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Tracking Spoilage and Foodborne Pathogenic Bacteria in Refrigerated Milk, Chicken, and Lettuce Using Full-Length 16S rRNA Sequencing

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Abstract

Food systems represent a critical interface linking microbial ecosystems across animal, plant, and environmental matrices. Microbial spoilage is a major contributor to food waste in the European Union and also influences food safety through the persistence and succession of spoilage and pathogenic bacteria along the food chain. Species-level characterisation of food-associated bacterial communities, and their temporal dynamics, is therefore essential for developing targeted intervention strategies. This study aimed to characterise bacterial community composition and succession in raw and pasteurised milk, chicken fillets and unwashed lettuce during refrigerated shelf life using species-level 16S rRNA profiling. Full-length 16S rRNA sequencing was used to analyse the bacterial communities in raw and pasteurised milk, chicken fillets and unwashed lettuce at 4 time points (product dependent) over their shelf life stored under refrigerated conditions. Product-specific temporal changes in bacterial community composition were observed, reflecting differences in product matrix and initial microbiota. Pasteurised milk showed substantial community restructuring, with Firmicutes declining and Proteobacteria becoming dominant. Raw milk displayed greater initial diversity, comprising Firmicutes, Actinobacteria and Proteobacteria, but similarly shifted towards Proteobacteria dominance during storage. Raw chicken fillets remained phylum-stable, although spoilage-associated Firmicutes (*Brochothrix*, *Carnobacterium*) increased. Unwashed lettuce communities reflected plant-associated microbiota and changes consistent with refrigerated storage. These results demonstrate that refrigerated storage drives predictable yet matrix-specific bacterial succession, creating opportunities for precise control of spoilage and potential foodborne hazards. Species-level knowledge of dominant taxa and their temporal proliferation supports optimisation of preservation and storage strategies, predictive shelf-life modelling, and improved spoilage monitoring. By integrating species-level microbiome data into food system surveillance, this work highlights pathways to reduce food waste while maintaining food quality and safety across perishable food products.

Keywords: Microbial spoilage, Food waste reduction, Full-Length 16S rRNA, Bacterial succession