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Changes in the microbial communities of air-chilled and water-chilled yellow-feathered broilers during storage
(#363)

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Introduction
Microbial control during processing and storage of broiler is a key factor that influences the quality and shelf-life of the final products (Kim, Hong Park, In Lee, Owens, & Ricke, 2017). The hypothesis for the present study was that different chilling systems would influence the initial microbiome on broiler carcasses and may contribute to the development of spoilage bacterial community.

Here, yellow-feathered broiler carcasses were subjected to an air or water chilling process at the slaughterhouse and then stored at 2 °C for up to 12 d. A high-throughput sequencing technique of 16S RNA gene amplicons was used to characterize bacterial communities of broiler carcasses during storage. Specifically, we aimed to determine whether chilling broiler carcasses in air or water would affect the microbiome on the carcasses differently.

Methods
A total of 96 yellow-feathered broilers were used in this study. Air chilling (AC) was conducted in a 180 m^2 refrigerated room that maintained at 2 °C. Water chilling (WC) used a pilot-scale chiller tank filled with 120 L mixture of ice and tap water without agitation. For each chilling group, eight chilled carcasses were packed randomly and stored at 2 °C. After 3, 6, 9, and 12 days of storage, one package of carcasses from each treated group was selected randomly for analysis.

Extraction of bacterial DNA and PCR amplification were performed according to the published method (Liu, Li, Li, & Luo, 2018). Sequencing (2 ×300 bp) was carried out on Illumina MiSeq platform (Illumina, San Diego, USA). Differences of bacterial richness (Chao 1) and diversity (Shannon) between AC and WC groups were explored by t-test. Principal coordinate analyses (PCoA) were conducted to compare similarities among samples using the R package software.

Results
A total of 2716407 high-quality reads were obtained and the high-quality sequences were clustered into 1161 OTUs. During storage, Chao1and Shannon index of both groups decreased consistently ($p < 0.05$) (Fig. 1). AC carcasses showed greater species richness (Chao1) than that from WC carcasses after 3 days of storage. For diversity, AC carcasses showed higher level of Shannon in comparison to WC carcasses initially (at day 0 and day 3), while no significant difference ($p > 0.05$) was found between AC and WC carcasses stored from day 6 to day 12.

The initial bacterial communities on broiler carcasses were dominated by *Proteobacteria*, *Firmicutes*, *Bacteroidetes*, and *Actinobacteria*, while *Proteobacteria* was the most prevalent phylum in the spoiled carcasses (Fig. 2A). At the genus level, the bacterial community structure was revealed to become less complex during storage (Fig. 2B). Despite the low abundances of *Pseudomonas* on the initial samples, a trend towards the succession of *Pseudomonas* with time during storage was observed in both chilled groups. At the end, *Pseudomonas*, *Psychrobacter* and *Shewanella* were the prevalent genera on AC carcasses, accounting for 46.4, 35.6%, and 8.5% of total microbial community, respectively. For WC carcasses, *Psychrobacter* and *Pseudomonas* were the main genera, representing 53.7% and 27.6% of the total genera, respectively. Principal coordinates analysis (PCoA) results revealed distinct separation of bacterial communities between the AC and WC carcasses stored at different day (Fig. 3), suggesting the strong effect of chilled methods on microbiota of broiler carcasses.

Conclusion
The present work describes an investigation on the microbiota of air chilled and water chilled yellow-feathered broiler carcasses during storage under aerobic conditions. Different chilling systems exerted their effects on the surface bacterial communities of broilers, and subsequently influenced the succession of bacterial diversity on carcasses during storage.

Notes

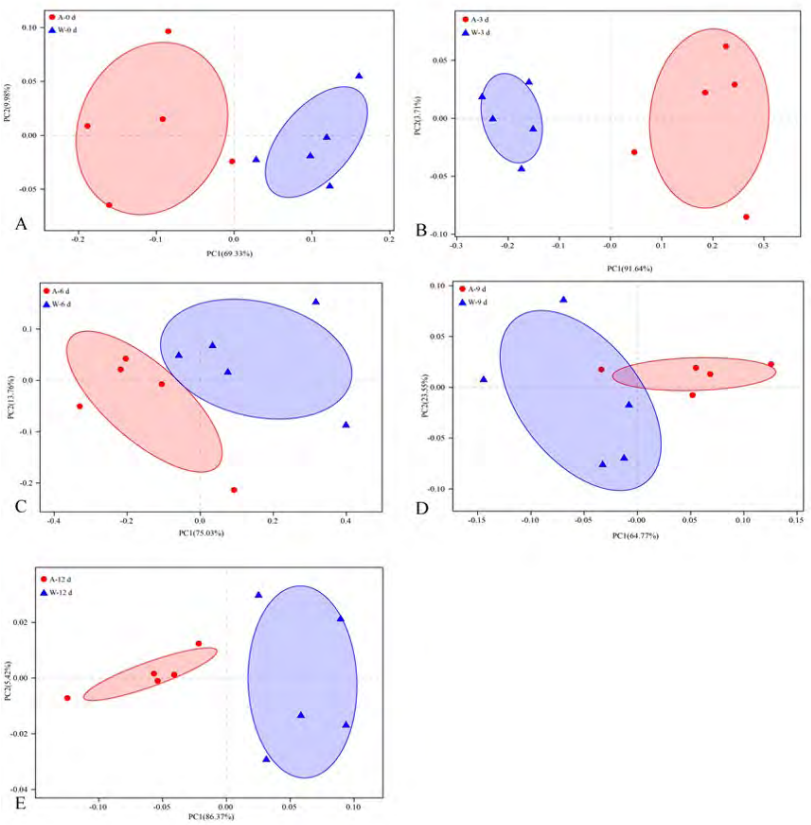

Fig.3
Principle coordinates analysis (PCoA) of microbial communities at different storage days. A, B, C, D, and E represent the storage time of 0, 3, 6, 9 and 12 days, respectively.

Notes

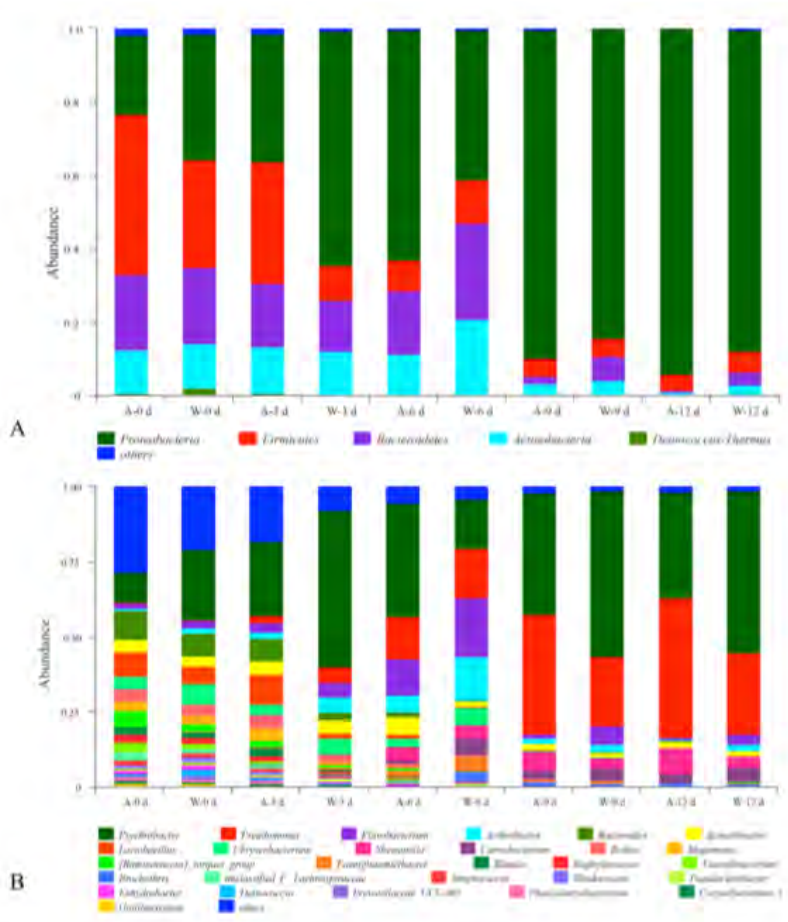

Fig.2
Characterization of the broiler surface-associated microbiota during storage.
(A) Relative abundance at phylum level;
(B) Relative abundance at genus level

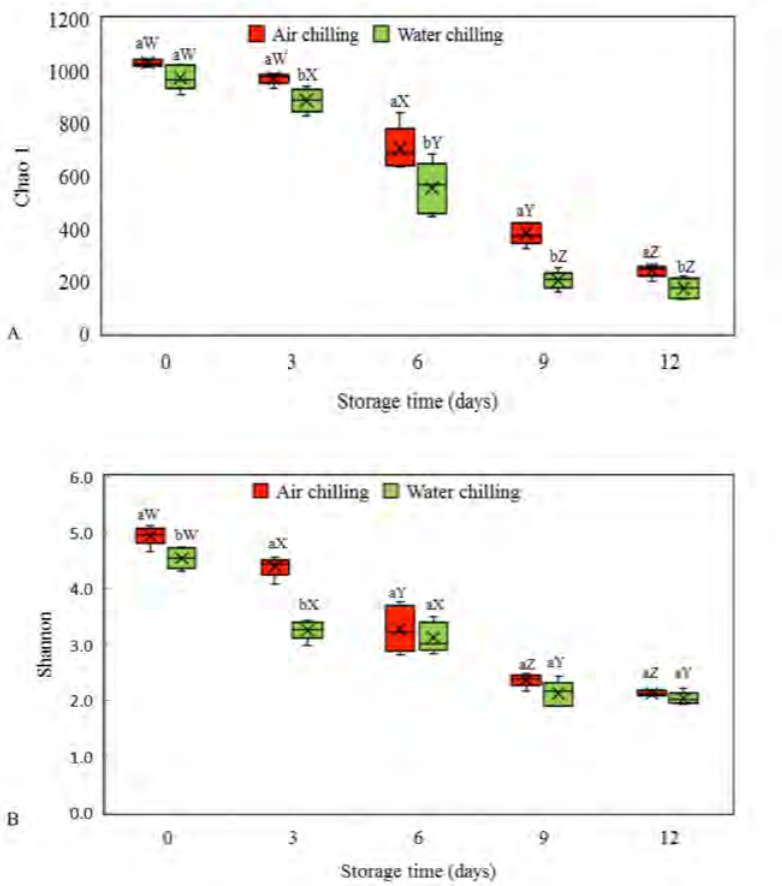

Fig.1
Alpha diversity indexes of bacterial community on broiler carcasses during storage. (A): Chao 1; (B): Evenness; n=5.

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