The effect of two different production systems on pig fecal microbiota composition

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Different production systems (conventionally and pasture-raised pigs) and co-rearing of pigs with other livestock have both been shown to influence pig fecal microbiota composition. In this study, we assessed 16S fecal microbiota composition of pigs kept at three different locations: (i) pigs reared on pasture with small ruminants and cattle (group L1), (ii) pigs reared indoors and without other farm animals and fed only organic commercial feed (group L2), and (iii) pigs reared on pasture with cattle (group L3). Fecal samples were rectally collected from 18 pigs in all four seasons of 2022. Pigs from groups L2 and L3 were raised on the same organic farm and maintained by the same livestock workers, whereas pigs from L3 were raised on another organic farm and were maintained by other livestock workers. All pigs were fed the same type of organic commercial feed. Total DNA was extracted from 72 fecal samples using QIAamp Fast DNA Stool Mini Kit (Qiagen). Sequencing of 16S rRNA gene (V3–V4 region) to a depth of 50,000 tags per sample was performed with Illumina paired-end (2×250 bp) technology. Operational taxonomic unit (OTU)-based microbiome analysis was performed using QIIME 1.9.1. Alpha diversity was comparable between study groups; the average number of observed OTUs ranged from 1,500 to 1,800 in all seasons and in all study groups. The two predominant bacterial phyla in all three groups were Firmicutes and Bacteroidetes. Significant seasonal changes in microbiome composition were observed between all seasons (nonparametric MANOVA, p < 0.008). Microbiome composition differed significantly between the study groups L1 and L2–L3, as demonstrated by principal coordinate analysis of weighted UniFrac distances and nonparametric MANOVA (p = 0.001), whereas groups L2 and L3 did not differ significantly (p = 0.2). Linear discriminant analysis Effect Size (LefSe) identified several bacterial taxa that were most differentially abundant between different study groups and different seasons.

Pig microbiota composition is not stable over time and is influenced by external (rearingrelated) factors. In the present study, the production system or co-rearing with other animal species did not significantly affect pig microbiome composition. Rather, the main observed differences in microbiota composition could be explained by the farm and livestock workers.