



Fluctuations in the Microbial Community and the Volatile Organic Acids Created During Aerobic Storage of Ground Beef

J. R. Levey^{1*}, I. Geornaras¹, D. Woerner², J. Prenni³, J. L. Metcalf¹, K. Belk¹, and J. Martin¹

¹Animal Science, Colorado State University, Fort Collins, CO, USA

²Animal Science, Texas Tech University, Lubbock, TX, USA

³Horticulture and Landscape Architecture, Colorado State University, Fort Collins, CO, USA

*Corresponding author. Email: jennrlevey@gmail.com (J. R. Levey)

Keywords: 16S rRNA sequencing, GC-MS, ground beef, quality, shelf life
Meat and Muscle Biology 3(2):81

Objectives

Degradation due to microbial and chemical mechanisms occurs throughout the storage life of ground beef. These pathways are intertwined and the microbial community and the volatile organic acids (VOCs) that evolve in ground beef are dynamic. Evaluation of microbial growth using traditional culture-dependent techniques can be misleading due to the presence of unculturable organisms. Therefore, utilizing culture-independent techniques allows for a more thorough understanding of the microbial community within a meat matrix during storage life. The objective of this study was to employ 16s rRNA amplicon sequencing and VOC identification using GC-MS to explore diversity and changes of the microbial community and VOC production during shelf-life of ground beef.

Materials and Methods

Finely ground beef (80/20) was procured from beef processing facilities in the West (one lot) and Midwest (two lots). The lots were separated into three physically separate replicates. Ground beef lots were transported in chub packaging to Colorado State University (Fort Collins, CO), and the chubs were stored in the dark at 2°C for either 16/17 d or 23/24 d. After dark storage, chubs were reground, and 454 g fluff-packs were placed on polystyrene trays before overwrapping with polyvinyl chloride film. The trays were placed in retail display cases maintained at 2–4°C for 5 d. Samples were collected every day of retail display for evaluation of the microbial community and VOC development. Following standardized extraction, 16S rRNA amplicon sequencing was used to explore microbial communities. Sequencing data were analyzed using the programs in

the QIIME2 (version 2018.4) pipeline. Similarly, volatile organic compounds were extracted prior to analysis of targeted VOCs using a GC-MS. The project was designed as a split-plot design and was analyzed using R packages (version 3.4.3), lme4, lmerTest, and emmeans. Least squares means were separated using an α of 0.05.

Results

The top orders of bacteria found in the meat samples were from *Enterobacteriales*, *Lactobacillales*, and *Pseudomonadales*. No differences ($P \geq 0.05$) in Faith's Phylogenetic Diversity Index, or a measure of diversity of the bacterial species within a sample, were observed between Days 0, 2, and 4 of retail case display. A targeted analysis identified eighteen VOCs associated with ground beef spoilage. In previous studies, the presence of hexanal, acetoin and acetic acid are identified as spoilage indicators. Hexanal, Acetoin and acetic acid increased ($P \leq 0.05$) over the 5 d of retail display.

Conclusion

The use of 16s rRNA amplicon sequencing technology is a relatively recent tool that has rapidly advanced the study of microbial deterioration during beef storage and shelf-life. Moreover, the combination of 16s rRNA amplicon sequencing and identification of VOCs in this study, afforded an exploration of the relationship between chemical and biological changes which occur during ground beef storage. These analytical technologies, when used in unison, can highlight the dynamic relationships and evolution of chemical and biological constituents in ground beef. Further research in ground beef shelf-life should incorporate such measures.