

P40 – The grapevine Pectin Methylesterases gene family and its involvement in *Botrytis* bunch rot control

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Abstract

Plant Pectin Methylesterases (PMEs) represent a group of tissue-specific and developmentally regulated proteins. The gene family is involved in the plant cell wall (CW) remodelling process, by the control of the degree of cell wall pectin methylesterification. Pectin methylesterification also influence the susceptibility to pathogens as *Botrytis cinerea* (*Bc*), a necrotrophic fungus responsible of the *Botrytis* bunch rot in grapevine. In *Botrytis*, PME as well as other CW degrading enzymes have been identified as virulence factors. To further characterize the *PME* gene family and its role in the *Botrytis* bunch rot, the latest genome assembly and annotation were revised and through sequence homology search, a total of 63 PME domain containing proteins were identified, 16 more than a previous identification in grapevine. The *in-silico* analyses of the family by means of the *Vitis* gene expression database VESPUCCI as well as Aggregated Gene Co-expression Network approach (AggGCNs) allowed us to identify and enrich gene co-expression modules and build gene co-expression networks. Interestingly, one of the co-expression modules showed a high modulation in presence of *Botrytis cinerea* infection and particular attention was paid to it. To investigate the contribution of the genes of that module, their expression level in different organs and developmental stages from two grapevine cultivars with divergent *Bc* susceptibility was investigated. Furthermore, berries were artificially infected with *Bc* at mature stage to evaluate *PME* gene expression level and their possible role in the grapevine bunch rot susceptibility. The results obtained contribute to characterize the grapevine *PME* gene family and the role of specific members in the grapevine-*Bc* interaction and to select *PME* genes candidate to the control of *Botrytis* bunch rot in grapevine.

Keywords: grapevine, pectin methylesterase, cell wall, *Botrytis cinerea*, bunch rot, gene expression, co-expression, network analysis