

Zinc oxide (ZnO) is commonly supplemented at pharmacological dosage in piglets' diets in order to reduce diarrhoea incidence and support performance through the regulation of the intestinal integrity and microbiota. Nevertheless, the use of pharmacological levels of ZnO will be soon banned in European Union and Canada. The objective of this study was to evaluate different levels of Zn from regular ZnO or from a potentiated Zn source on growth performance and microbiota of piglets at 14 days after weaning. A total of 1440 piglets (25 days of age) were divided in 12 dietary treatments: 150, 300, 600, 900, 1500, or 3000 mg/kg of regular ZnO or potentiated Zn. Growth performance data was collected at day 14 after weaning, as well as the faecal samples for microbiota analysis. Piglets were healthy and did not present diarrhoea during the period of the trial. The ADG was higher ($P < 0.01$) on pigs fed potentiated Zn at 300, 600, and 900 mg/kg of Zn compared to pigs fed ZnO at the same dose. The ADFI was higher ($P < 0.05$) in pigs fed potentiated Zn at 300 and 600 mg/kg of Zn compared to pigs fed same levels of Zn from ZnO. Finally, FCR was higher ($P < 0.05$) for pigs fed 300 mg/kg of Zn from potentiated Zn than from ZnO. Other doses comparisons were not different between Zn sources ($P > 0.05$). At day 14 after weaning, when comparing 3000 mg/kg of Zn from ZnO with 150 or 300 mg/kg of Zn from potentiated Zn, piglets' performance was not different ($P > 0.05$). In conclusion, potentiated Zn at intermediate dose may be an alternative to the pharmacological level of regular ZnO.

P157. Role of the cecum on faecal microbial community structure in finisher pigs using a caecectomized pig model

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The cecum is a major site of fermentation of dietary nutrients. In the pig, there is a knowledge gap pertaining to the role of the cecum in nutrient metabolism and health. The objective of this preliminary work was to develop a caecectomized pig model and to evaluate cecum microbial community structure in caecectomized finisher pigs fed a high fibre diet. Caecectomies were performed at the nursery to grower phase transition (~ 63 d of age) prior to the experiment. A total of 10 barrows (initial BW = 83 kg; ~112 d of age) were allotted to 1 of 2 treatments (5 replicates/treatment) in a 4 wk experiment. Treatments consisted of caecectomized (CEC-) or cecum intact (CTRL) pigs. All pigs were fed a moderately complex, high fibre (soy hulls included at 25%) finisher diet (3,006 ME kcal/kg) during the entirety of the trial. Data was analysed using PROC MIXED procedures of SAS with treatment as fixed effect and initial BW block as random effect. No differences were observed in BW on d 0 (82.92 vs 83.92 kg) or d 28 (110.78 vs 114.36 kg) between treatments (CEC- vs CTRL, respectively). During wk 4 CTRL pigs tended to have greater ($P < 0.09$) ADFI compared to CEC- pigs (4.39 vs. 3.45 kg/d). Faecal samples (obtained on d 0, 14, and 28) were used to evaluate phylum-level bacterial community structure by sequencing the V4 region of the 16S rRNA gene. No significant differences were observed in microbial community structure between treatments over the time course of the experiment. Preliminary data suggests there may be utility in development of a caecectomized pig model to evaluate the role of the caecum in pig nutrient metabolism and health. Additional analyses are in process to investigate fibre digestion kinetics and bacterial community structure at the genus/species levels.

P158. The evaluation of caecal and faecal microbial community structure in caecum-cannulated grower pigs fed a high fibre diet

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The cecum is a major site of fermentation of dietary nutrients. There is a knowledge gap pertaining to the role of the cecum in nutrient metabolism and health. The objective was to examine the role of the cecum in fibre digestion by evaluating caecal and faecal microbial community structure in caecum-cannulated grower pigs fed a high fibre diet. A total of 12 barrows (initial BW = 26.79 kg, ~63 d of age) were fitted with caecal cannulae 2 wk prior to application of dietary treatments. Pigs were allotted to 1 of 2 dietary treatments (6 replicates/treatment): Control diet (CTRL; 3,289 ME kcal/kg) or CTRL + 22.5% soy hulls were corn oil was used to ensure the diets were isoenergetic (HIFI; 3,153 ME kcal/kg). All pigs were fed treatment diets from wk 0 to 4. Caecal and faecal samples collected at wk 0, 2, and 4 were used to evaluate bacterial community structure by sequencing V4 region of 16S rRNA gene. Data were analysed by PROC MIXED procedures of SAS. Growth performance was analysed to support model development. Pigs fed HIFI diet had reduced ADFI compared to CTRL pigs during wk 2 (2.81 vs 2.25 kg/d, $P = 0.014$). CTRL pigs had greater ($P < 0.05$) BW at wk 0 and 2 and tended ($P < 0.07$) to have greater BW at wk 4 (43.32, 58.68, and 76.28 vs 40.01, 55.74, and 73.39 kg, CTRL vs HIFI, respectively). Overall, community structure was different comparing caecal to faecal samples ($P < 0.001$). Samples obtained at the conclusion of experiment (wk 4) indicate significant effects of dietary treatment (HIFI vs CTRL) in both caecal and faecal microbial community structure ($P < 0.01$). This data demonstrates caecal and faecal microbial communities are different and those communities change in response to dietary fibre.

P159. Standardization of the C:N ratio in ileal digesta of pigs alters relationships among fermentation end-products during in vitro hindgut fermentation

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Undigested protein that becomes available for the microbiota in the hindgut can be used as building blocks for bacterial cells or can enter different catabolic pathways. Degradation via protein fermentation pathways is least preferred, as fermentation end-products released can be toxic for the host. Gearing microbial protein metabolism towards protein synthesis or degradative pathways that result in less toxic end-products, for example through nutritional interventions, is an interesting strategy for improving health. We studied variation in protein fermentation patterns, as a result of substrate composition. Ileal digesta, obtained from cannulated pigs fed a variety of protein sources, were subjected to hindgut fermentation in vitro under different conditions; 1) ileal digesta were fermented as is, and 2) ileal digesta were fermented after standardizing the C:N ratios. Gas production was monitored as an indirect measure of microbial activity, and fermentation end-products at different points in time were analysed by gas chromatography and high resolution mass spectrometry. Using principal component analysis, we identified

patterns in protein fermentation end-products and related them to the ileal digesta composition using stepwise regression. Protein associated fermentation end-product concentrations of e.g. isovaleric-, isobutyric-, phenylacetic-acid and p-cresol, were negatively affected by the available amount of high fermentable carbohydrates combined with a high C:N ratio. The aforementioned fermentation end-products positively correlated with NH_3 concentrations and negatively with short chain fatty acids (SCFA) concentrations. Standardization of the C:N ratio changed their relationship; isovaleric-, isobutyric-, phenylacetic-acid and p-cresol lost their correlation with NH_3 concentrations, became positively correlated with SCFA concentrations, and now showed a positive correlation with available amounts of high fermentable carbohydrates. Our observations demonstrate an important role of the C:N ratio in the relationship between fermentation end-products. At constant C:N, protein fermentation end-products follow carbohydrate fermentation and NH_3 , often considered as a proxy for protein fermentation, loses its predictive power.

P160. Particle size of commonly consumed grains and brans: An important functional property affecting fermentability by gut microbiota

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Grains are an essential component of pig feeds and human diets. However, it is unclear whether their particle size affects gut microbial fermentation. It was hypothesized that larger grain particles will be less fermentable, resulting in lower SCFA and total gas production most likely due to the smaller relative surface area.

In this study, sorghum and wheat grains, were ground to obtain particles of four sizes (i.e., 1000 ~ 1200 μm , 600 ~ 710 μm , 250 ~ 500 μm , 63 ~ 125 μm). These substrates were treated to remove free starches. Physical structure of substrates (either compact or expanded) were characterized by microscopy, prior to in vitro fermentation using a pooled faecal inoculum.

The SCFA and gas production were determined, and analysis of variance followed by Tukey test were performed (significant if $P < 0.05$). Pearson correlation coefficients (ρ) between particle sizes and fermentation outcome parameters were determined.

For all particle sizes, microscopy revealed a compact structure for sorghum, but by contrast an expanded structure for all wheat particles. Sorghum followed expectations- the two larger particles had reduced total SCFA ($\rho = -0.865$, $P < 0.001$) and gas production ($\rho = -0.850$, $P < 0.001$) compared with the smaller sizes. Generally, wheat did the opposite, i.e. the smallest size had a significantly lower total gas (~127 mL/g DM, $P = 0.014$), compared with a mean of ~157 mL/g DM for the larger three particles (no significant difference between them). Wheat total SCFA was positively correlated to its particle size with the total greatest for the larger particles, and smallest for the smaller particles ($\rho = 0.909$, $P < 0.001$). This contrast between sorghum and wheat must be partially due to physical structure as indicated by microscopy.

We suggest that for a compact structure, the surface area may be important for fermentability, while an expanded structure means that surface area is less important as it allows greater bacterial accessibility.

P161. Impact of supplementing lactating sows' diets with an Aspergillus oryzae-derived prebiotic

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Grains are an essential component of pig feeds and human diets. However, it is unclear whether their particle size affects gut microbial fermentation. It was hypothesized that larger grain particles will be less fermentable, resulting in lower SCFA and total gas production most likely due to the smaller relative surface area.

High prolific sows' productivity is limited by the sufficient nutrient intake required to meet lactation requirements, partly compromising their maternal ability and piglet survivability. Dietary-supplementation with an *Aspergillus oryzae*-derived prebiotic (AO) could stabilize the gut microbiota, improve feed digestibility, and nutrient absorption, enhancing production and swine health. This study intended to assess the influence of supplementing lactation diets with AO on sow and litter performance and piglet survivability. Eighty-four Large White sows (mean 2.3 parities) equally-divided into a control-group (CON) or a treated-group (AOF), balanced by farrowing order and backfat depth (42 sows \times group) were used in a commercial farm. The Control group was fed a commercial diet meeting lactation requirements (NRC, 2012), whereas the AOF group was fed the same diet top-dressed with 4g of AO-derived prebiotic/head/day. Groups received their respective diets from allocation into the farrowing house until weaning (24 days), trice daily as part of a broth mix with water in a ratio of 3.5 : 1 (water : feed) increasing from 2.5 up to 6.5 kg dry-diet/sow/day after 15 days. Sow bodyweight, backfat depth, Body-condition-score at farrowing, and weaning and feed intake were recorded. Recorded piglet variables included bodyweight at birth, after cross-fostering (conducted within treatment within 48 h from birth), and at weaning, number of piglets born, born alive, stillborn, mummified, mortality during lactation, and weaned. Productive data were analysed with one-way ANOVA. Mortality was analysed using a Chi-Square test. Sows and piglets' production traits measured, were not significantly affected ($P > 0.05$). However, feeding AO to sows reduced piglet mortality by 29% ($P < 0.05$) during lactation compared to CON group (11.4% vs. 16.1%, respectively). This might be explained by the transmission of balanced intestinal microflora from sows to piglets and the feed intake increment observed in sows from the AOF-group. Results suggest that AO-supplementation in lactating sows can increase piglet survivability.

P162. Combination of functional amino acids can promote performance and gut morphology in piglets

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Functional amino acids have many physiological roles as modulators of immunity, cell proliferation and as a source of energy in the intestine. We hypothesized that functional amino acids (AA) supplemented as a combination might improve piglet growth through the modulation of gut morphology after weaning.