

scarce. This study aimed to characterize the microbiota of the ileal digesta and faeces of pigs fed with different Ca levels and phytase. In a completely randomized row column design with four periods, eight ileal-cannulated barrows (initial body weight 27 kg) were fed four maize-oilseed meal-based diets containing 5.4 (LowCa) or 8.5 (HighCa) g Ca/kg (limestone addition) and supplemented or not with 1,500 FTU/kg of a hybrid-6-phytase (+ and -). No mineral P was added and the P concentration was 4.3 g/kg. In each period, faecal samples were collected on day 6-9 and 10-11 and ileal digesta on day 10-11. DNA was extracted and analysed with target amplicon sequencing, followed by bioinformatics and statistical analysis. Faecal microbiota data showed a trend for the interaction phytase and limestone ($p=0.085$). Without phytase, HighCa led to lower faecal phytate degradation (87%) than HighCa+ (96%) ($p<0.05$). Bifidobacterium in faeces was more abundant after administration of HighCa+ (25.3%) than HighCa- (17.7%) ($p<0.05$). The HighCa+ diet showed an increase in the abundance of Limosilactobacillus and Ligilactobacillus (3.6% and 1.6%) compared to HighCa- (2.2% and 0.6%). Lactobacillus was more abundant in faeces than ileal digesta when HighCa- and HighCa+ was provided (4.1 vs. 1.9% and 5.1 vs. 2.1%) ($p<0.05$). HighCa- and HighCa+ led to an increase in the abundance of Prevotella in faeces (4.7% and 5.6%) compared to ileal digesta (1.7% and 1.3%) ($p<0.05$). Limestone addition to the feed increased the abundance of bacteria known to be phytate degraders and short-chain fatty acids producers. The higher abundance of phytate degraders in faeces than ileal digesta gives hints on hindgut fermentation of phytate.

O21. Effects of copper source on bile acid profiles and intestinal microbiota in finishing pigs

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Bile acids (BA) are synthesized in the liver (primary BA) and converted by the gut microbiota into secondary BA. Quantitatively, the most relevant microbial transformations include deconjugation of bile salts, via the enzyme bile salt hydrolase (BSH), and 7 α -dehydroxylation of primary BA into secondary species. The objective of this study was to explore whether high levels of Cu from different sources have differential actions on BA metabolism and gut microbiota. Samples of colon and liver were obtained from a study in which 120 pigs were randomly allotted to 3 treatments (8 pens/treatment) for 120 days. Treatments were negative control diet (NC, 25 mg Cu/kg) plus the NC supplemented with 250 mg/kg of Cu from either CuSO₄ or Cu₂O. On day 120, 8 pigs/treatment were sacrificed to obtain samples of tissues and colonic digesta that were later used to quantify BA via UPLC-MS and characterize gut microbiota via 16S rRNA gene sequencing. Compared with the other two treatments, feeding Cu₂O increased ($P < 0.004$) the contents of total bile salts and chenodeoxycholic acid (primary BA) in colonic mucosa. Compared with CuSO₄ group, feeding Cu₂O reduced ($P < 0.03$) the hepatic concentration of lithocholic acid (secondary BA), but this effect was not different from the control group. Although treatments did not affect gut microbiota alpha diversity, both sources of Cu altered the abundance of several genera of BA-metabolizing bacteria compared with the control group, being the repression ($P < 0.10$) of some of them

(Lactobacillus, Clostridium CAG:306) more pronounced in animals fed Cu₂O. These results demonstrate that high levels of Cu alter BA profiles, most likely by modifying intestinal BSH activity and microbial metabolism of BA. Furthermore, findings suggest that the growth response elicited by Cu in the performance study might have been associated with BA-mediated improvements in lipid digestion and/or metabolism.

O22. Early oral faecal filtrate transplantation to improve gut health in pigs before and after weaning – a pilot study

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Gut microbial colonization starts immediately after birth and the subsequent composition and succession of microbes play an important role for gut function. Transplantation of faeces or bacteria-free filtrates of faeces has shown gut protective effects in neonatal pigs. We therefore, hypothesized that transplantation of a filtrate of faeces (FFT) from lactating sows to neonatal pigs would prevent diarrhoea and enhance survival rate and growth. Methods: On the day of farrowing, two piglets from each of 10 litters were randomly selected for faecal filtrate filtration (FFT, $n=20$) and two piglets from each of nine other litters were selected as controls (CON, $n=18$). On day one to six of life, FFT piglets received oral inoculations of filtrate derived from 1 gram of sow donor faeces per day while CON piglets received equivalent volumes of sterile saline. Individual growth and faecal scores were recorded at day one to six, day 14, 21, and 27. On day 27, one piglet from each litter was euthanized and tissue collected (FFT: $n=7$, CON: $n=6$), while the remaining piglets (FFT, $n=8$ and CON, $n=6$) were weaned on day 28. Individual growth and faecal score were recorded daily for these weaned pigs until day 35 where they were tissue collected. Results: Growth performance, haematology and biochemistry, small intestine morphology, brush border enzymes, organ weights and 16S rRNA sequencing data were similar between the two groups in both the suckling period and the post-weaning period. However, FFT showed lower diarrhoea prevalence in the suckling period (1.9 % vs. 6.2%; tendency $p=0.09$) and in the post-weaning period (16.1% vs. 33.3%; $p=0.04$) compared to controls. Conclusion: sow faeces derived filtrates provided as oral transplants during the first week of life, may reduce diarrhoea episodes before and after weaning. The mechanism remains to be resolved.

O23. A blend of medium-chain fatty acids and organic acids accelerates microbial maturation in newly weaned piglets

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The inclusion of medium-chain fatty acids and organic acids (MCOA) in the post-weaning diet has been shown to alter gut microbiota and improve pig performance during the weaning transition. However, there