Cell wall remodeling mediated by specific *PME* genes plays a role in grapevine response to *Botrytis cinerea*

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Abstract (250 words)

Botrytis cinerea (*Bc*) is one of the main pathogens affecting the cultivated grapevine. A key role in grapevine tissue colonization is played by cell wall (CW) remodeling driven by CW Modifying Enzymes (CWMEs), expressed both by the host and the pathogen. Their action can impact CW integrity and trigger specific immune signaling, thus influencing *Bc* infection outcome. To further characterize the role of the CW in the grapevine response to *Bc*, two contrasting genotypes in their resistance to the fungus were artificially inoculated at full bloom. RNA-seq analysis and biochemical characterization of the CW and its modification in samples collected at 24 hours post-inoculation highlighted significant differences between genotypes. A gene set enrichment analysis indicated several over-represented categories upon infection, with a general down-regulation of those genes related to CW organization and pectin modification, mostly in the resistant genotype. Within the down-regulated *CWMEs*, *Pectin Methyl-Esterase* (*PME*) genes were found highly represented. Unlike, *VviPME10* was significantly induced upon infection and was further characterized since its putative ortholog in Arabidopsis was associated with resistance to *Bc*. *VviPME10* promoter hosts several predicted binding sites for VviWRKY3, a defense-associated transcription factor, as highlighted by DAP-seq analysis. This evidence is under confirmation by luciferase assays. In addition, the artificial inoculation with *Bc* of leaves from six *VviPME10* knock-out (KO) edited lines showed significantly larger lesion areas when compared to control plants at 5 dpi. Together, these results suggest that pectin modification, mediated by *VviPME10,* plays an important role in the grapevine response to *Bc*.

Keywords: *Botrytis cinerea,* transcriptomics, DAP-seq analysis, Cell wall, grapevine pectin methyl-esterase