Published April 25, 2019

2018 Reciprocal Meat Conference – Meat and Poultry Processing, Ingredient Technology and Packaging

Meat and Muscle Biology™

Evaluation of the Spoilage Microbiota Associated with Sliced Pre-Packaged Deli-Style Ham

C. G. Bower*, S. Fernando, and G. Sullivan

Animal Science, University of Nebraska– Lincoln, Lincoln, NE, 68588, USA
*Corresponding author. Email: cbower357@gmail.com (C. G. Bower)

Keywords: bacterial community, ham, microbial spoilage
Meat and Muscle Biology 2(2):58 **doi:10.221751/rmc2018.050**

Objectives

The objective of this study was to evaluate the spoilage microbiota of various sliced, case ready deli-style hams and identify differences between their microbiological communities.

Materials and Methods

Ham samples were procured at local retail stores from products available on the shelf. Three brands (A, B, C) of smoked, sliced, Ham, Water Added were purchased with a brand being considered the same product and establishment number. Replication was defined as having the same sell-by date indicating a common date of production; 3 different sell-by dates for each brand created 3 replications. Multiple packages of each brand and sell-by date were purchased to allow an unopened package to be used for each sampling date and were stored at 4°C. Sampling times were determined as follows: –4, –2 (4 and 2 wk prior to sell-by, respectively), 0 (sell-by date), 2, and 4 (2 and 4 wk after the sell-by day, respectively). Water activity and salt concentration were sampled at –4 only. Objective color (CIE L^*, a^*, b^*), pH, aerobic plate count (APC) and anaerobic plate count (AnPC) were evaluated throughout storage time. Bacterial community analysis was performed using high throughput 16S rRNA gene sequencing on the Illumina MiSeq platform. Sequences were processed using QIIME, binned into operational taxonomic units (OTUs) at 97% similarity and assigned taxonomy using the Greengenes database as reference. Water activity and salt concentration data were analyzed using R. Color, pH, and plate counts were analyzed as a 3 (brand) by 5 (storage time) factorial using R. Alpha and β diversity of bacterial communities were analyzed using QIIME and R. Alpha diversity was estimated using observed OTUs and Chao1 estimates, and β diversity was determined using a weighted UniFrac distance matrix.

Results

Salt and water activity were different between brands ($P \leq 0.007$). Brand A had less salt compared to brands B and C, while brand B had a lower water activity than brands A and C. Objective color values for L^* and a^* were not different ($P \geq 0.182$) between brands or storage times, but b^* was different between brands ($P < 0.001$). Brand A had greater b^* (yellowness) than brands B and C. There was a brand by storage time interaction for pH ($P = 0.021$). At wk 0, the pH of brand B was lower than any time during the study. There was a significant main effect of brand on both APC and AnPC ($P < 0.001$). Brand A had greater APC and AnPC when compared to brands B and C. Observed OTUs and Chao1 diversity estimates indicated there was a brand by storage time interaction for bacterial richness, where brand A wk –4 had the greatest bacterial richness followed by brand A wk 0. There was a main effect of storage time on the bacterial community structure ($P < 0.001$). Brand B and brand C were more similar in community structure compared to brand A.

Conclusion

The lower salt concentration in brand A may affect bacterial spoilage. Furthermore, results from this study indicate that the spoilage community associated with similar types of sliced ham is dependent on brand, implying that spoilage patterns and characteristics are related to environmental bacteria composition of the initial post-lethality contamination.

