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Probiotic bacteria may exert a wide spectrum of effects on the host gut and its microbiome. Our study aimed to investigate the effect of feeding the suckling piglets and their dams ($n=10$) with probiotic (2.75×10^9 CFU/g viable spores of *Bacillus subtilis* (DSM25841) and *Bacillus amyloliquefaciens* (DSM25840) in creep and sow feed (0.4 g/kg feed) on the suckling piglet's health and gut function at weaning. Ten sows and their offspring not fed with the probiotic served as a control. Sow's blood and colostrum samples were taken at farrowing for IgA, IgM and IgG ELISA assay. At weaning (day 28 postnatal), one piglet randomly selected from each control and probiotic treated sow was sampled for blood and killed to obtain ileal samples for analyses. Probiotic treated sows showed significantly reduced back fat and body weight loss during lactation and tended to have better body condition score (BCS) after weaning as compared to controls. No effect of probiotic on colostrum immunoglobulins was observed, but in the blood plasma the concentration of IgG was significantly elevated. Probiotic administration increased creep feed consumption by 0.3 kg ($P=0.03$), litter gain by 5.4 kg ($P=0.01$), and piglet weaning weight by 0.34 kg ($P=0.03$) as compared to control. Probiotic also reduced faeces score, in the second week of life ($P=0.01$). At weaning in probiotic treated piglets, IgM concentration in the blood plasma and in the ileal mucosa were significantly increased (1.08 vs 0.69 mg/mL, $P=0.03$ and 10.25 vs 5.08 $\mu\text{g/g}$ tissue, $P=0.05$), whilst ileal mucosa IgG concentration was reduced. Also, a clear-cut trophic effect on the ileal mucosa (including longer villi, thicker mucosa, and more developed Peyer's patch architecture) concomitant with an inhibition of epithelium maturation was observed as compared to control. Concluding, probiotic supplementation improved piglet's performance, and the gut immune system before weaning challenge.

P145. Growth performance and gut microbiome of weanling pigs fed dietary enzyme complex and fibrous feed ingredients

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This study was conducted to test the hypothesis that the enzyme complex (EC) in diets containing fibrous feed ingredients may improve the growth performance and nutrient digestibility and alter gut microbiome of weanling pigs. A total of 192 weanling pigs (6.70 ± 0.97 kg) were randomly assigned to 4 diets prepared as a 2×2 factorial with 2 diet types (low [LF] or high [HF] fibre) and 2 EC levels (not added or added). The LF diets were based on corn and wheat, whereas the HF diets were prepared by adding barley, wheat middlings, and canola meal into the LF diets at the expense of corn. Soybean meal, soybean oil, and

supplemental amino acids concentrations were adjusted to maintain the metabolizable energy and amino acid contents. The LF and HF diets contained neutral detergent fibre (NDF) at 88 and 127 g/kg, respectively. The EC provided 4,000 U/kg xylanase, 200 U/kg β -glucanase, 100 U/kg amylase, and 2,000 U/kg protease. Adding EC increased ($P<0.05$) body weight on d 42 (26.7 vs. 28.0 kg) and average daily gain and gain-to-feed ratio from d 0 to 42. On d 42, dietary EC increased ($P<0.05$) the apparent total tract digestibility of gross energy (82.4 vs. 88.4%) and NDF (58.7 vs. 72.1%) in the HF diets, but not in the LF diets. On d 28, the alpha diversity indexes of microbiome in faeces were greater ($P<0.05$) in pigs fed the LF diets than in those fed the HF diets. Relative abundance of several bacteria including *Eubacterium* and *Faecalibacterium* in faeces on d 42 increased ($P<0.05$) by EC addition. In conclusion, added EC in diets containing fibrous ingredients improved growth performance and nutrient digestibility. Gut microbial community structure in pigs was beneficially influenced by dietary EC addition.

P146. Feed efficiency in grower-finisher pigs in relation to faecal microbiota functionality

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This study aimed to relate feed efficiency in pigs (i.e., feed intake (ADFI), body weight gain (ADG), and feed conversion ratio (FCR)) to the functionality of their faecal microbiome. We hypothesised that functionality of faecal microbiome was stronger related to feed efficiency in pigs than composition of the faecal microbiome. Data were collected from 692 three-way crossbred male grower-finisher pigs. Pigs were offered feed ad libitum in a three-phase feeding program with a commercial diet based on wheat, barley and by-products. On the day before slaughter (mean body weight 125 kg), individual faecal samples were collected. Faecal samples were sequenced for the 16S hypervariable region of bacteria (V3/V4) to profile the faecal microbiome, sequences were grouped, and functionality was obtained through KEGG orthologs (KOs) using the R package 'Tax4Fun2'. On average, 36% of the sequences could be used to obtain KO. We calculated the proportion of variance in feed efficiency related traits that was explained by variation in the relative abundance of the faecal microbiome (m_2), or the relative abundance of the KO (k_2). The values for m_2 were 0.44 for ADG, 0.32 for ADFI and 0.39 for FCR, and were higher than those found for k_2 with 0.28 for ADG, 0.20 for ADFI and 0.22 for FCR. The most important KO contributing to the explained variance by microbiota functionality were related to antibiotic resistance and carbohydrate metabolism for ADG and ADFI. For FCR, the most important KO were related to energy metabolism, signalling and cellular processing, and genetic information processing. Hence, even though less than half of the microbial sequences could be linked to KO, functionality of faecal microbiota was related to feed efficiency traits. This study was part of the Feed-a-Gene Project, funded from the European Union's H2020 Programme under grant agreement no 633531.

P147. Apple pomace supplementation modulates colonic microbiota promoting health benefits in post-weaning piglets

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