

INNOVATIVE APPROACHES TO BOTRYTIS BUNCH ROT CONTROL: UNVEILING PME10 FUNCTION FOR SUSTAINABLE VITICULTURE

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The ripening of grapevine (*Vitis vinifera* L.) berries is a complex, tightly regulated process involving a cascade of physiological, transcriptional, and biochemical changes that collectively determine fruit quality and resilience to environmental stresses. A key event during ripening is berry softening, driven largely by modifications to the cell wall (CW), which confer the flexibility necessary for textural development. However, these structural changes can also compromise cell wall integrity, increasing susceptibility to biotic stresses, notably fungal pathogens. Among these, *Botrytis cinerea* (Bc), the causal agent of Bunch Rot (BR), poses a major threat to grape production. The progression of *B. cinerea* infection is closely linked to host cell wall remodeling, which facilitates pathogen colonization. Central to this interaction are cell wall-modifying enzymes, particularly pectin methylesterases (PMEs), which are produced by both the host and

the pathogen. These enzymes play a pivotal role in regulating cell wall (CW) structure and defense, ultimately influencing the outcome of the infection. The functional inactivation of specific pectin methylesterase (PME) genes has been shown in various plant-pathogen systems to influence resistance against fungal invasion, suggesting a conserved role in defense modulation. In grapevine, a combined biochemical, histochemical, and transcriptomic analysis of flowers and berries from genotypes with contrasting susceptibility to *B. cinerea* (Bc-BR) underscored the involvement of specific PME isoforms in mediating resistance. Notably, an unbiased transcriptomic analysis of infected flower tissues revealed a more pronounced transcriptional response in the susceptible genotype, indicative of an ultimately ineffective defense reaction. Detailed expression profiling of *PME* family members—integrating this dataset with publicly available transcriptomes of Bc-infected berries—identified *PME10* as the most strongly induced gene upon infection. Functional characterization further supported its role in defense: *PME10* knockout mutants exhibited reduced total PME activity and increased susceptibility to *B. cinerea*, whereas overexpression lines displayed elevated PME activity and significantly attenuated disease symptoms. Using DAP-seq, DAP-qPCR, and dual luciferase assays, WRKY03—a defense-related transcription factor—was identified as a putative regulator of *PME10*. Analysis of transcriptional changes in infected flower tissues revealed preliminary insights into the potential interplay between hormone signaling pathways and cell wall remodeling during Bc infection in grape berries. This project aimed to deepen our understanding of grape berry resistance to Bc and identified *PME10* as a novel genetic determinant of grapevine defense. These findings provide a promising target for the development of Bc-resistant cultivars through the application of advanced New Genomic Techniques.