Bacterial Community Succession in the Intestinal Tract of Broiler Chicken Raised in an Open-sided House System

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INTRODUCTION

❖ The government began a program aimed to support small-scale poultry production, as part of the Omani government's strategy to develop and strengthen the country's food security and bridging the protein demand-supply gap.

❖ The majority of small and medium scale farmers in Oman uses an open-sided housing system to grow their chickens because of the simplicity of its construction, ease of heat management and minimal management cost.

OBJECTIVE

❖ The objective of this study was to assess the relative abundance of the intestinal microbial composition in duodenum, jejunum, ileum, and cecum of broiler chicken (Cobb500) raised in an open-sided house system using 16SrDNA-based analysis.

METHODOLOGY

Experimental Procedure
❖ Ninety-one-day-old chicks of Cobb500 were raised in an open and fed a conventional corn-soybean meal diet from Day 0-35 days of age. At 5, 15, 25, and 35 days of age, samples of gastrointestinal tract contents were collected from Duodenum ,Jejunum, Ileum and Caecum.

DNA Extraction
❖ Total DNA was extracted from contents of each luminal content samples using a QIAamp DNA Stool Mini Kit (QIAGEN, CA, Hamburg, Germany). The DNA concentration was evaluated by measuring optical density using Nano-Drop 2000 at a wavelength of 260 & 280 nm. The integrity of the DNA extracts was assessed visually using 1.0% agarose gel electerophoresis.

Polymerase Chain Reaction Amplicon Production and High-Throughput Sequencing:
❖ The variable regions V3-V4 of the 16S rDNA gene were amplified and sequenced. Amplicons produced from different intestinal luminal content samples were sent to a commercial company (BGI Genomic Lab, Tai Po Industrial Zone, New Territories, Hong Kong, China) for sequencing on the Illumina MiSequencing platform.

Bioinformatics and Statistical Analyses
❖ Bioinformatics and statistical analyses were performed using the QIIME and R package (v3.1.1). The alpha-diversity indices (ACE, Chao1, Shannon and Simpson index) were calculated to establish the relative abundance and diversity of the sequences. Metastats and R package (v3.1.1) (James et al., 2009) were used to compare and determine which taxonomic groups were significantly different ($p < 0.05$) among groups of samples based on intestinal segments and age period. The obtained p-value was adjusted by a Benjamini–Hochberg false discovery rate correction (Function 'p. adjusts' in the stats package of R (v3.1.1)).

RESULTS

❖ Microbial composition of the different intestinal segments differed significantly ($p<0.05$), implying that each region established its own unique bacterial population.
❖ At the Phylum level (Figure 1),
   ❖ Firmicutes sequences were the dominant group whereas, detected across different gut sections at all age periods.
❖ At the Family level (Figure 2),
   ❖ Across different age periods, Lactobacillaceae sequences were the most dominant group across different gut sections at all age periods.
❖ The microbial communities of the duodenum, jejunum, ileum, and cecum formed clusters as evident in the PCoA plot (Figure 3), There were overlaps among the four clusters, indicating that microbial communities of the duodenum and ileum were more similar.

CONCLUSION

❖ 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.
❖ This study adds to the existing body of literature by providing further characterization of the developmental patterns observed in the intestinal microbiota of chickens reared in an open-sided house.
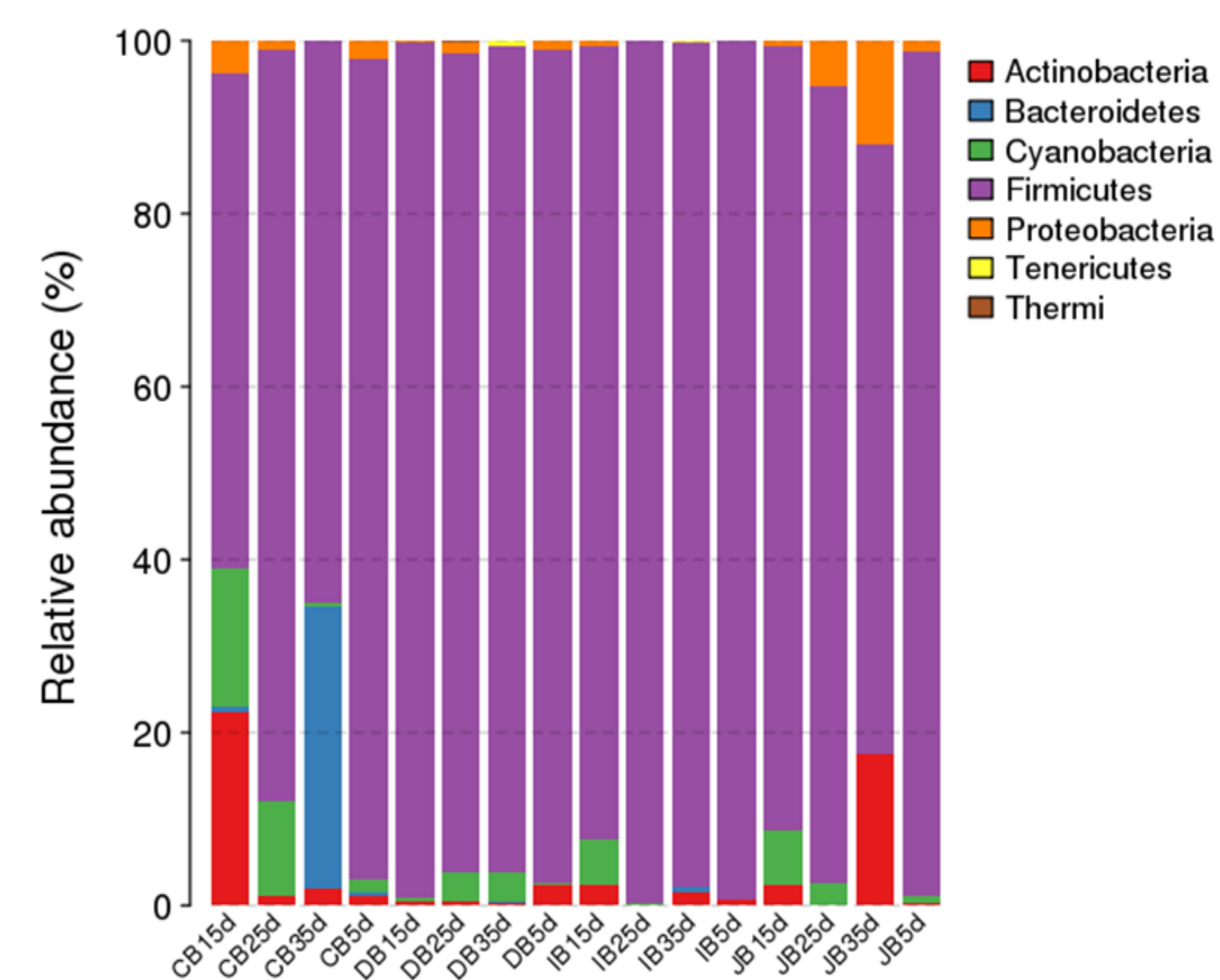❖ Future investigations should prioritize examining histological alterations associated with intestinal function.

Fig 1. Percentage of relative abundance of bacterial community of broiler chicken at Phylum level
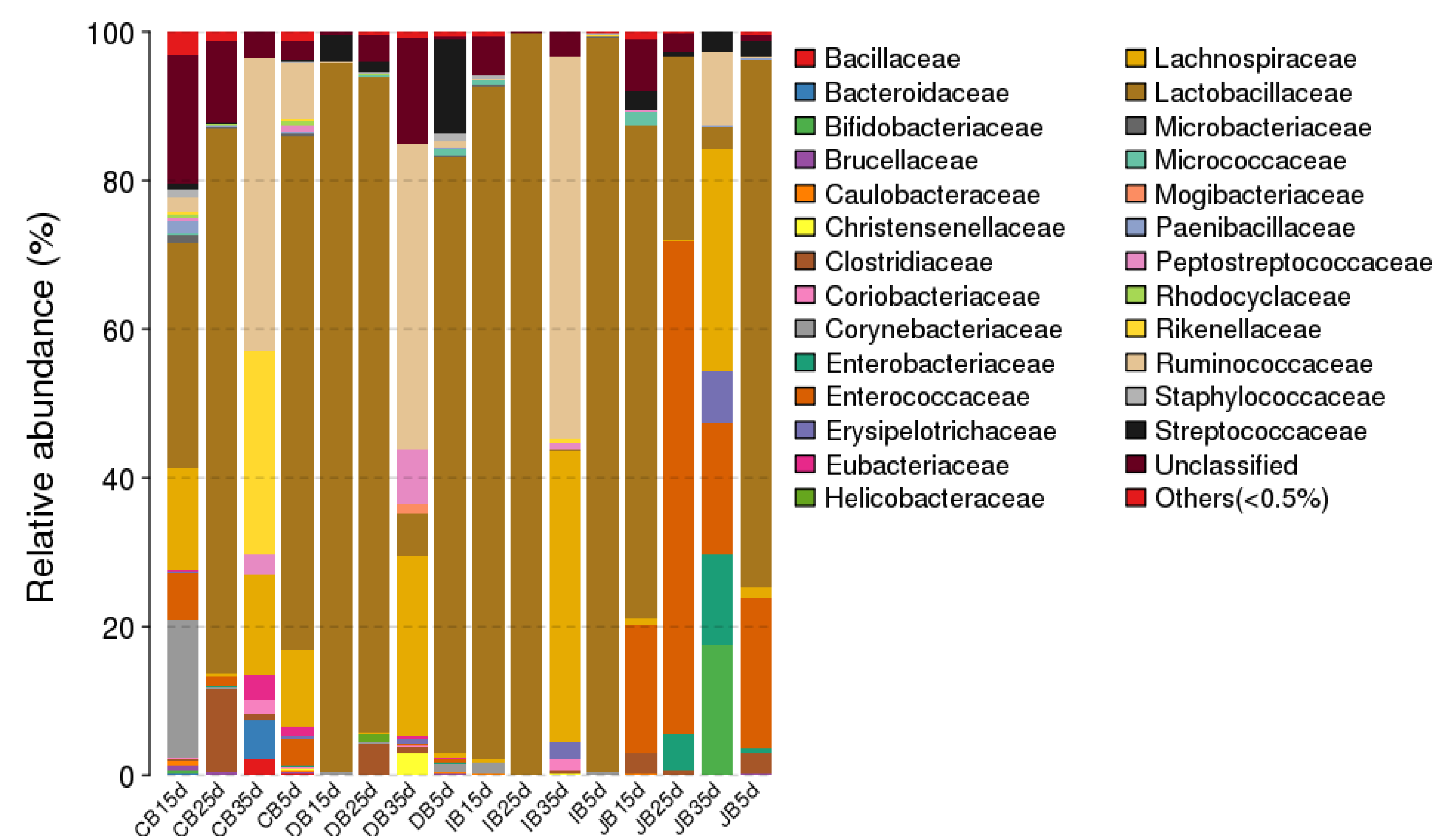

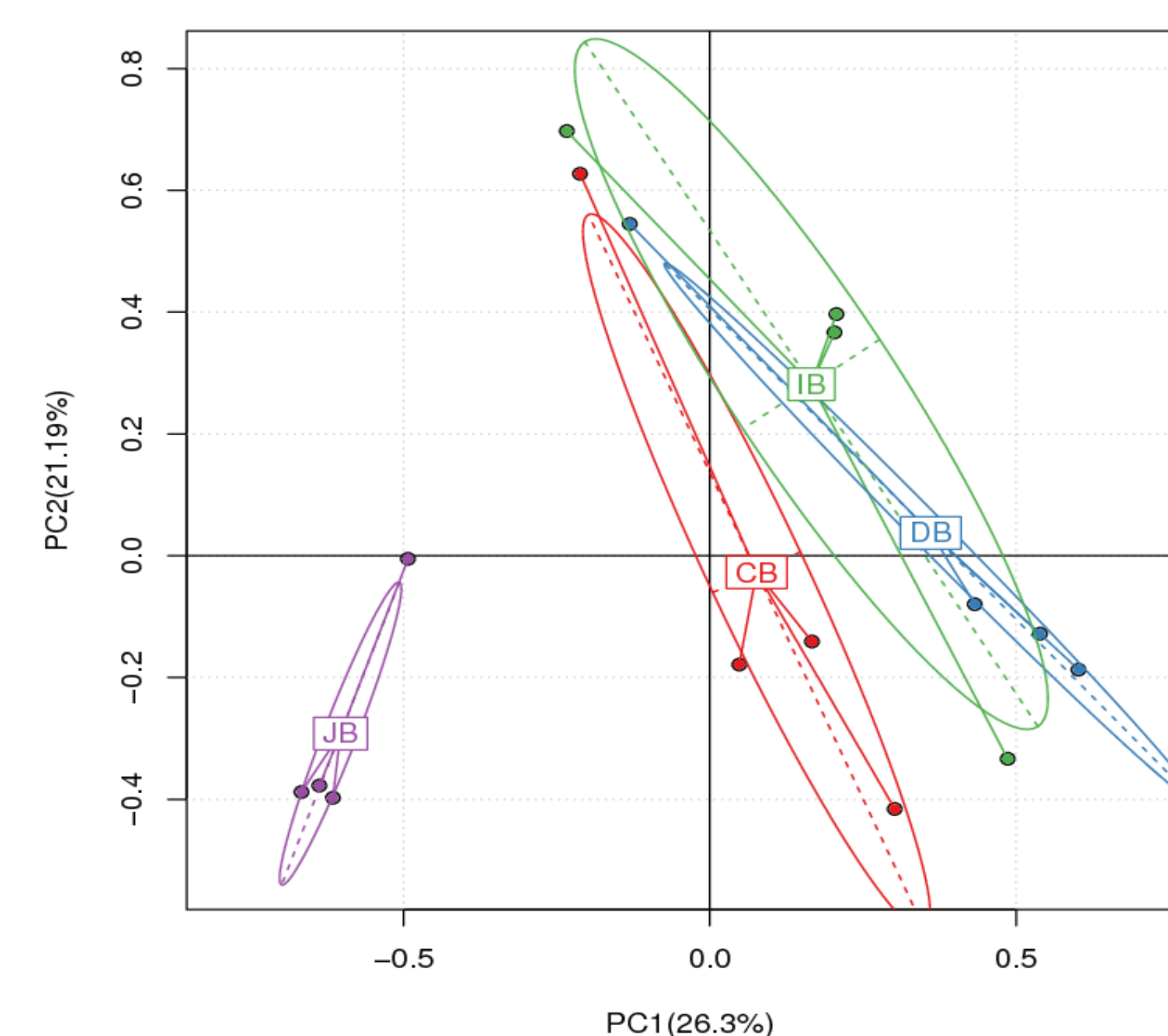**Fig 2.** Percentage of relative abundance of bacterial community of broiler chicken at Family level.

Fig 3. Principal coordinate analysis (PCoA) of dissimilarity between the microbial samples.

ACKNOWLEDGMENTS