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Chicken caeca microbiome is altered by feed supplementation of phosphorous and calcium

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This study investigates the disturbance of the chicken microbiome under the influence of minerals phosphorus (P) and calcium (Ca). Microbial taxonomy was elucidated targeting the taxonomic marker 16S rRNA gene, and functionality was acquired through metagenome sequencing. Both tasks comprise bioinformatic processing, which demands computational calculations, and they were done in the bwHPC infrastructure. A significant difference in the microbiota was observed in all diets. Lachnospiraceae was the most abundant family, in the treatment supplemented with P (33% digesta, and 37% mucosa). In the Ca supplemented diet, the presence of Peptococcaceae (11%, and 8%, respectively) was increased when compared with the other treatments. At the functional level, for both digesta and mucosa, the metabolite information registered higher abundance of genes (50%) in P and Ca diets, while in control was only 40%. Thus, changes in supplementations result in important modifications on the microbiome.

Abstract (optional)

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