes, Firmicutes, and Proteobacteria phyla were predominant at all ages, while specific microbial groups (e.g. Lactobacillus) were more represented in the youngest animals. In this sense, a temporal trajectory of bacterial communities in 31 piglets revealed a stratification of piglets in two main groups after weaning that were primarily distinguished by the levels of unclassified Ruminococcaceae and Prevotella, respectively. This results were confirmed in phylogenetic network and clustering analyses in 518 60-days old pigs. A Dominance of Prevotella was positively correlated to increased concentrations of luminal secretory IgA, average daily gain and body weight. In parallel, the genetic parameters of the gut microbiota composition were estimated and, among a set of 63 genera, 7 had low ($0.1<h2<0.2$), 15=" 8=" and=" h2=" high=" medium=">0.4) heritabilities for abundance variation. Finally, regularized canonical correlations and sparse Partial Least Squares analyses highlighted both positive and negative correlations between health traits (e.g. monocytes, eosinophils, platelets) and genera such as Prevotella, Roseburia and Dialister. Thus, the gut microbiota composition is both influenced by the host's genetics and linked to health and growth traits, which confirms the relevance of this ecosystem for the porcine production.</h2<0.2),>