

Variable characteristics of microbial communities on the surface of sweet cherries under different storage conditions

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Abstract

Ripe fruit is susceptible to postharvest rotting induced by microbial pathogens. The development of fruit storage technologies requires a comprehensive understanding of the overall microbial community involved in fruit storage. In this study, we investigated the microbiota of bacteria and fungi on cherry surfaces under room-temperature storage condition (25 °C) and low-temperature storage condition (0 °C) using high-throughput sequencing. The results demonstrated that *Enterobacter*, *Erwinia*, *Botrytis*, and unidentified *Pleosporales* were significantly enriched in the rotten samples, while *Bacillus* and *Aureobasidium* were enriched in the unrotten samples. After the fruit rotted, more dramatic changes were observed in fungal microbiota than in bacterial microbiota. Rotting significantly reduced fungal α -diversity without noticeably altering bacterial α -diversity, under both room-temperature storage and low-temperature storage conditions. Furthermore, temperature condition significantly impacted the composition of the surface microbiota of cherries, and the microbiota changed more significant when rotting under room-temperature storage condition than under low-temperature storage condition. Low-temperature storage reduced the α -diversity and network complexity. Significant correlations among potential pathogens, beneficial microorganisms, and other microbiota members indicated that in addition to pathogens, microbiota along with pathogens also influences fruit rot. This study provides new insight into the dynamics of the microbiome in cherries during storage.