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Mining microbiome data to identify antagonists of grapevine downy mildew (*Plasmopara viticola*)

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Abstract (250 words)

Vineyards are home to a myriad of microorganisms that interact with each other and with the vines. Some microorganisms are plant pathogens, such as the oomycete *Plasmopara viticola*, causing grapevine downy mildew. Others have a positive effect on vine health, such as disease biocontrol agents. These beneficial plant-microbe and microbe-microbe interactions have gained more attention in recent years because they could represent an alternative to the use of fungicides in viticulture. The aim of the present study is to identify bacterial and fungal taxa naturally present in vineyard soil and grapevine leaves and significantly more abundant in plots with low susceptibility to downy mildew (DM), susceptibility being defined by the intensity and frequency of DM symptoms over several years. Seven pairs of vineyard plots with contrasting susceptibility to DM were selected on the basis of a long-term epidemiological survey conducted in the Bordeaux region by the IFV. In each plot, we sampled young leaves (at phenological stage of 2-3 spreading leaves) and surface soil (top 5 cm) before the first fungicide treatments of the growing season. We used metabarcoding approaches to explore the entire microbial community of the samples. Up to 1974 and 769 taxonomic units of bacteria and fungi respectively were identified. Using differential abundance analyses, we could identify taxa that were significantly more abundant in plots of vines with low susceptibility to DM. As perspectives, the antagonistic activity of these taxa will be studied experimentally to develop microbial biocontrol of downy mildew and move viticulture towards pesticide-free viticulture.

Keywords: *Plasmopara viticola*, phyllosphere, pest management, sustainable viticulture, grape-associated microorganisms