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Jordi Estellé, Núria Mach, Yuliaxis Ramayo Caldas, Marie-Hélène Pinard-van Der Laan, . Inra-Denmark-Bgi Consortium, Claire Rogel Gaillard

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Pig's gut microbiota: composition, and links with host genetic parameters, immunity and production traits

J Estellé¹, N Mach¹, Y Ramayo-Caldas¹, MH Pinard van der Laan¹, INRA-Denmark-BGI consortium, C Rogel-Gaillard¹

¹INRA, UMR1313 Génétique Animale et Biologie Intégrative, Domaine de Vilvert; F-78350 Jouy-en-Josas

Contact

Claire Rogel-Gaillard

INRA, UMR1313 Génétique Animale et Biologie Intégrative, Domaine de Vilvert; F-78350 Jouy-en-Josas

claire.rogel-gaillard@jouy.inra.fr

We are developing a research line that targets the Pig's gut microbiota with two objectives: i) to study the interplay between the gut microbiota and its host for shaping host's phenotypes with a focus on production and immunity traits, and ii) to build a reference gene catalogue of the gut microbiome to implement quantitative metagenomics.

French Large White piglets from 14 to 70 days old were assessed for fecal microbiota composition by 454-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. The dynamic analysis of bacterial communities for 31 piglets revealed a shift after weaning with stabilization at 36 day-old, and a stratification of piglets in two main groups after weaning, distinguished primarily by levels of *Ruminococcaceae* and *Prevotella*. These results were confirmed by phylogenetic network and clustering analyses from 518 60 day-old pigs. Clusters according to microbiota were positively correlated with growth rate and increased concentrations of luminal secretory IgA. Among a set of 63 genera, 15 had medium ($0.2 < h^2 < 0.4$) and 8 high ($h^2 > 0.4$) heritabilities for abundance variations. Positive and negative correlations between health traits (e.g. monocytes, eosinophils, platelets) and genera such as *Prevotella*, *Roseburia* and *Dialister* were found.

We have established a gene catalogue of the gut microbiota by sequencing fecal DNA from over 287 French, Danish and Chinese pigs, representing 17 breeds, 11 farms, and various ages. Over 7.6 million non-redundant genes representing 719 metagenomic species were identified. The pig gut microbiota is influenced by gender, age and breed. Analysis of the prevalence of antibiotic resistance genes (ARGs) reflected antibiotics supplementation in each country and farm.

These studies create a resource for targeted and whole metagenomics-based studies and pave the way towards sustainable knowledge-based pig farming.