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Feed efficiency and the faecal microbiome at slaughter weight in pigs

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Feed efficiency (FE) is an important trait in the pig industry, as feed costs are responsible for the major part of production costs. Availability in the market and cost of feed ingredients dictate changes in feed composition. As a result, fibre level and composition can vary between pig diets. Microbiota in the gastrointestinal tract play an important role in fibre digestion, because they produce enzymes that break down fibre structures and deliver volatile fatty acids (VFA) to the pig. These VFA can be used as metabolic energy sources. As such, microbial fermentation could influence FE in pigs. The aim of this study was to investigate the association between FE and faecal microbiome in commercial grower-finisher pigs. Three-way crossbreed grower-finisher pigs (154) were either fed a diet based on corn/soybean meal (CS) or a diet based on wheat/barley/by-products (WB). Faecal samples were collected on the day before slaughter (mean body weight 122 kg), and sequenced for the V3-V4 16S ribosomal DNA regions. Sequences we clustered according to operational taxonomic units (OTU) for each individual. A partial least square regression was applied to the dataset, together with a discriminant analysis using principal components of FE extreme groups (10 high and 10 low FE animals for each diet by sex-combination). Pigs on different diets and males vs females had a very distinct microbiome, needing only two OTUs for diet ($P=0.018$) and 18 OTUs for sex ($P=0.002$) to separate the groups. Faecal microbiome was not related to FE groups fed the CS diet, but there were sex specific OTUs related to FE in male and female pigs in the groups fed the WB diet. In conclusion, our results show a diet and sex dependent relationship between the faecal microbial composition and FE in grower-finisher pigs at slaughter weight. This study is part of the Feed-a-Gene project and received funding from the European Union's H2020 program under grant agreement no. 633531.