

# The influence of grinding intensity and compaction of diets on the microbial community in the gastrointestinal tract of young pigs

J. Bullermann<sup>1</sup>, Saara J. Sander<sup>1</sup>, M. Arlinghaus<sup>1</sup>, Jutta Verspohl<sup>2</sup> and J. Kamphues<sup>1</sup>

<sup>1</sup>Institute of Animal Nutrition and <sup>2</sup>Institute of Microbiology, University of Veterinary Medicine Hannover, Foundation, Germany



Supported by:



Federal Ministry of Food, Agriculture and Consumer Protection

based on a decision of the Parliament of the Federal Republic of Germany

## Introduction

Several studies already showed that a coarse feed particle size (feed structure) reduces *Salmonella* prevalence in pig herds indicating that feed physical form affects the intestinal flora. The aim of the present study was to evaluate the influence of feed structure, determined by grinding intensity and further compaction, on the resident flora in the gastrointestinal tract of young pigs. Therefore the counts of lactobacilli, enterococci and coliform bacteria as selected microbial groups as well as the gastrointestinal milieu (e.g. pH, dry matter) were evaluated.

## Material and methods

**Animals:** weaned female piglets (n = 60)  
age: 33 d, BW: 7.96 ± 1.09 kg

**Diets:** based on wheat, barley, soybean meal  
213 g crude protein, 43.2 g crude fiber, 13.6 MJ ME per kg dry matter

Table 1: Feed processing and particle size distribution of the diets

diet	FP fine, pelleted	CM coarse, meal	CP coarse, pelleted	CE coarse, extruded
mill type	hammer mill	roller mill	roller mill	roller mill
> 1 mm (%)	8.97	45.8	41.6	29.3
< 0.2 mm (%)	42.4	27.2	32.7	43.7
dMEAN (mm) <sup>1</sup>	0.463	0.880	0.836	0.659

**Experimental design:** 15 animals in each group, 3 consecutive trials individual housing without bedding material ad libitum feeding (fed dry), free access to fresh water dissection after 4 weeks (age: 61 d; BW: 21.5 ± 3.16 kg)

### Physicochemical parameters:

pH in the stomach content of the cardia and pyloric region  
dry matter content and concentration of lactic acid in the stomach content  
particle size distribution in the digesta throughout the GIT (wet sieve analysis)

### Microbial populations:

Counts of enterococci, coliform bacteria and *Lactobacillus* spp. in the ingesta of the stomach, the distal third of the small intestine and the cecum

### Microbiological methods:

homogenized digesta samples (stomach, distal third of the small intestine, cecum) serial 10-fold dilution steps of each ingesta sample (1.0 g) in PBS 0.1 mL plated on selective blood agar (enterococci), Gassner agar (coliform bacteria) and Rogosa agar (lactobacilli) counting of cfu after 24 h or 48 h (lactobacilli only) of incubation

### Statistics:

Statistical analysis was performed by SAS 9.3 for Windows using 1-way ANOVA Values are expressed as mean ± standard deviation

## Results and discussion

The most pronounced effects of the feed structure on the physicochemical parameters measured were seen in pigs fed the CM diet. The other two coarsely ground, but further processed diets did not lead to dry matter contents (dm) or pH values significantly different from those obtained in pigs fed the FP diet (see table 2).

Table 2: pH, lactic acid and dry matter content of the stomach ingesta

diet	FP fine, pelleted	CM coarse, meal	CP coarse, pelleted	CE coarse, extruded
dm (g/kg digesta)	195 <sup>a</sup> ± 54.2	299 <sup>b</sup> ± 31.7	220 <sup>a</sup> ± 56.2	228 <sup>a</sup> ± 47.8
pH cardia	3.79 <sup>aA</sup> ± 0.557	5.15 <sup>bA</sup> ± 0.475	4.00 <sup>aA</sup> ± 0.979	3.79 <sup>aA</sup> ± 0.838
pH pylorus	3.76 <sup>aA</sup> ± 0.716	2.83 <sup>bB</sup> ± 1.06	3.62 <sup>aA</sup> ± 0.630	3.31 <sup>abA</sup> ± 0.634
lactic acid (mmol/kg fm)	5.71 <sup>a</sup> ± 6.01	17.6 <sup>b</sup> ± 8.28	9.69 <sup>ab</sup> ± 14.0	18.0 <sup>b</sup> ± 11.7

<sup>a,b</sup> within a row, means without a common superscript differ ( $P < 0.05$ )

<sup>A,B</sup> within a column, means without a common superscript differ ( $P < 0.05$ )

With the significantly higher dm content in the stomach of pigs fed the CM diet, the ingesta formed layers within the stomach, specified by highly significant pH gradients between the cardia and the pyloric region ( $P < 0.001$ ). As shown in figure 1, the different particle size distribution of the diets was also reflected in the digesta with the "coarsest structure" after feeding the CM diet. In contrast to poultry, in the GIT of pigs no marked mechanical comminution occurs.

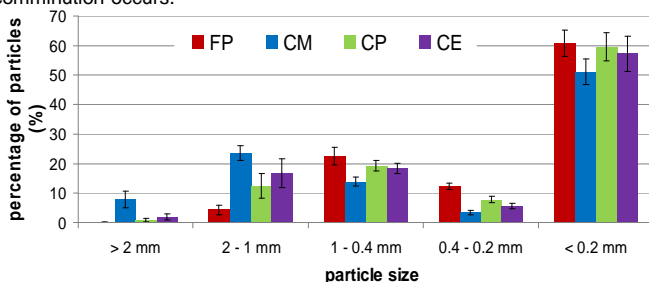


Figure 1: Particle size distribution in the colon content (in %); wet sieve analysis

To reveal effects of the feed structure on the resident microflora, lactobacilli, enterococci and coliform bacteria were chosen, because these bacteria represent major groups of the microbial community in the gastrointestinal tract. Counts of these microbial groups were significantly influenced by feed structure, as shown in table 3.

Table 3: Microbial counts (log<sub>10</sub> cfu/g digesta) at different localizations of the GIT

diet	FP fine, pelleted	CM coarse, meal	CP coarse, pelleted	CE coarse, extruded
<b>lactobacilli</b>				
stomach	6.9 <sup>a</sup> ± 0.851	7.9 <sup>b</sup> ± 0.461	7.4 <sup>ab</sup> ± 0.782	7.5 <sup>ab</sup> ± 0.992
small intestine	7.4 <sup>a</sup> ± 0.696	7.7 <sup>a</sup> ± 0.742	7.7 <sup>a</sup> ± 0.690	7.8 <sup>a</sup> ± 0.915
cecum	7.5 <sup>a</sup> ± 0.600	8.2 <sup>b</sup> ± 0.657	8.1 <sup>b</sup> ± 0.564	8.0 <sup>b</sup> ± 0.749
<b>coliform bacteria</b>				
stomach	2.3 <sup>a</sup> ± 2.30	4.4 <sup>b</sup> ± 1.42	2.5 <sup>a</sup> ± 2.42	1.8 <sup>a</sup> ± 2.41
small intestine	6.1 <sup>a</sup> ± 0.743	4.9 <sup>b</sup> ± 1.18	5.7 <sup>ab</sup> ± 0.752	5.3 <sup>ab</sup> ± 0.972
cecum	6.3 <sup>a</sup> ± 1.13	6.0 <sup>a</sup> ± 0.772	6.1 <sup>a</sup> ± 0.750	5.8 <sup>a</sup> ± 0.742
<b>enterococci</b>				
stomach	6.0 <sup>a</sup> ± 1.10	6.4 <sup>a</sup> ± 0.442	6.0 <sup>a</sup> ± 1.89	6.9 <sup>a</sup> ± 0.693
small intestine	7.3 <sup>a</sup> ± 0.888	6.1 <sup>b</sup> ± 0.831	7.4 <sup>a</sup> ± 0.750	7.2 <sup>a</sup> ± 0.696
cecum	7.5 <sup>a</sup> ± 0.808	7.1 <sup>a</sup> ± 0.578	7.6 <sup>a</sup> ± 0.843	7.7 <sup>a</sup> ± 0.766

<sup>a,b</sup> within a row, means without a common superscript differ ( $P < 0.05$ )

Perhaps due to a more efficient stomach barrier, characterized by high lactobacilli counts, high lactic acid content and marked pH gradients in the stomach content, significantly lowest counts of coliform bacteria ( $P = 0.011$ ) were found in the distal part of the small intestine of pigs fed the CM diet, although this group showed the significantly highest number of these bacteria in the stomach ( $P = 0.012$ ).

Significantly higher numbers of lactobacilli in the cecum in all three groups fed the coarsely ground diets (CM, CP, CE) can probably be explained by a higher substrate availability in the hindgut due to preceally undigested starch.

## Conclusion

In conclusion, in young pigs the feed structure influenced the resident gastrointestinal flora represented by lactobacilli, enterococci and coliform bacteria. The shift to higher numbers of lactobacilli and lower counts of enterococci and coliforms in pigs fed the coarsely ground diets might contribute to positive effects on gut health firstly due to a more efficient stomach barrier and secondly due to prebiotic effects of higher amounts of starch reaching the hindgut. This presumably resulted in changes of fermentation patterns with higher proportions of propionate and butyrate.

Literature: <sup>1</sup> Fritz, J., W.J. Streich, A. Schwarm, and M. Clauss. 2011. Condensing results of wet sieving analyses into a single data: a comparison of methods for particle size description. J. Anim Physiol Anim. Nutr., ESVN Suppl. 1-14 DOI: 10.1111/j.1439-0396.2011.01183.x.

The project is supported by funds of the Federal Ministry of Food, Agriculture and Consumer Protection (BMELV) based on a decision of the Parliament of the Federal Republic of Germany via the Federal Office for Agriculture and Food (BLE) under the innovation support program. It is further financially supported by Amandus Kahl & Co. KG, Bühler Feed and Biomass, and Wolking Maschinenbau GmbH