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Comparison of Microbial Communities on Dry Aged Beef between Aging Facilities

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Objectives

Despite the high cost and significant attention to detail in the processing of dry aged beef, there is very little information about how quality attributes are incorporated into the meat. Consequently, there are many different dry-aging techniques that are thought to impart unique flavors into the finished product. Many artisanal meat professionals believe the microbial populations present on the outer crust contribute to these flavor profiles; however, to-date there is very little information about the microbial species that grow on dry-aged beef. The fungal and bacterial communities of 9 dry aged beef loins from 5 aging facilities were compared to assess differences in the types of microbes present and relative ratios of detection.

Materials and Methods

The loins were aged for 49 d in refrigerated conditions. The average temperatures for the aging facilities ranged from 35.0 to 39.4°F, and average relative humidity ranged from 75.9 to 91.0%. Of these 5 facilities, 1 facility aged the meat under Ultraviolet light. Each loin was sampled in multiple spatial locations for DNA extraction and the fungal and bacterial sequences present in the samples were identified using a next-generation sequencing approach and subsequent bioinformatic computational pipeline.

Results

Insufficient microbial DNA was isolated from UV-treated loins, indicating that this treatment eliminates all or most microbial growth on the meat. The results indicated that each aging establishment, with the UV-treated facility removed from the dataset, was producing meat with different microbial communities, based on PERMANOVA ($p < 0.01$) and visual analysis of clustering in the principal coordinates analysis plot of Bray-Curtis dissimilarity. The position on the loins from which samples were taken had negligible influence on microbial community structure. Aging facility was determined to be the only observed driver of community structure. Notable operational taxonomic units (OTUs) that were detected in a majority of samples included the bacterial spoilage-associated species *Pseudomonas fragi*, and the fungal species *Debaryomyces udenii* and *Penicillium polonicum*. Additionally, an OTU identified as *Mucor* sp. PG272 was found to be present in over 75% of all samples. While this specific species is not known to be associated with dry aged beef or related products, we believe this OTU may represent a species similar to *Thamnidium*, a mold to which industry insiders often associate with product quality.

Conclusion

The proportions of these populations were variable depending on the meat's location of origin, and may have significant consequences in the resulting sensory properties of the edible, cooked meat produced from their host loins. This study established a general core microbiome for dry aged beef, as well as confirmed that there can be significant differences in the microbial communities on dry aged beef from different aging facilities, which may be contributing to distinct flavors and improved tenderness of dry aged beef.

