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Grapevine responses to trunk pathogens: potential genes involved in plant-pathogen interactions

Mariana Patanita[1*], André Albuquerque[1], Maria do Rosário Félix[2], Patrick Materatski[1], Carla M. R. Varanda[1], Joana Ribeiro[1], Maria Doroteia Campos[1]

[1]MED – Mediterranean Institute for Agriculture, Environment and Development, Instituto de Investigação e Formação Avançada, Universidade de Évora, Pólo da Mitra, Ap. 94, 7006-554 Évora, Portugal.

[2]MED – Mediterranean Institute for Agriculture, Environment and Development & Departamento de Fitotecnia, Escola de Ciências e Tecnologia, Universidade de Évora, Pólo da Mitra, Ap. 94, 7006-554 Évora, Portugal.

*Email: mpatanita@uevora.pt

Grapevine trunk diseases (GTDs) have increased considerably in the last two decades and are currently considered the most spread and destructive diseases that affect grapevines, influencing the productivity and longevity of vineyards in all the major growing regions of the world. The simultaneous presence of multiple trunk pathogens in a single plant, together with the inconsistent expression of symptoms, their isolation in asymptomatic plants, and the absence of effective treatments, make these diseases extremely complex to early detect and eradicate, being currently one of the most relevant challenges for the sustainability of viticulture. Aiming to search for sustainable alternatives to limit their development, the present study intended to investigate plant molecular responses against GTDs following a real-time qPCR approach on a set of candidate genes, and associate this data with phenotypical differences. Samples were collected from GTDs asymptomatic and symptomatic plants of two cultivars with different levels of susceptibility to GTDs, 'Alicante Bouschet' and 'Trincadeira'. Target genes included defence-related genes, genes involved in sugar transport or metabolism, genes previously identified in grapevine response to pathogens, and other differentially expressed genes (DEGs), selected in a previous transcriptome analysis, totalling 18 genes. Several genes were found to be significantly overexpressed (p<0.05) in symptomatic plants namely *GIN2*, *TLP3*, *TLP8* and *PR1*. On the other hand, the genes *MAPKKK17* and *PER42*, already recognized as involved in responses to biotic stresses, were overexpressed in the asymptomatic ones. Similarly, *STS1*, *cwINV* and *HT5* were significantly overexpressed in the less susceptible cultivar, 'Trincadeira', and *PR3* was the only one overexpressed in the most susceptible cultivar, 'Alicante Bouschet'. Altogether, these results can help to explain the phenotypical differences that occur between plants and shed light into the underlying mechanisms of resistance and susceptibility of grapevines against these pathogens. However, further research is required to gain better knowledge of these diseases and their expression in order to limit their propagation and contribute to the development of effective protective methods, through the activation or inhibition of potential plant responses regulators.

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