Effects of feed structure on the microflora in the gastrointestinal tract of broiler chickens

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Introduction

Reducing the use of antimicrobial substances in rearing and fattening period of food producing animals will be a major task. Not all possible measures to fulfil this goal are researched yet. It is for example well known that the diet composition acts upon the broiler intestinal microflora. Therefore, the aim of this study was to evaluate the impact of feed structure (grinding intensity, type of compaction) on the development and composition of the microflora and some digesta parameters of broiler chickens.

Material and methods

Trials: 3 consecutive trials, 5 weeks/trial
Animals: 100 male ROSS 708 broilers/trial, 4 groups with 25 birds each
Diets: d1 – d7: conventional starter diet
> d 8: chemically and botanically identical diets

BUT: different grinding intensity and processing

- group 1: finely ground, pelleted
- group 2: coarsely ground, pelleted
- group 3: finely ground + whole wheat, pelleted
- group 4: coarsely ground, extruded

Table 1: Feed ingredients, same for every group

Feed ingredient	% of the diet
Wheat	64.0
Soybean meal	30.0
Soybean oil	2.0
Mineral supplement	2.5
$CaCO_3$	1.5

Table 2: Particle size distribution (wet sieve analysis, mass-%)

Diet	Pellet fine	Pellet coarse	Pellet, whole grain	Extruded diet
> 1.0 mm	15.5	41.7	37.0	12.0
< 0.2 mm	40.4	31.6	31.4	48.9
dMEAN mm	0.520	0.856	0.972	0.437

Birds from every group were slaughtered at d 7/21/35.
On days 7 and 21: Digesta samples from gizzard, ileum and caecum were tested quantitatively on the counts of

- Staphylococci/Streptococci
- *E. coli*
- Lactobacilli
- *Clostridium perfringens*.

From the same locations: pH values in the content.
Particle size of the digestain the ileum was analysed on days 21 and 35.
Counting of bacteria: 1g of the intestinal content was serially diluted in 10–fold steps using PBS medium and plated on:

- Staphylococci/Streptococci on Staph/Strep agar
- Lactobacilli on Rogosa agar
- *E. coli* on Gassner agar
- *Clostrdium perfringens* on SPS agar

Both SPS and Rogosa agar had to be kept anaerobically.
The Campylobacter testing was done on trial day 35 by the Department of Food Quality and Safety, University of Veterinary Medicine Hannover.

Picture 1: Agar plates after a dilution series

Results

The birds fed the diet “Pellet coarse” had significantly more particles > 0.4 mm in the digesta, sizes both in ileal and rectal content compared to all other groups (Figures 1 and 2).

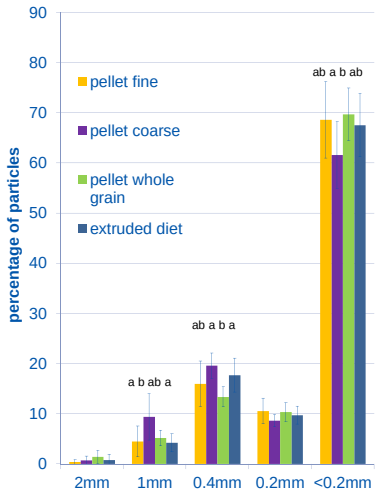

Fig. 1: Particle size distribution in the ileal content day 21, n per group = 9

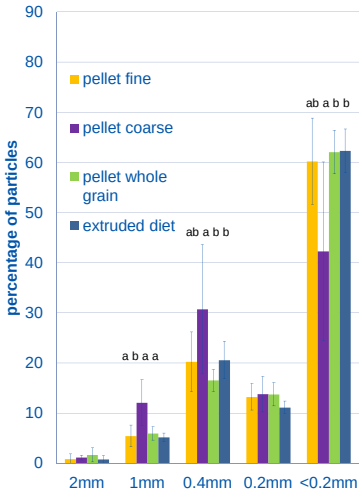

Fig. 2: Particle size distribution in the rectal content day 21, n per group = 9

In addition, both the lowest pH values and the lowest bacterial counts in the gizzard on trial day 21 were found in this group (Tables 3 and 5). The pH value changed extremely in this feeding group, once the digesta entered the small intestine: In this location, a comparison to the other feeding groups shows that the birds fed the diet “Pellet coarse” had the highest pH values in the digesta.
Regarding the counts of Campylobacter, in the groups fed the extruded diet the highest and in the group “Pellet, whole corn” the lowest values were determined (Table 4).

Table 3: pH values in the digesta (day 21, n per group = 15)

	Pellet fine	Pellet coarse	Pellet, whole grain	Extruded diet
Gizzard	3.55 ± 0.70	3.27 ± 0.50	3.40 ± 0.74	3.34 ± 0.79
Ileum	6.82 ± 0.96	7.19 ± 0.89	7.04 ± 0.95	6.60 ± 0.83
Caecum	6.44 ± 0.63	6.52 ± 0.57	6.64 ± 0.54	6.58 ± 0.44

Table 4: Counts of Campylobacter (d 35, n per group = 15)

Pellet fine	Pellet coarse	Pellet, whole grain	Extruded diet
2.64^{ab}	2.12^{ab}	$\mathbf{1.45^{a}}$	3.52^{b}
± 2.74	± 2.78	± 2.23	± 3.07

While feed structure had no impact on bacterial counts of *E. coli* or *Clostridium perfringens*, especially in the caecum significant differences between the feeding groups were found for the gram positive bacteria Staphylococcus/Streptococcus and for lactobacilli. In all three parts of the GIT that were examined in this study the birds of the group fed the extruded diet showed higher numbers of Staphylococci/Streptococci than the other feeding groups. Additionally, numbers of lactobacilli in the caecum were also significantly higher in the group “Extrudate” compared to the other ones (Table 5).

Table 5: Bacterial counts (lg CFU/g digesta) in the gastrointestinal contents (day 21, n per group = 9)

Species	part of GIT	Pellet fine		Pellet coarse		Pellet, whole grain		Extruded diet	
Staphylococci/ Streptococci	gizzard	$\mathbf{5.67^{ab}}$	± 1.36	$\mathbf{4.44^{a}}$	± 2.55	$\mathbf{6.03^{ab}}$	± 0.86	$\mathbf{6.20^{b}}$	± 0.69
	ileum	7.74	± 0.62	7.55	± 0.61	7.37	± 0.88	7.98	± 0.47
	caecum	$\mathbf{7.84^{ab}}$	± 0.46	$\mathbf{7.87^{ab}}$	± 0.48	$\mathbf{7.66^{a}}$	± 0.37	$\mathbf{8.29^{b}}$	± 0.49
E. coli	gizzard	2.84	± 1.86	2.64	± 1.53	2.70	± 1.86	3.39	± 1.63
	ileum	6.40	± 0.98	5.68	± 0.67	5.51	± 1.09	6.03	± 0.89
	caecum	7.62	± 0.64	7.51	± 0.42	8.02	± 0.55	7.55	± 0.67
Cl. perfringens	ileum	3.64	± 2.88	3.60	± 2.92	2.61	± 2.75	3.08	± 3.10
	caecum	2.60	± 2.13	3.84	± 2.62	2.29	± 2.49	3.41	± 2.85
Lactobacilli	gizzard	4.76	± 2.20	3.60	± 2.20	4.74	± 1.18	4.94	± 1.43
	ileum	6.72	± 1.00	6.57	± 1.06	6.44	± 0.93	7.02	± 1.21
	caecum	$\mathbf{6.72^{a}}$	± 0.97	$\mathbf{6.90^{a}}$	± 1.07	$\mathbf{6.82^{a}}$	± 0.67	$\mathbf{7.77^{b}}$	± 0.86

Conclusions

The milling intensity and feed processing had an impact on the microflora of the broilers‘ gastrointestinal content and influenced particle sizes and pH values of the digesta. In this study the gizzard could cope better with bigger particle sizes than it did with medium sized particles, which is impressively shown by the particle distribution figures of both ileal and rectal content. The low pH value of the group with the pellet coarse shown within the gizzard could have reduced the numbers of bacteria at this location as well. This might have consequences on bacterial counts in the following parts of the intestine. The extruded diet had a significant impact upon the caecal microflora, an effect which might have influenced the Campylobacter counts, too. Further investigations to understand the underlying mechanisms are necessary, especially the potential role of feed processing regarding campylobacter.

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