## Contribution of fruit microbiome to raspberry volatile organic compounds emission

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## Abstract

Raspberry fruit (Rubus idaeus L.) is highly appreciated by consumers for its quality characteristics and aromatic profile, determined by nearly 300 volatile organic compounds (VOCs). Although several microbes produce VOCs, their direct involvement in fruit aroma determination has been largely overlooked. In this study, the contribution of fruit-associated microbiota to fruit volatile emissions was evaluated by performing an untargeted GC–MS analysis of VOCs occurring in control (C), sterile (S) and artificially reinoculated berries (R). C and R bacterial fruit microbiomes were characterised by next generation sequencing (NGS). The treatments significantly affected the fruit volatilomes, thus confirming the role of bacteria in fruit aroma construction. In particular, aldehydes, monoterpenes, norisoprenoids, and other aroma-active compounds were significantly lower in S raspberries, and recolonisation could only partially restore the emission of terpenoid compounds. Significant correlations were found among NGS data and volatile emissions, including a positive correlation between Lactobacillus and Paenibacillus spp. and norisoprenoids, and a negative correlation between Enterobacteriaceae and monoterpenes. Several VOC-emitting bacterial taxa (including Bacillus, Lactobacillus, Methylobacterium, Paenibacillus, Pseudomonas spp.) are recurrently found in the raspberry-associated microbiome, suggesting that future applications aimed at the control of microbial colonisation may enhance fruit aroma.