

Feed size and texture influence propionic and butyric acid concentrations and bacterial community compositions in the pig gastrointestinal tract

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Certain *Escherichia coli* are associated with postweaning diarrhoea and oedema disease in pigs, others are important zoonotic pathogens in the food chain. Antibiotics are commonly used to control this pathogen at the farm level, but natural approaches, such as feed strategies, are now being considered to replace antimicrobials in their use as growth promoters and therapeutic agents, to reduce the risk of antimicrobial resistance development. This has put new emphasis on using diet to control bacterial infections in pigs. Some strategies, such as use of probiotics, prebiotics, organic acids and plant extract supplements have shown promising results, although inconsistently, underlining the need for new reliable approaches. Thus, dietary modifications that lead to a modulation of the bioregulation of volatile fatty acids (VFA) can have an potential impact on the intestinal microflora.

Our objectives were to assess the effect of feed particles size and texture on the intestinal VFA profiles and concentrations, bacterial community composition, and pathogenic *E. coli* populations, and on growth performance. Fattening pigs (n=840) received one of six different diets (mash feed 500, 750 and 1250 µm and pellet feed 500, 750 and 1250 µm). Weight gain was monitored in pigs fed each diet formulation over the fattening period. At the slaughterhouse, caecal and colon contents from 165 pigs were sampled for enumeration of lactobacilli, enterobacteria, *Bifidobacterium* spp. and *E. coli* by quantitative PCR (qPCR) and VFA quantification. Acetic, propionic, butyric, valeric, isobutyric, isovaleric and caproic acids were quantified by capillary gas chromatography. The lactobacilli/enterobacteria ratio was determined with the 16S rRNA genes. Total intestinal *Bifidobacterium* spp. were also quantified using the 16s rRNA gene. The *yccT* gene was used to enumerate total *E. coli*, whereas the genes *eae*, *faeG*, *estB* and *cnf1* were amplified for quantification of virulent *E. coli* populations. All standard curves were constructed using PCR products. A decrease in feed conversion associated with pellet texture and/or 500 µm particle size was observed for each diet formulation (p<0,05;Least Significant Difference). In addition, caecal (p=0,0271) and colon (p=0,0012) propionic acid concentrations were lower for pellet than for mash fed animals, after comparison based on multiple linear regression. Similarly, caecal (p=0,0167) and colon (p=0,0008) butyric acid concentrations were also lower for pellet than mash fed animals. With respect to the feed particle size, caecal (p=0,0208) and colon (p=0,0006) butyric acid concentrations were higher for 1250 µm than for 500 µm. For total *E. coli* enumeration, caecal (p=0,01;Multiple linear regression) and colon (p=0,04;Multiple linear regression) *yccT* gene copies were higher for pellet than mash fed animals. Lactobacilli, enterobacteria and *Bifidobacterium* spp. qPCR results also support an impact on intestinal microflora of diet strategies involving feed size and feed texture.

This is the first report of the effect of feed texture combined with feed particles size on intestinal bacterial communities and the digestive system in pigs. Moreover, economic disadvantages of mash feeding can be countered by optimizing strategies, such as the use of mash feed for curative purposes or in the maternity and during stressful periods associated with greater vulnerability of animals. Thus, such strategies provide interesting alternatives to antibiotic use.