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Gut microbiota composition in swine: genetic parameters and links with immunity traits

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The intestinal microbiome plays a major role in host's physiology and homeostasis. It participates in the immunological barrier against infections, helps to develop and mature the immune system, and contributes to extract nutrients and energy from food. Despite large scale studies in human, little is known on gut microbiota composition and potential associations with individual traits in livestock species.

The objective of this study was to estimate the host genetic parameters of the gut microbiota composition and analyze its links with immunity traits in French Large White pigs.

The genetic microbiota content is genetically controlled

The microbial diversity of the gut microbiota was characterized by sequencing the variable region of the v3-v4 segment of the 16s ribosomal DNA by 454 Roche pyrosequencing in a cohort of 299 60 days-old piglets. Results showed a predominance of *Prevotella* followed by *Oscillibacter*, *Dialister*, *Roseburia* and *Treponema* genera. The heritability of the bacterial relative abundances was estimated for 63 genera. Among this set of 63 genera, 7 had low ($0.1 < h^2 < 0.2$), 15 medium ($0.2 < h^2 < 0.4$) and 8 high ($h^2 > 0.4$) h^2 (Table1).

Table 1. Heritabilities (h^2) and standard error of h^2 (SE) estimated for the relative abundances of bacterial genera that characterize individual variability of the gut microbiota composition.

Genus	h^2	SE
Gemmiger	0.82	0.13
uncl_Rikenellaceae	0.55	0.15
Faecalibacterium	0.54	0.14
Coprococcus	0.51	0.15
Clostridium_XIVa	0.45	0.14
Prevotella	0.45	0.13
Coriobacterineae	0.44	0.14
Oribacterium	0.41	0.14
Phascolarctobacterium	0.39	0.13
Lactobacillus	0.37	0.13
Dorea	0.33	0.12
Anaerovibrio	0.31	0.52
Mitsuokella	0.30	0.48
Treponema	0.30	0.13
Blautia	0.25	0.12
Butyrivibrio	0.25	0.12
Streptococcus	0.25	0.12
Oxobacter	0.24	0.52
Selenomonas	0.24	0.12
uncl_Ruminococcaceae	0.23	0.12
Dialister	0.22	0.37
Acidaminococcus	0.21	0.46
Anaerovorax	0.20	0.11

Genera identified as the most predominant are in bold letters.

The relative abundances of sets of bacterial genera are genetically correlated

At the genetic level, the relative abundance of *Prevotella*, *Oribacterium*, *Selenomonas*, *Dialister* and *Megasphaera* were found positively correlated with each other and tended to be negatively correlated to other genera (Fig. 1).

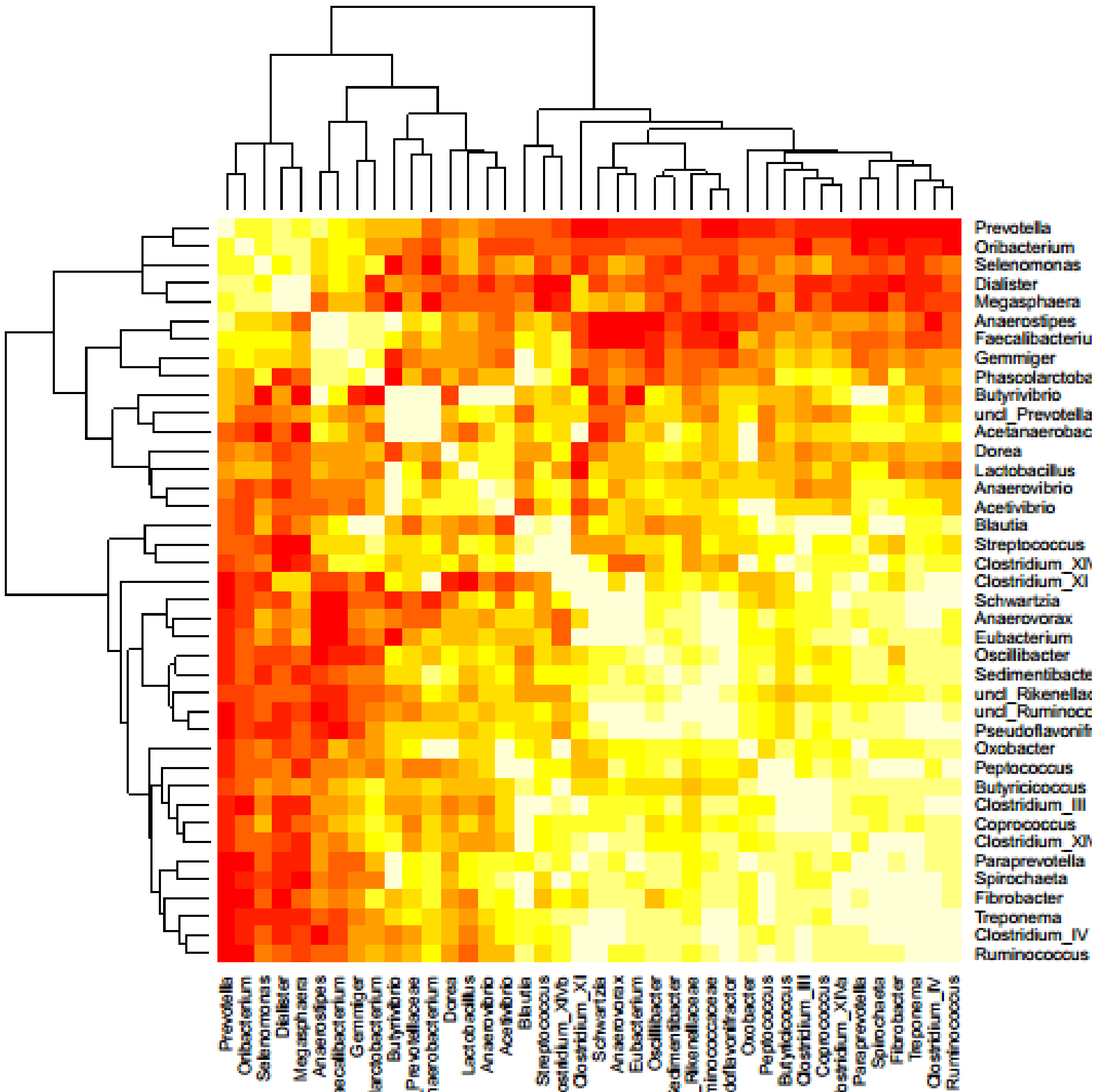


Figure 1: Genetic correlations between relative abundances of genera (positive correlations are shown in white, negative correlations in red and yellow colors indicate no correlation).

Covariations of microbiota composition with immunity traits

Multivariate statistical analysis with the rCCA approach highlighted both positive and negative links between immunity traits such as monocytes, eosinophils, platelets, haemoglobin or red blood cell parameters, and genera such as *Prevotella*, *Roseburia* and *Dialister* (Fig. 2). Inverse trends were observed for genera belonging to Firmicutes and Bacteroidetes phyla.

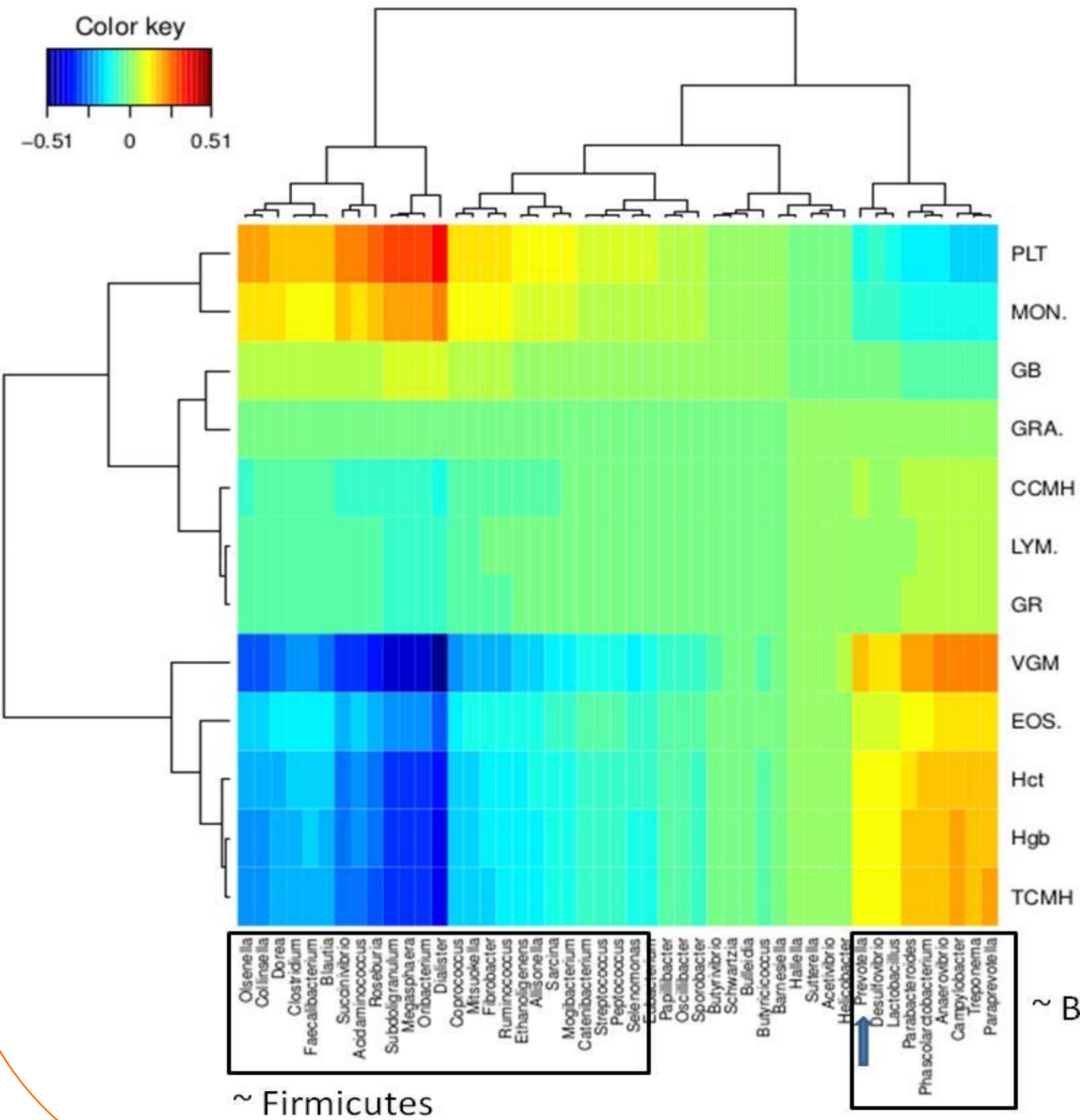


Figure 2: Canonical correlation analyses (rCCA) between bacterial genera and immune traits

- PLT: platelets;
- MON: monocytes;
- GB: white blood cells;
- GRA: granulocytes;
- CCMH: mean cell hemoglobin concentration;
- LYM: lymphocytes;
- GR: red blood cells;
- VGM: red cell distribution width;
- EOS: eosinophils;
- Hct: hematocrit;
- Hgb: hemoglobin;
- TCMH: mean cell hemoglobin.

The blue arrow points to the predominant *Prevotella* genus.

In this report we demonstrate for the first time that the gut microbiota composition in swine is influenced by the genetics of the host. In addition, we have found covariations between microbiota composition and immunity traits. These results pave the way for studying the microbiota as a new component of phenotype construction in pigs.

It may be anticipated that microbiota parameters, together with zootechnical and immunity traits, will help to better decipher the driving forces that shape animal performances and robustness.