

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

Meat and Muscle Biology™



Effects of Salt and Nitrite on the Spoilage Microbiota of Deli-Style Ham

C. G. Bower*, R. Stanley, S. Fernando, D. Burson, 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, nitrite, salt, shelf life
Meat and Muscle Biology 2(2):57

doi:10.221751/rmc2018.049

Objectives

The objective of this study was to determine the effect of salt and nitrite concentration on the microbial shelf life characteristics of deli-style ham.

Materials and Methods

Three replications of deli-style ham treatments were manufactured in a 3 × 4 factorial arrangement of salt concentration (0.7, 1.4, or 2.1%, meat block basis) and nitrite concentration and source (0, 100, or 200 ppm sodium nitrite, SN, or 100 ppm sodium nitrite equivalent from pre-converted celery juice powder, CP). All treatments contained 1% sugar, 0.35% sodium phosphate and either 495 ppm sodium erythorbate or 440 ppm of ascorbic acid from cherry powder with the balance added as water to achieve a 25% extension. After cooking and chilling overnight, hams were sliced, vacuum packaged, and stored at ~4°C in covered lugs. Samples were stored for 14 wk and evaluated every 2 wk for aerobic plate count (APC), anaerobic plate count (AnPC), and microbial community structure. Data were analyzed using PROC GLIMMIX of SAS, and means were separated using the LSMEANS PDIF option ($\alpha = 0.05$) with Tukey's adjustment. Bacterial community analysis was performed using high throughput 16S rRNA gene sequencing on the Illumina Miseq platform. Sequences were processed using QIIME, and binned into operational taxonomic units (OTUs) at 97% similarity and assigned taxonomy using the Greengenes database as reference. Alpha and β diversity of the bacterial community was performed using QIIME and R to determine differences in the overall bacterial community structure. Alpha diversity was estimated using observed OTUs and Chao1 diversity estimates, and β diversity was calculated using a weighted UniFrac distance matrix.

Linear discriminant analysis effect size (LEfSe) was performed to identify differential OTUs between treatments.

Results

There was a salt by nitrite and a nitrite by week interaction for aerobic plate count (APC). In all treatments containing SN or CP, APC decreased as salt increased, however in the 0 ppm SN treatments, APC did not change based on salt. Throughout storage time, APC decreased with greater concentrations of nitrite, while 0 SN treatments had the most growth throughout the sampling period. Bacterial community richness estimates of observed OTUs and Chao1 were affected by storage time ($P = 0.016$ and $P < 0.001$, respectively), where communities showed greater richness in wk 0 than the rest of storage time. Nitrite concentration affected bacterial community composition, where uncured and 100 ppm CP were more similar than 100 ppm or 200 ppm. Bacterial communities consisted of mostly *Pseudomonadaceae*, which composed $\geq 73.2\%$ of the bacterial community, regardless of treatment. Based on differentially abundant bacterial species, *Pseudomonas* and *Janthinobacterium lividum* were less abundant in the 100 ppm CP treatments compared to all others, and *Prevotella* were greatest in 100 ppm SN.

Conclusion

Treatments with 200 ppm of sodium nitrite provided the longest shelf life to deli-style ham. Furthermore, 0.7% salt resulted in the shortest shelf life. When aiming to reduce sodium and reduce or use alternative sources of nitrite in, processors should bear in mind implications on the microbial shelf life of deli-style hams.