

### **S3-0226 Impact of *Lactobacillus acidophilus* d2/csl (CECT 4529) supplementation on broiler caecum microbioma and metabolic functions**

Gerardo Manfreda, Paola Moniaci, Federica Palma, Alessandra De Cesare

*Dept. of Agriculture and Food Sciences, University of Bologna, Ozzano dell' Emilia (BO), Italy*

Corresponding author: [alessandra.decesare@unibo.it](mailto:alessandra.decesare@unibo.it)

This study examined the effects of the dietary supplementation of *Lactobacillus acidophilus* D2/CSL (CECT 4529) on broiler caecal microbioma and metabolic functions. A total of 14 caecal contents were tested. Four samples were collected at day 0, before dietary treatment. Moreover, five samples were collected from both control and treated groups at 41 days. At the end of the rearing period the relative abundance (%) of Lachnospiraceae was significantly higher in treated birds in comparison to the control (17.07 vs 14.39;  $P=0.036$ ). The bacterial species significantly higher in the chickens treated with  $1 \times 10^9$  CFU/kg of *Lactobacillus acidophilus* were *Ruminococcus obeum*, *Clostridium clostridioforme*, *Roseburia intestinalis*, Lachnospiraceae bacterium 14-2T and *Coprococcus eutactus*. Part of these species belongs to *Clostridium* cluster IV, positively impacting gut health through the production of butyrate and short chain fatty acids. The metabolic functions significantly higher in the treated group at 41 days belong to the biosynthesis of other secondary metabolites, glycan biosynthesis and metabolism, folding, sorting and degradation, carbohydrate as well as amino acid metabolisms. Particularly interesting is the higher level of the  $\beta$ -glucosidase contributing to the hydrolysis of glucose monomers from non-starch polysaccharides playing an important role in the fermentation of undigested carbohydrates and ultimately in animal performance and health.

**Keywords:** *Lactobacillus acidophilus*, metagenomic analysis, microbioma, metabolic functions, gut health