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Gut microbiota of growing rabbits fed diets with different fibre and lipid contents

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Fibre with its different fractions, both insoluble and soluble, is the main dietary component guaranteeing the normal functioning of the rabbit digestive physiology and gut health. Thus, the present study aimed to evaluate the effect of an increase of ADF from 18.1 to 18.8% associated with a decrease in dietary starch from 14.3 to 13.8% and an increase in dietary fat from 2.9 to 3.8% on the microbiota composition of caecal content and hard faeces. To this purpose, 576 crossbred rabbits (Hypharm, Groupe Grimaud, Roussay, France) were weaned at 31 d, assigned to the two dietary treatments, and fed the experimental diets until slaughtering (73 d of age), when hard faeces and caecal contents were sampled from 20 rabbits (10 per diet) in the afternoon (h.15:00-16:00) and analysed using a 16S rDNA multi-amplicon sequencing approach. Firstly, sequencing results showed that the microbial diversity and the bacterial community structure of the hard faeces barely differed from that of the caecal content ($P>0.05$). The overall microbial composition was dominated by the phylum of Firmicutes, the Clostridia and Bacilli classes, followed by Ruminococcaceae and Lachnospiraceae as dominant families. Then, as for the diet effect, no differences in alpha and beta diversity of microbiota were detected in rabbits fed the two diets. However, twelve genera, mostly belonging to the family of Lachnospiraceae, increased (Wald test, $P<0.05$) in rabbits fed the diet with the highest fibre and fat contents. Overall, these findings enhance our understanding about gut microbiota in growing rabbits and indicate that even small changes in fibre and fat of the diet may affect the composition of gut microbiota.

Gut microbiota-metabolome response to dietary porcine intestinal mucosa hydrolysate in piglets

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In piglets, a healthy gut microbiota contributes to regulating the immune system and enhancing resistance to pathogens. The use of porcine intestinal mucosa hydrolysate (PIMH) as an alternative to other protein sources has been reported to improve performance and profitability in piglets. The present study aimed to assess the effects on gut microbiome and metabolome of incorporating PIMH in the diet in piglets. The trial consisted of two treatment groups (n=16 pens/treatment; 6 piglets/pen). Pigs in the negative control (NC) group received a weaner I diet containing 3.5% skimmed milk powder and a weaner II diet containing 2.5% soy protein concentrate. In the PIMH group, these protein sources were replaced by 5% PIMH (Palbio 50RD®, Bioiberica S.A.U.) in weaner I and 2.5% PIMH in weaner II. Diets were iso-energetic and iso-protein and with a similar lactose content. At day 34 post-weaning, ileum content from the last 1.5 m before the cecum was collected from ten pigs (1:1 gender ratio) from each group. Digesta was homogenized and snap-frozen and used for microbiota analysis with 16S ribosomal RNA (rRNA) sequencing as well as metabolomics using ultra-high-performance liquid chromatography coupled with a time-of-flight (UHPLC-TOF). A permutational multivariate analysis of variance (PERMANOVA) was used for microbiota data, and an ANOVA comparison was done for metabolomics. Microbiota alpha- and beta-diversity were not significantly different ($P>0.10$) between study groups, but a significantly decreased (FDR<0.05) relative abundance of amplicon sequence variants (ASVs) of opportunistic pathogens from the Streptococcus genera was seen with PIMH. Metabolomics showed significantly ($P<0.05$) higher concentrations of spermine (protein-derived biogenic polyamine) and lower amino acid concentrations of N-acetyl-L-methionine and L-glutamine in the PIMH group, which could be related to an antioxidant action, and a positive modulation of metabolism, intestinal barrier and maturation, and protein digestibility. In conclusion, the use of PIMH may improve gut health in piglets through modulation of their gut microbiota and metabolome, which could explain the improvements in performance observed previously.