



Relationship between intestinal and blood metabolome and fecal digestive efficiency in chicken

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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 were 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.

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Relationship between intestinal and blood metabolome and digestive efficiency in chicken

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Digestive efficiency (DE) is an essential component of feed efficiency, especially in the context of increasing variety of feedstuffs with variable quality used in poultry diets. However, measuring fecal DE during balance trials is time-consuming and constraining as birds are placed in individual cages. Moreover, not all the mechanisms controlling DE are known. The aim of our study was thus to identify biomarkers of DE using intestinal and blood metabolomics. Our study used 60 chickens of an advanced intercross line (8th generation) between 2 broiler lines divergently selected for fecal DE, based on metabolisable energy corrected to zero nitrogen retention (AMEn). At 3 weeks, fecal AMEn and coefficients of digestive use of lipids, nitrogen, and starch were measured during a balance trial, ileal and caecal contents were sampled and blood collected. Metabolome was determined by proton high resolution NMR. Correlation models (canonical partial least squares) were fitted to assess the links between efficiency and metabolites of the 3 sample collection sites. Metabolites differences between animals with high or low levels of DE were mainly involved in amino acids metabolism (lysine, isoleucine, methionine) and energy metabolism (glutamate, glucose) in the 3 collection sites. High positive correlations were found between glucose in caecal content and AMEn and coefficient of DE of nitrogen, which is consistent with the large divergence found in the divergent lines on these criteria. This result suggests an effect of microbial fermentation on DE. These metabolic profiles provide information on the mechanisms implied in feed digestion in chickens. Further analyses will estimate if the blood metabolome can be used as an indirect criterion of selection of feed efficiency and DE. 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 and by the INRA program GISA-GALMIDE.