

Genetic characterization of poultry gut microbiota by 16S-rRNA gene sequencing.

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Genomic studies applied to animal gut content have made possible the discovery of microbiota composition, the identification of novel microorganisms, even those unculturable, and their relationship to diseases and environment. Understanding avian gut microbiome may provide clues to develop tools to increase broiler production and even allow antibiotic-free avian production. The aim of this study was to characterize the gut microbiota from healthy broiler flocks. DNA samples, isolated from ceca content of 18 Cobb male broilers fed with standard corn-soybean diet, with 42 days of age were employed to produce 16S rRNA (V3 - V4 region) libraries. Those were sequenced in an Illumina MiSeq using a paired-end protocol (2x300 bp). Sequence quality control analysis and taxonomic classification using SILVA Database (release 111) were performed with Mothur software Version 1.33.3. The results have shown that the most prevalent bacteria were from the Rikenellaceae (53.47%), Ruminococcaceae (24.57%), and Lachnospiraceae (7.41%) families, followed by Porphyromonadaceae (3.27%), Lactobacillaceae (1.25%) and unclassified families (6.19%). Genus *Alistipes* sp. (Rikenellaceae) showed the highest prevalence (52.63%) among all genera. Bacteria from this genus (previously *Bacteroides*) are strictly anaerobic gram-negative rods that resemble the *Bacteroides fragilis* group, in that most species are bile-resistant and indole-positive. They are weakly saccharolytic and most species produce light brown pigment on laked rabbit blood agar. Some species have human sources, such as *Alistipes obesi* sp. nov., *Alistipes indistinctus* sp. nov., *Alistipes onderdonkii* sp. nov., and *Alistipes shahii* sp. nov. The Ruminococcaceae and Lachnospiraceae families, members of the Clostridia class, are anaerobic, Gram-positive gut microbes. Members from Ruminococcaceae may play a role in biohydrogenation, and may also stimulate mucin production and degradation, required to keep the intestinal barrier integrity. Bacteria from Lachnospiraceae, abundant in the digestive tract of mammals and relatively rare elsewhere, have been linked to obesity and protection from colon cancer in humans, probably due to the production of butyric acid by many species within that family. This acid is important for both microbial and host epithelial cell growth. This study will base additional research applied to poultry production, pointing out microorganisms with potential biological use as probiotics and litter inoculum.

Key words: 16S rRNA, poultry production, , gut microbiome, *Alistipes*, Ruminococcaceae, Lachnospiraceae

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