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Immune traits are affected by genetic selection for faecal enterotypes in pigs

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The faecal microbiota of 60-day-old Large White pigs reared in same conditions can be structured into two enterotypes, for which the keystone genera are *Prevotella* (*P*) and *Mitsuokella* (*M*) or *Ruminococcus* (*R*) and *Treponema* (*T*). We generated two pig lines HPM and HRT selected for the relative abundance of either P and M or R and T, respectively. Each line showed an increase in the prevalence of the selected enterotype over three successive generations. We used 40 animals per line from the 3rd generation to investigate if at 60 days of age, they display differences in the microbiota of the small and large intestines, and in immune traits. Using 16S gene sequencing, the two lines were shown to harbour strong microbiota differences at the descending colon (648/1334 ASV and 79/144 genera differentially abundant), with less differences at the ileal Peyer's patches (38/435 ASV and 18/126 genera). Piglets from the HPM line exhibited a higher number of eosinophils and natural IgM, while piglets from the HRT line showed higher counts of CD4⁺ CD8⁺ T cells and stronger phagocytosis activity. Overall, our results show that direct genetic selection for the composition of the faecal microbiota is not only associated with changes in the microbiota of other sections of the gut, but also with host traits related to immunity. Those divergent pig lines are therefore a powerful tool for better understanding the combined effects of host genetics and gut microbiota on phenotypes relevant to sustainable livestock systems, including health and immune traits.

Keywords: microbiota, genetics, immune traits

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