

Impact of mash feed on *Escherichia coli* populations and the digestive metabolites in the pig gut

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Escherichia coli causes postweaning diarrhea and oedema disease leading to substantial mortality and morbidity in fattening pigs. Various approaches are being considered to replace antimicrobials in their use as growth promoters and therapeutic agents, due to the risk of developing antimicrobial resistance. This has put new emphasis on using the diet to control bacterial infections in pigs. Some strategies such as probiotics, prebiotics, organic acids and plant extract supplements showed results, although inconsistently. Thus, new approaches are needed. The effect of feed texture in conjunction with feed size has never been extensively studied. Diet modifications can lead to diverse metabolic activities, for example a modulation in the bioregulation of volatile fatty acids (VFA). VFA concentrations increase in the gastro-intestinal tract when the peristalsis is decelerated and VFA possess antibacterial properties that are extremely pH-sensitive (between 5,6 and 6,6). The objectives of this study were to assess the effect of mash feed on the prevalence of pathogenic *E. coli* populations in relation to gut content, volatile fatty acid concentrations and growth performance. Fattening pigs (n=144) were submitted to one of six different diets (mash feed 500, 750 and 1250 µm and pellet feed 500, 750 and 1250 μm). Faecal samples and weight gain data were collected from pigs fed each diet formulation during fattening. At the slaughterhouse, caecal contents were sampled for E. coli virulence gene detection using multiplex PCR and ileal, caecal and colon contents were sampled for pH determination and detection of acetic, propionic, butyric, valeric, isobutyric, isovaleric and caproic acids by capillary gas chromatography. Evolution of *E. coli* gut populations in relation to VFA concentrations was explored. Thus, this study is the first to evaluate the effect of feed texture combined with feed size on intestinal *E. coli* and the digestive system in pigs.