

Analyzing changes in the microbial profile of long-term stored tuna and salmon using next-generation sequencing technology

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Outline

1. Introduction
2. Metabolomics and bacterial diversity of packaged yellowfin tuna (*Thunnus albacares*) and salmon (*Salmo salar*) show fish species-specific spoilage development during chilled storage
3. Characterization of bacterial communities of cold-smoked salmon during storage
4. Conclusion

Abstract

Fish are rich in valuable unsaturated and Omega-3 fatty acids, yet they are highly prone to spoilage due to strong internal enzymes and microbial activities. Consequently, various preservation methods such as vacuum packaging, salting, and smoking are often required, combined with low temperatures. However, the complexity of preservation environments and conditions makes predicting the evolution of microbial communities and metabolite profiles challenging. Therefore, next-generation sequencing technology, capable of rapidly identifying complex samples, has recently been applied in the food sector. The first study utilized high-throughput sequencing (HTS) and proton nuclear magnetic resonance spectroscopy (^1H NMR) to analyze vacuum-packed tuna and salmon stored for 13 days. At the end of storage, salmon had an average bacterial colony count of 7.3 log CFU/g, with *Photobacterium* being the dominant genus. Trimethylamine was identified as a primary spoilage product in salmon, alongside a decrease in glucose concentration, an increase in organic acids, indicating glucose fermentation. In tuna, the average colony count at the end of storage was only 4.6 log CFU/g, with *Pseudomonas* being the dominant genus. A significant decrease in lactic acid was observed, suggesting it as a potential carbon source for bacteria on tuna, without identifying the main spoilage product. Overall, salmon was more prone to spoilage compared to tuna. The second study applied high-throughput sequencing (HTS) to analyze 45 samples of cold-smoked salmon (CSS) from three different processing plants over 28 days of storage, identifying operational taxonomic units (OTUs) specific to each processing environment. Despite the 45 CSS samples sharing a core microbiome, processing plant-specific traits were observed, indicating the influence of the processing environment on CSS. These findings from both studies provide enhanced insights into the changes and characteristics of microbial community compositions on fresh fish meat.

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