



Tropentag, September 20-22, 2023, hybrid conference
“Competing pathways for equitable food systems transformation:
Trade-offs and synergies”

Bacterial community succession in the intestinal tract of broiler chicken raised in an open-sided house system

WALEED AL-MARZOOQI

Sultan Qaboos University, Animal & Veterinary Sciences, Oman

Abstract

This study assessed the relative abundance of the intestinal microbial composition in duodenum, jejunum, ileum, and cecum of broiler chicken (Cobb500) raised in an open-sided house fed a nonmedicated corn-soybean meal diet from 0–35 days of age. A total of 1,179,68 sequences of 16S rDNA-based analysis were clustered into 253 operational taxonomic units at the 97 % sequence similarity which identified seven phyla and twenty-six Families. Of the total sequences, Firmicutes constituted a dominant phylum in duodenum, jejunum, ileum and cecum, accounting for 96.4 %, 88.8 % and 96.8%; respectively. The least dominant were Tenericutes and Thermi phyla, ranging from 0.12–0.01 % in the same gut order. At the Family level, Lactobacillaceae was dominant in duodenum, jejunum, ileum and cecum accounting for 73.87 %, 43.30 %, 77.81 % and 46.30%; respectively of the total sequences. Both Ruminococcaceae and Lachnospiraceae were the most prominent Families, accounting for 30.8 % and 28.61%; respectively of the total sequences of the reads obtained from the four intestinal sections. One of the most intriguing findings of this study is that, in addition to differences in relative abundance, the statistical comparisons of the 16S rDNA libraries of microbial communities revealed that each gut segment harbors its unique bacterial community. This was supported by Principal Coordinate Analysis (PCoA) which showed a clear separation of bacterial communities between jejunum and cecum samples compared to those from duodenum and ileum, suggesting some similarity in microbial community structure between the duodenum and ileum. The results obtained characterises the development of the chicken intestinal microbiota over time period under naturally ventilated housing system. The study provides unique insight into bacterial community and relative abundance of these were quite diverse and significant differences in microbial community composition from different intestinal segments were identified.

Keywords: 16S rDNA, broiler, chicken, house, intestine, microbiota