

P212. Intestinal barriers in intrauterine growth restricted piglets

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Intrauterine growth retarded (IUGR) neonatal piglets show morbidity and mortality much higher than in their normal birth weight (NBW) littermates. Diarrhoea is second after crushing major reason of death in IUGR piglets. The development of the gut barrier systems, including epithelium and immune structures, in IUGR piglets is little known. Study aimed to evaluate microscopically (light, confocal and scanning electron microscopy) the epithelium and the Peyer's patch structures in IUGR piglets. Whole tissue samples were collected from the duodenum, jejunum and ileum of IUGR - NBW littermate pairs on postnatal day (PD) 7, 14 and 180. In IUGR neonates the continuity of epithelium was maintained, however, the foetal-type enterocytes were more abundant, filled with foamy cytoplasm (lack of large vacuoles), and showed poor expression of cytoskeleton proteins as compared to NBW. Moreover, in IUGRs the goblet cell number was reduced, as well as the intraepithelial leukocytes population. The number and size of Peyer's patches in the distal small intestine was low at birth but from the PD14 did not differ from NBW. Also, the cellular structure of Peyer's patch was like in NBW from the PD14 onward. Concluding, the immune system development in the gut mucosa of IGUR makes significant compensatory progress between PD7 and PD14. Though the Peyer's patch architecture is not different from that in NBW pigs at PD14, the reduced percentage of goblet cells and the increased number of intraepithelial leukocytes may ease the tendency of the neonates to develop inflammatory process in the gut.

P213. Specific fibre fractions can decrease E.coli adhesion and intestinal inflammation in weaned piglets

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Enterotoxigenic E.coli is associated with post-weaning diarrhoea in piglets. The initial step of an E.coli infection is to adhere to host-specific receptors present on enterocytes, thereby inducing immune responses. This study aimed to examine if specific fibre fractions in the piglet diet can prevent E.coli adhesion and immune responses. In total, 200 piglets were included in the trial: 10 piglets/pen × 10 pens/dietary treatment × 2 dietary treatments. Piglets (Danbred × Piétrain) were fed a control diet or test diet with 2 kg/ton of a mixture of specific fibre fractions derived from Araceae root and citrus, from weaning until 14 days post-weaning. Afterwards, 1 piglet per pen was euthanized, and a section at 75% of small intestinal length was taken for quantification of E.coli colonization on the mucosal epithelium by scraping and conventional plating. Samples of intestinal content (small intestine, caecum, colon) were taken for microbiota (qPCR) and SCFA (GC) analyses. Faecal samples were taken to measure myeloperoxidase (MPO) as biomarker for intestinal inflammation. Data were analysed by mixed model

analysis using R. Pen was considered as experimental unit, and differences were considered significant at $P < 0.05$ and trends at $P < 0.1$. Piglets fed the fibre mixture tended to have lower E.coli colonization to the mucosal epithelium (5.65 vs. 4.84 log₁₀ CFU/g; $P = 0.07$), less E.coli in the caecum (8.91 vs. 7.72 log₁₀ CFU/g; $P = 0.03$) and more Lachnospiraceae, which are known butyrate producers, in the colon (11.3 vs. 11.6 log₁₀ CFU/g; $P = 0.03$). Furthermore, the fibre mixture tended to increase caecal butyric acid ($P = 0.07$), and decrease faecal MPO concentration (20.2 vs. 10.4 ng/g; $P = 0.07$), indicating less intestinal inflammation. To conclude, this study indicated that specific fibre fractions from Araceae root and citrus in piglet weaner diets may reduce the risk of pathogen overgrowth by decreasing E.coli adhesion and intestinal inflammation.

P214. Enzymatically treated yeast in diets of weanling pigs

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Abating the weaning-induced disturbance in gastrointestinal function is essential for ameliorating the reduction in post-weaning performance of weanling pigs. Prebiotics are gaining wider use for their benefits however, the benefit of enzyme-treated yeast in the diet of weanling pigs has not been adequately explored. This study was conducted to determine the physiological response of weanling pigs to dietary enzymatic digest of whole yeast (HY40). At 21-d weaning age (6 kg BW), 192 piglets in 32 pens of 6 piglets per pen with 8 pens/diet were assigned to 4 corn-soybean-based diets supplemented with 0 (control), 1, 2, or 4 g HY40/kg. Diets were provided in two phases from days 0 to 14 and 14 to 43 post-weaning. General linear models procedure was used in data analyses and preplanned contrasts of HY40 to control were used to separate means. Total tract digestibility of dry matter, energy, and N increased ($P < 0.05$) by 3.5, 5.7, and 8.0% points, respectively with age; concentrations of serum immune markers increased ($P < 0.05$) with age. Supplementing diets with HY40 increased ($P < 0.05$) serum catalase and IgG on days 14 and 43 respectively. Ileal mucosa nutrient transporters, pro- and anti-inflammatory marker genes measured on day 43 were not affected by diets but ileal mucosa glutathione peroxidase-4 increased ($P < 0.01$) linearly. Ileal villus height/crypt depth ratio was greater ($P < 0.01$) in pigs fed HY40-supplemented diets relative to control pigs. No dietary effects on total ileal eubacteria, Lactobacilli sp., Streptococcus, Enterococcus, or E. coli 16S rRNA gene copies; ileal short-chain fatty acids, branched-chain fatty acids, and volatile fatty acids were observed. However, ileal butyrate concentration increased ($P < 0.05$) in pigs fed HY40 supplemented diets. The observed changes in serum and mucosal antioxidant markers, intestinal butyrate concentration in piglets fed HY40-supplemented diets may be indicative of beneficial gastrointestinal improvement in weanling pigs.

P215. Higher amino acid demand in portal drained viscera of post-wean piglets

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Little is known about amino acid (AA) requirements of piglets right after weaning where piglets face multiple stressors. Stress level was hypothesized to affect AA requirements. To study this, piglets were exposed to a smooth transition onto solid feed by giving them regular meals until day 3 post weaning (C-d3, n = 8) or until day 10 (C-d10, n = 8). Another group of piglets were exposed to a higher stress level, i.e., withholding feed until 24 h after weaning (F-d3, n = 8). On day 3 and 10, piglets were fed ½ hourly test meals at a level of 2.4 × the energy requirements for maintenance. After 5.5 h, the test meal was mixed with U-13C labelled Spirulina hydrolysate and fed in the same way for another 6 h. Jugular and portal vein blood plasma samples were taken and analysed on tracer and tracee AA by LCMS and GC-C-IRMS. Differences in levels of jugular and portal blood were taken as a proxy for the arteriovenous difference over portal drained viscera (PDV). Net balances (NB) over the PDV were calculated for tracer and tracee, yielding an enteral and endogenous part of the NB. Data were analysed using a MIXED model.

F-d3 had a higher protein breakdown due to weaning stress as indicated by higher urea plasma levels compared to C-d3 (P = 0.09). F-d3 showed a negative NB for essential AA (EAA) from the feed (P = 0.05), resulting in a 19% lower flux of EAA from PDV (P = 0.05) compared to C-d3. The uptake of arginine by the PDV was 3x higher in F-d3 and C-d3 (P = 0.01) compared to C-d10 that showed a net release of arginine (P = 0.05). It can be concluded that a high level of nutritional stress influenced EAA flux from PDV and stimulates protein breakdown. A high arginine uptake by the PDV probably plays a role in this.

P216. Transcriptomic and DNA methylation response to feed intake in the duodenum in high- and low-feed efficiency pig lines

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Feed efficiency is a complex trait of interest in animal breeding to reduce environmental impact of livestock herding and the cost of animal feed. A divergent selection on feed efficiency was carried out in pigs for more than 10 generations at an INRAE experimental unit, establishing lines of relative high- and low-feed efficiency in large white pigs. The objective of this study was to identify the molecular mechanisms underlying the divergence in feed efficiency between the two pig lines in the duodenum. We focused on the duodenum because of its sensory role in the hunger satiety pathways.

Duodenum mucosal samples were collected in post-weaning pigs from the two divergent lines either after a 12 h period of feed restriction, or with a 10 h period of feed restriction followed by a 2 h period of ad libitum feed access (n = 6 per group and per line). Transcriptomes and methylomes were analysed by poly-A RNA sequencing (RNA-seq) and by methylated DNA precipitation followed by sequencing (MeDP-seq), respectively. Transcriptomic reads were analysed with nf-core/rnaseq and limma-voom. MeDP-seq reads were analysed with nf-core/chipseq and the BayMeth method.

A total of 962 genes were differentially expressed in the duodenum mucosa between the conditions (fasted vs fed), in contrast with 318 differentially expressed genes when comparing the divergent lines. The

DNA methylome of the duodenum mucosa was unaffected by short term feed intake, but was distinct between the lines. More transcripts were affected by short term feed intake in the feed-efficient line than in the other line, including genes of the incretine secretion pathways involved in the production of GIP and GLP-1.

Thus the duodenum transcriptomic response to short term feed intake was distinct in feed efficient and less efficient pig lines. These differences might in part be due to differences in DNA methylation profiles.

P217. Influence of n-3 fatty acids in sow and piglet diets on ileal transcriptome of piglets 28 days post-weaning

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Selection for hyperprolific sows has increased litter size and the frequency of piglets with low birth weight which are more vulnerable to the challenges of weaning. Due to their anti-inflammatory properties, there is growing interest in the use of n-3 fatty acids (FA) in post-weaning diets. However, very little is known about their mode of action. This study aims to determine changes in the ileal transcriptome of post-weaned piglets fed n-3 FA provided either through maternal diet (lactation) or directly in the post-weaning diet. We used piglets from six litters (3 control sows and 3 n-3 FA sows). From each litter, 2 piglets with low and 2 with large birth weight were selected at weaning. For each weight category one piglet was offered a control diet and the other one an n-3 FA diet. At day 28 post-weaning (±56 days of age) ileal tissue samples were collected and total RNA was extracted. RNA-seq reads were mapped and quantified against reference genome Sscrofa11.1 using STAR and RSEM, respectively. Differential expression analysis was performed with DESeq2 using a Wald test to compare the different groups, adjusting for the factor sex in the model. Genes were considered differentially expressed with an adjusted P < 0.05 and absolute fold-change > 1.5. While n-3 FA in maternal diet modified the expression of only 8 genes, a total of 371 genes, 328 upregulated and 43 downregulated, were identified in n-3 FA piglets compared to control piglets. A functional categorization of the overexpressed genes revealed biological functions associated with intestinal and mineral absorption, and the metabolism of lipids. Furthermore, downregulated genes were related to gap junction channel activity and glutamate neurotransmitter release cycle. No effects of birth weight were observed. In conclusion, the inclusion of fish oil, mainly in piglet diet, modifies the ileal transcriptome regardless of piglet's birth weight.

P218. Dietary protein sources affect uremic toxin excretion in pigs

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Metabolites produced during protein fermentation by the microbiota in the hindgut, e.g. phenols and indoles, are known precursors of uremic