Compositional shifts in the strawberry fruit microbiome in response to near-harvest application of *Metschnikowia fructicola*, a yeast biocontrol agent

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Abstract

Plant-associated microbial communities form complex co-associations that play a role in promoting plant productivity and health, although the underlying mechanisms have not been fully elucidated. The functional role of the microbiome provides a new perspective on how we can potentially utilize the microbiome to maintain the postharvest quality and health of produce. While the composition and dynamics of the microbiome on fruit and vegetables over time and in response to postharvest management practices has begun to be explored, an understanding of their functional role in harvested produce is still lacking, especially in fruit. Therefore, the present study was undertaken to characterize the effect of near-harvest field application of a yeast biocontrol agent Metschnikowia fructicola, on the strawberry fruit microbiome. Highthroughput sequencing revealed significant shifts in the bacterial and fungal community in response to the application of the yeast biocontrol agent sampled at the time of application, after harvest, and after storage and shelf life. Alterations included an increased bacterial diversity, distinct shifts in community composition and structure, specific microbial interactions and differential enrichment of several potentially beneficial genera Methylobacterium, Sphingomonas, Rhizobium, Bacillus and others) in M. fructicola treated fruit leading to subsequent postharvest disease suppression. Results of this study provide new insights into the dynamics of the postharvest fruit microbiome that will assist in the development of a targeted, microbiome-driven approach to robust and sustainable disease control strategies.