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Utilizing Microbiome and Bioinformatic Tools to Reduce Food Waste in Poultry

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Objectives

In chicken harvest, the post-harvest chilling process is a crucial step for food safety. Most facilities use either water immersion chilling (WC) or air chilling (AC) to rapidly cool the chicken. A holistic assessment of the consequences of each method to meat quality and shelf life is necessary to determine the impacts of each method. To address this knowledge gap, a multifaceted project was conducted to determine how the chilling system influenced the microbial ecology and subsequent deterioration of chicken breasts.

Materials and Methods

The study was conducted using a 2 × 2 × 2 factorial design to evaluate the impacts of chilling method (AC vs. WC), fabrication method (bone-in vs. boneless; BI vs. BL), and cold storage period (7 vs. 14 d) on the microbial ecology of chicken breasts. A total of 256 chicken carcasses were used for this study. Carcasses were obtained from a commercial processing plant following dressing and a single antimicrobial treatment. Twenty carcasses were removed for sampling as warm carcasses, and the remaining 236 were divided into eight groups for processing (AC-BI, AC-BL, WC-BI, WC-BL tray-wrapped for 7- and 14-d storage). Collection time-points included: warm, post-chilling, post-fabrication, post-storage, and after 3-d retail display. Microbiome samples were collected at each sampling using a PBS rinsate. Then, samples were further processed for microbiome analysis following standard methods, sequenced for the V4 region of the 16S rRNA gene, and analyzed using the QIIME2 pipeline.

Results

There were significant differences in microbial diversity between different chilling methods, fabrications methods, and cold storage times. Both chilling methods were different from the warm carcasses based on α diversity metrics, though the two chilling methods were not different from each other. However, there were differences in the β diversity between all three groups. Storage day significantly altered the faith's phylogenetic α diversity but had no impact on Shannon's α diversity. By both metrics, the diversity was reduced with increased length of storage, suggesting that a few organisms begin to dominate the product during dark storage. The fabrication methods also resulted in significantly different diversities when phylogenetic metrics (Faith's, unweighted UniFrac) were used. The products that were sampled prior to dark storage, regardless of chilling method, were dominated by Enterobacteriaceae, while those that were subjected to cold storage were dominated by Pseudomonadaceae. In the stored samples, AC samples tended to have a greater abundance of Moraxellaceae and Enterobacteriaceae than WC.

Conclusion

These results suggest that different treatments of chicken breasts, including chilling, fabrication, and storage time, all correspond with changes to the product microbiome. These data will be combined with microbiology, physiochemical, nutritive, and taste and color data as well as a techno-economic analysis to provide a deeper understanding of impacts of processing methods on poultry quality and shelf life.