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Agroecosystem management modifies the rhizosphere microbiome via soil and host responses: an integrated study of host physiology and root multiomics

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Abstract

The composition of the rhizosphere microbiome is structured by many factors, including the bulk soil microbial pool, microbe-microbe interactions, and the plant host. Our ability to manipulate the rhizosphere environment for agricultural production will be improved with greater understanding of how management practices may modify the rhizosphere, both by altering the soil environment and/or the host plant physiology. To better understand how management practices modify the composition of rhizosphere bacteria and fungi, we implemented an experiment within a long-term study in a vineyard (*Vitis* spp.) located in Pennsylvania, USA in 2020. Two management practices are under study at the site: 1) rootstock grafting (101-14 mgt. and Riparia) and 2) increased plant diversity with a grass groundcover (*Festuca rubra*). Roots and soils up to 1 meter were accessed through root boxes and categorial sources of data (root traits, soil properties, transcriptomics, metabolomics, and microbiome) were analyzed both sequentially and integrated methods. PERMANOVAs on Bray-Curtis similarity indicate that rootstock management practices influence rhizosphere bacterial composition ($p<0.001$), primarily by host effects. In contrast, groundcover management practices altered soil properties, shifted root growth and increased bulk soil microbial diversity (up to 13%); these shifts may have had stronger consequences for the composition of rhizosphere fungi ($p=0.054$) than bacteria. Preliminary integrated analyses indicate that in this study rhizosphere microbiota were more strongly structured by bulk soil microbes, root gene expression, and new root growth than soil properties. This study demonstrates that integrating physiology and multiomics can clarify how management practices alter rhizosphere microbiome composition.