



Characterization of Caecal Microbiota in Broilers that Differ in Genetic Strain, Nutrition, and Development of Woody Breast

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Objectives

Woody breast (WB) meat from broilers has undesirable textural characteristics, including, crunchiness and stickiness. Genetic, nutritional, and environmental factors are associated with the mechanism of WB development. A diverse microbiota plays an important role on the growth performance and health of the host, and greater than 900 species of bacteria have been isolated in the gastrointestinal tract of chicken. However, minimal information is known about the microbiota in the guts of broilers that yield WB meat. Therefore, the objective of this research was to characterize and compare the bacterial diversity of caecal microbiota in broilers with normal and woody breast fillets.

Materials and Methods

The Institutional Animal Care and Use Committee of Mississippi State University (IACUC-16-542) reviewed and approved all protocols. One-day-old mixed sex broilers from two strains (A2 and B2) were raised in 32 pens in a chicken house. Birds of each strain were randomly assigned to 16 pens (15 birds per pen) and 8 pens were fed a control diet and 8 pens were fed an amino acid reduced diet (digestible lysine, total sulfur amino acids, and threonine reduced by 20% as compared to the control diet). After 8 wk of growth, 4 male broilers with normal breast (1 chick per pen) and 4 male broilers with WB (1 chick per pen) determined by palpation were selected for each treatment (breed × diet). The cecum samples were collected after birds were euthanized and bled. DNA was extracted and amplified using universal primers that target the V3~4 regions of bacterial 16S rRNA for sequencing in Illumina MiSeq. Raw sequences were processed, and the quality was filtered using the default parameters of Quantitative Insights into Microbial

Ecology (QIIME 2). Differences between species were assessed using the unpaired two-tailed Student *t* test assuming unequal variance at $\alpha = 0.05$.

Results

Data suggested that the most abundant phyla in all samples were *Firmicutes*, followed by *Bacteroidetes* and *Proteobacteria*. Accounting for both abundance and evenness of the species present in each sample (α diversity), results indicated that there was no difference ($P > 0.05$, pairwise Kruskal–Wallis test) in the diversity of gut microbiota between two phenotypes (normal vs. woody), two strains (A2 vs. B2) or two diets (control vs. reduced). However, principal coordinate analysis plots (β diversity) revealed that the samples were clustered based on the phenotype rather than by the strain or diet. These results revealed that the microbiota of each bird with normal breast was more similar to each other than the microbiota of birds with WB. Among all species (300–400) identified, no difference ($P < 0.05$) existed in bacterial abundance between the two genetic strains. However, 16 and 13 species were differentially abundant ($P < 0.05$) between normal and woody breast and between control and reduced diet treatments, respectively. In the ceca of WB birds *Selenomonas bovis* (12.6%) and *Bacteroides plebeius* (12.3%) were the top two predominant bacteria; however, the relative abundances of these two bacteria were only 5.1% and 1.2% in normal birds, respectively.

Conclusion

Differences in the microbiome may be associated with the development of WB. Further studies are needed to investigate the potential mechanism and how to reduce broiler WB incidence by regulating their gut microbiota.