

Dietary rye supplementation affects immune competence related parameters in broilers

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Background and objectives

- Literature: dietary inclusion of rye increases viscosity of intestinal digesta → affecting nutrient absorption, gut morphology, microbiota composition, and immune-related processes in gut mucosa.
- Objectives: To investigate whether rye might be a helpful model-ingredient to investigate the effects of nutrition on immune competence related parameters of broilers.

Material and methods

- 960 day-old male Ross 308 chicks, randomly allocated to 24 pens
- 3 dietary treatments with 8 replicates/treatment (40 birds/pen)
- Birds were fed a control starter (d1-d13) and finisher diet (d29-d35)
- Three experimental iso-caloric and iso-nitrogenous grower diets (0%, 5%, and 10% rye) (d15-d28).
- Immune competence related parameters: microbiota composition in jejunum, genes expression in jejunal mucosa (microarray), and jejunal morphology.

Results

- No effect of treatment on microbial diversity in jejunum (Fig. 1)
- Exchange between *Lactobacillus* species occurred (Table 1).
- 5% or 10% rye in the diet (d15-28) decreased performance and litter quality (Table 2), but increased villus height, crypt depth, and surface of goblet cells in the jejunum (Table 4).

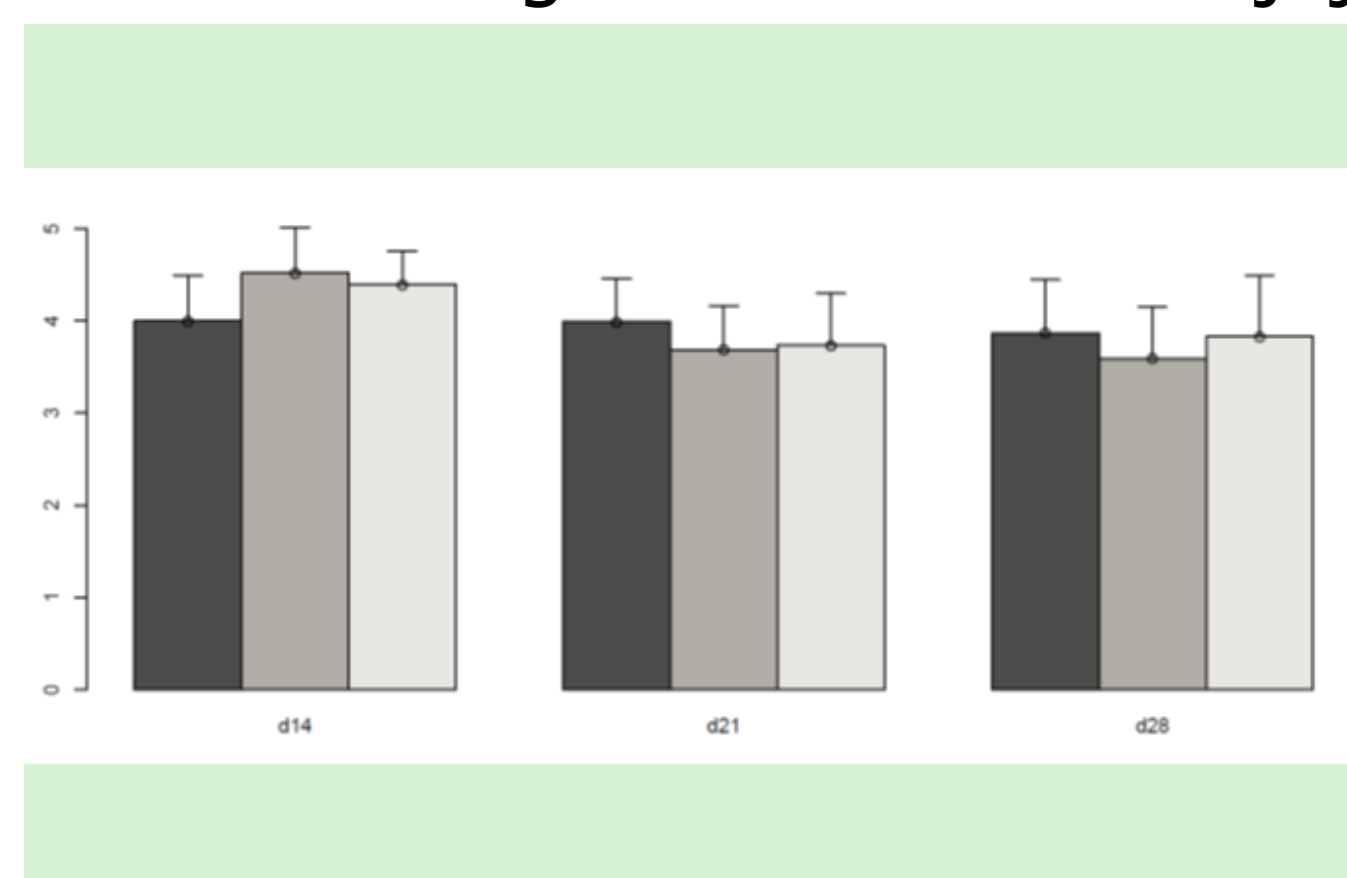


Figure 1. Shannon diversity index of jejunal microbiota in 0% (left), 5% (middle), and 10% (right bar) rye-diets at d14, 21 and 28.

Family	Genus	Species	0% rye	5% rye	10% rye	P-value
Lactobacillaceae	<i>Lactobacillus</i>	<i>reuteri</i>	27.98	34.96	38.99	< 0.001
Lactobacillaceae	<i>Lactobacillus</i>		33.23	38.92	17.82	< 0.001
Lactobacillaceae	<i>Lactobacillus</i>	<i>salivarius</i>	16.84	11.68	21.98	< 0.001
Planococcaceae	<i>Staphylococcus</i>	<i>saprophyticus</i>	4.50	1.73	5.11	0.002
Enterococcaceae	Other	Other	2.64	1.51	2.05	0.006
Corynebacteriaceae	<i>Corynebacterium</i>	<i>stationis</i>	2.73	1.79	3.06	0.261
Streptococcaceae	<i>Streptococcus</i>	<i>luteciae</i>	0.96	0.40	0.86	< 0.001
Aerococcaceae	<i>Aerococcus</i>		1.45	0.95	1.18	< 0.001
Staphylococcaceae	<i>Jejunalicoccus</i>	<i>psychrophilus</i>	1.89	1.32	1.77	0.641
Aerococcaceae	<i>Facilamia</i>		1.64	1.72	1.53	0.110
Other	Other	Other	1.14	0.74	0.56	0.004
Total			95.02	95.72	94.92	

Table 1. Microbiota composition in the jejunal digesta (% of total) per treatment at 21 days of age.

Table 2. Growth performance per treatment; rye supplemented diets were only provided from d15-d28; Litter quality score ranged from 0 (wet and 100% caked) to 10 (dry and friable litter)

	Rye (%)			P-value	LSD
	0	5	10		
BWG (g/bird)					
0-14 days	503	511	501	0.290	14
15-21 days	569 ^{ab}	577 ^a	555 ^b	0.034	16
22-28 days	756	749	720	0.214	44
29-35 days	710	699	736	0.137	38
0-35 days	2538	2536	2512	0.746	80
Feed intake (g/bird)					
0-14 days	604	612	601	0.246	15
15-21 days	758	772	759	0.433	24
22-28 days	1128	1128	1124	0.985	67
29-35 days	1488	1485	1478	0.970	89
0-35 days	3603	3614	3612	0.976	115
FCR					
0-14 days	1.200	1.199	1.200	0.958	0.011
15-21 days	1.333 ^b	1.338 ^b	1.366 ^a	0.001	0.016
22-28 days	1.493 ^b	1.507 ^b	1.562 ^a	0.003	0.037
29-35 days	2.104	2.128	2.008	0.160	0.133
0-35 days	1.420 ^(b)	1.425 ^(ab)	1.438 ^(a)	0.075	0.016
Litter quality					
Day 21	7.0 ^a	6.5 ^b	5.6 ^c	<0.001	0.45
Day 28	6.8 ^a	6.4 ^{ab}	3.0 ^b	<0.001	0.53

^{a,b} Means in a row with different superscripts differ significantly (P < 0.05). (a,b) Means in a row with different superscripts between brackets indicate a trend (0.05 < P < 0.10).

- Genome-wide gene expression differed per treatment over time (d21 and 28; Fig. 2).
- At d21 and d28, numerous genes of the jejunal mucosa were down-regulated in the rye fed birds (Table 3).
- Only a few genes were upregulated (Table 3).

Table 3. Descriptive statistics of regulated probes/genes in jejunal tissue between dietary treatments at 21 and 28 days of the study.

Contrast	Probes ¹		Annotated genes ¹	
	Up	Down	Up	Down
Day 21				
5 vs. 0% rye diet	34	403	16	103
10 vs. 0% rye diet	14	313	3	103
10 vs. 5% rye diet	57	15	8	12
Day 28				
5 vs. 0% rye diet	4	22	4	6
10 vs. 0% rye diet	31	297	7	89
10 vs. 5% rye diet	5	282	2	94

¹ logFC > |1.3| and adjusted P-value < 0.05

- Expressed genes: involved in cell cycle processes of the jejunal enterocyte cells (cell growth, cell differentiation and cell survival; data not shown).
- Also complement and coagulation pathways (parts of the innate immune system) were affected.

Table 4. Gut morphology parameters per treatment of the jejunum at 14, 21 and 28 days of age

	Rye (%)			P-value	LSD
	0	5	10		
Villus height (µm)					
Day 14	1059 ^a	981 ^b	999 ^b	0.017	53
Day 21	1327	1408	1447	0.108	115
Day 28	1463	1548	1484	0.214	102
Crypt depth (µm)					
Day 14	244	227	230	0.459	30
Day 21	189 ^(b)	192 ^(ab)	219 ^(a)	0.074	29
Day 28	196	201	192	0.351	14
Surface of goblet cells (µm ²)					
Day 14	6628	6045	6098	0.926	1026
Day 21	8661	8256	9026	0.710	1971
Day 28	8333 ^(b)	9517 ^(a)	8329 ^(b)	0.093	1236

^{a,b} Means in a row with different superscripts differ significantly (P < 0.05). (a,b) Means in a row with different superscripts between brackets indicate a trend (0.05 < P < 0.10).

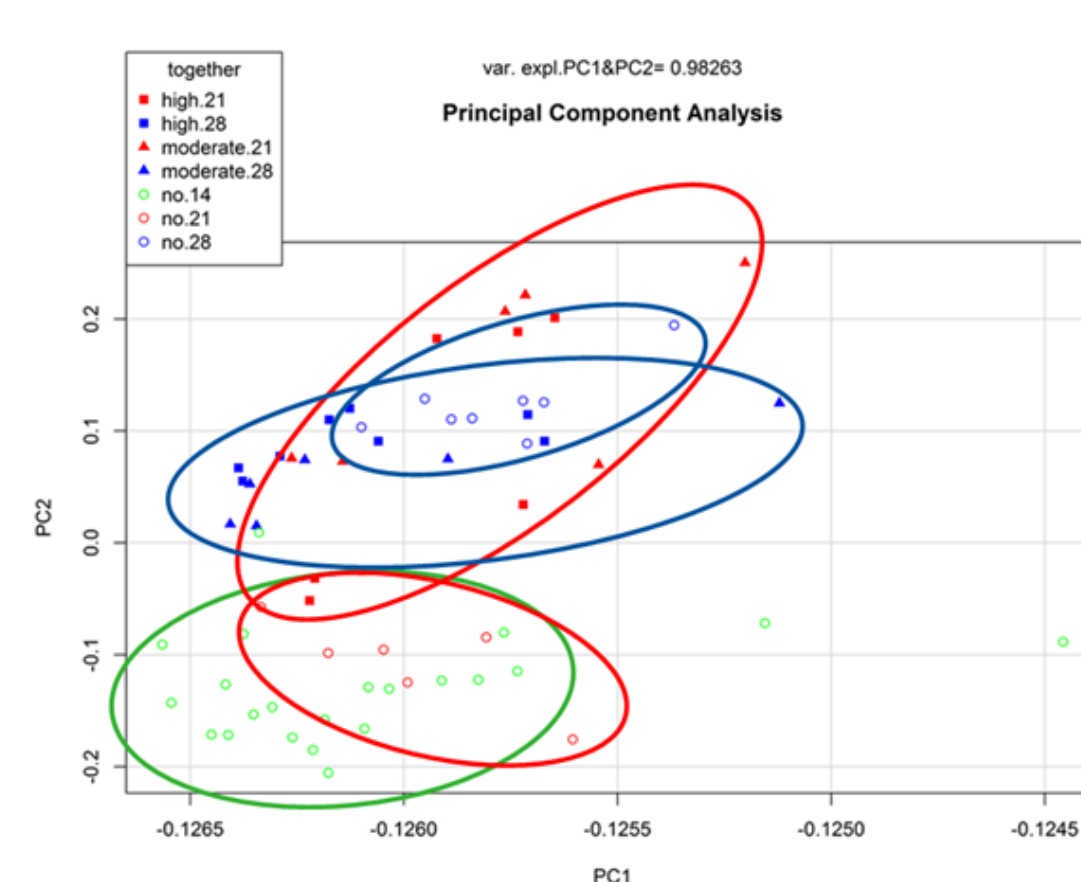


Figure 2. Principal Component Analysis.

Each symbol represents all expressed genes of one sample. Rye level: 0% (no; open circles), 5% (moderate; filled triangles), 10% (high; filled squares). Colors: time-points of sampling; d14 (green), d21 (red), and d28 (blue).

Conclusions

- Effect of rye in grower diet on broiler performance was limited.
- Dietary rye supplementation affected jejunal gut morphology, microbiota composition of jejunal digesta, and gene expression profiles of jejunal tissue
- Rye supplementation to grower diets is a helpful model to affect immune competence related parameters of broilers.

Acknowledgements

This research was commissioned and funded by The Feed4Foodure program line "Nutrition, Intestinal Health, and Immunity" (Feed4Foodure; BO-22.04-002-001).

