

Shared and unique features of bacterial communities in native forest and vineyard phyllosphere

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Phyllosphere bacteria have received little attention despite their important roles in shaping plant performance traits. In this study, we characterize the bacterial communities on leaves of native trees inhabiting sclerophyllous forests in central Chile, one of the world's biodiversity hotspots. Additionally, we provide profiles of bacterial communities on grape leaves and berries of organic and conventional vineyards. Results of 16S rRNA gene amplicon sequence analysis showed that 45% of OTUs were shared across forest leaves, grape leaves, and grape berries. Conventional management had higher number of OTUs shared with forest leaves than organic management. In addition, grape leaves subjected to conventional management had higher alpha diversity than those with organic management, while no significant effect of agricultural management was observed in grape berries. Indicator analysis showed that *Bdellovibrio*, *Beijerinckia*, and *Spirosoma* were typical for forest leaves, whereas *Enhydrobacter*, *Delftia*, *Proteiniclasticum*, *Arsenicicoccus*, and *Alkaliphilus* were typical for the vineyard phyllosphere. Regarding agricultural managements, *Beijerinckia*, *Sedimentibacter*, *Nesterenkonia*, *Gluconobacter*, *Conexibacter*, and *Anaeromyxobacter* were typical for conventional grape leaves, whereas no genus-level indicator was found for organic vineyard leaves. These results provide new insights of the diversity patterns of the phyllosphere microbiome in native and cultivated lands and suggest that both of these microbiomes are connected and integrated systems.