EFFECT OF PROCESSING PARAMETERS AND STORAGE TIME ON THE SPOILAGE MICROBIOME OF TURKEY PRODUCTS

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I. OBJECTIVES

This study aimed to identify changes in the microbial ecology of processed turkey products, as a function of storage time and degree of processing.

II. MATERIALS AND METHODS

Three replicates of products each representing varying degrees of processing were prepared from 3 separate lots of turkey breast meat: T1: raw ground turkey; T2: raw ground turkey with salt added; T3: raw ground turkey with salt and spices added; T4: cooked link; T5: cured cooked link; T6: sliced deli; and T7: sliced cured deli. Cooked products were processed to 74°C and chilled to 4°C. Aerobic plate counts (APC), anaerobic plate counts, lactic acid bacteria, *Pseudomona*s spp. Cephaloridine fucidin cetrimide agar and psychrotrophic plate counts (PPC) were evaluated in raw treatments every 7 d for 21 d, and cooked treatments were evaluated every 28 d for 84 d. Microbial communities were evaluated by sequencing the V4 region of 16S ribosomal RNA gene using 250 bp paired end sequencing on the Illumina MiSeq platform (Illumina Inc., San Diego, CA). Sequence reads generated were quality filtered and processed within R and Mothur. The DADA2 pipeline was used to identify amplicon sequence variants (ASV). ASV were assigned taxonomy using the Silva database 132. Alpha diversity was estimated using observed ASV and Chao1 estimates; beta diversity was evaluated using weighted and unweighted UniFrac distance matrices. Raw (3 treatment × 4 storage times) and cooked (4 treatment × 4 storage times) samples were analyzed independently for plate counts, alpha diversity with storage time as a repeated measure with an independent covariance structure using the nlme and emmeans packages.

III. RESULTS

In raw treatments, main effect of storage time on all plate count methods ($P < 0.01$) was identified, which can be observed as growth; there was a main effect of treatment on APC and PPC ($P < 0.05$). Treatments 2 and 3 had lower APC and PPC, implying that salt may be an effective microbial inhibitor. In cooked samples, storage time was significant on cephaloridine, fucidin, cetrimide plates ($P < 0.01$), as *Pseudomonas* spp. proliferated regardless of treatment. Treatment by storage time interaction was observed in APC, anaerobic plate counts, PPC, and lactic acid bacteria ($P < 0.04$). Sliced and noncured samples had more growth, illustrating post-process contamination and nitrite inhibition. Storage time significantly influenced Chao1 and observed ASV alpha diversity measures in raw samples ($P < 0.01$) and main effects of treatment ($P < 0.05$) and storage time ($P < 0.03$) on observed ASVs in cooked products. For both Chao1 and observed ASVs in raw treatments, storage times of 0 and 7 d had more bacterial richness than 14 and 21 d. Observed ASVs decreased over time in cooked products. There were main effects of storage time and treatment on beta diversity in both the weighted and unweighted UniFrac distance matrix ($P < 0.01$). Raw samples clustered by “freshness,” with day 0 and 7 samples clustering apart from day 14 and 21.

IV. CONCLUSION

Microbial communities are modulated by degree of processing, ingoing ingredients, and storage time. Bacterial diversity decreases as products spoil and spoilage species start to predominate. This loss of richness can be explained by the overgrowth of spoilage taxa, such as Pseudomonadaceae, Enterobacteriaceae, and Lactobacillaceae. Shelf life extension may be better achieved by employing methodology that is more targeted at these core organisms.

Keywords: poultry, *Pseudomonas*, shelf life