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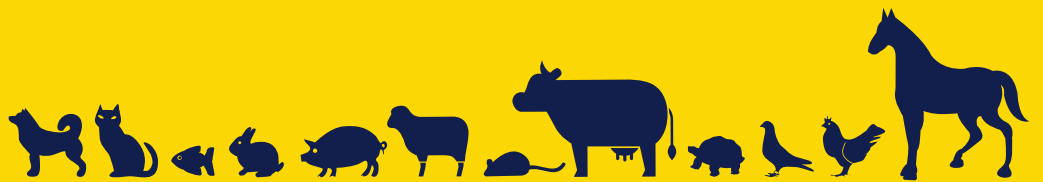


European Society of  
Veterinary & Comparative  
Nutrition



# CONGRESS PROCEEDINGS

## 23<sup>rd</sup> Congress of the European Society of Veterinary and Comparative Nutrition



University of Torino - Italy | September 18<sup>th</sup> - 20<sup>th</sup> 2019



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## Dietary supplementation with yeast cell walls affects feed conversion and gut transcriptome of broiler chickens

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**Introduction.** Dietary supplementation with yeast cell walls [1] has been found to reduce pathogenic bacteria load, to affect immune and inflammatory response, and to improve intestinal integrity and immunity in broiler chickens [2-5]. The present study aimed at evaluating growth performance and gut transcriptome in broiler chickens fed a yeast-supplemented diet.

**Animals, material and methods.** A total of 576 male chickens were randomly allocated to 2 diets, *i.e.* C (control) or Y (with 250-500 g/ton of yeast fractions as SafMannan® according to the growth period). Growth was monitored until 44 d of age. At 42 d, the jejunum of 24 chickens (12 per diet) was sampled for whole-transcriptome profiling. Strand-specific RNAseq libraries were prepared and sequenced on Illumina HiSeq4000 following a 50 single-end strategy. Performance data were analysed with diet as the main factor of variability for individual (PROC GLM) or pen data (with pen as a random effect, PROC MIXED: SAS, 2013). A pairwise Differential Expression (DE) analysis was made using Deseq2 (adjusted  $p < 0.10$ , fold change  $> 1.5$ ), followed by a Gene Set Enrichment Analysis (GSEA).

**Results and discussion.** The yeast supplementation did not significantly affect final live weight (2,959 and 2,968 g in birds fed diets C and Y, respectively), whereas it decreased feed intake (114 to 111 g/d;  $p < 0.10$ ) and improved feed conversion (1.74 to 1.70;  $p < 0.01$ ). As to gene expression, four genes were significantly over-represented in broilers fed with the diet Y compared to C (Table 1). When looking at genes under-represented in animals fed with the diet Y (no matter of the statistical significance), GSEA identified seven gene sets significantly enriched. A functional interpretation of these transcriptional differences showed that significant genes and gene sets play pivotal roles in immunity, NF- $\kappa$ B signalling, apoptosis, interferon-mediated pathways, and inflammation processes [6-7].

**Table 1.** Differentially expressed genes in gut transcriptome at 42 d in broiler chickens fed diet Y vs. diet C. Positive Fold Changes (FC) stands for an up-regulation in the former vs. the latter ones.

Gene ID	Gene name	Gene description	FC	p-value <sup>1</sup>
ENSGALG00000005795	CYP2C23b	cytochrome P450, family 2, subfamily C, polypeptide 23b	2.32	2.46E-08
ENSGALG00000017652	TTC9	tetratricopeptide repeat domain 9	2.47	0.015
ENSGALG00000048539	BHLHE41	basic helix-loop-helix family member e41	2.39	0.019
ENSGALG00000008997	STEAP4	STEAP4 metalloreductase	4.00	0.082

<sup>1</sup>Benjamini-Hochberg p-value correction.

**Conclusion.** Due to the limited number of DE genes, clear-cut conclusions about the impact of yeast on gut transcriptome cannot be drawn. Nevertheless, based on the biological functions of the few significant genes and the GSEA results, we hypothesize that yeast supplementation, besides improving feed conversion during growth, might improve anti-inflammatory state and immune responses of chickens against pathogens.

**References:** [1] Guang-Da Xue et al. (2018) Anim. Nutr. 3: 399-405; [2] Chacher et al. (2017) World's Poultry Science Journal 73: 831-844; [3] Hashim et al. (2018) Poult. Sci. 97:203-210; [4] Reisinger et al. (2012) Liv. Sci. 143: 195-200; [5] Tian et al. (2016) Anim. Feed. Sci. Tech. 215: 144-155; [6] Imig (2005) Am. J. Physiol. Renal. Physiol. 289: F496-503; [7] Inoue et al. (2012) Arthritis. Rheum. 64: 3877-3885.