

Identification of metabolic markers of grape infection with Esca complex disease

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Abstract

Grapevine trunk diseases (GTD) are caused by phytopathogenic fungi that degrade the woody part of the vine, leading to loss of vigor with decrease of grape production and quality, and eventually plant death. Widely spread, they are responsible for important economic loss for the viticulture industry worldwide. The Esca complex, caused by *Phaeoacremonium* spp., *Phaeoemoniella chlamydospora* and *Fomitiporia* spp., has been shown to be one of the major GTD but information is still very scarce. Early identification of GTD is crucial, however due to their cryptic nature, visible symptoms in wood and foliage may take years to manifest. The identification of molecular and metabolic markers in grape and leaves may allow early detection and a better understanding of the factors responsible for disease progression.

In this work, grape berries and leaves were collected in 2016, at harvest stage, from control and symptomatic grapevines (five biological replicates each) from a 17 years old vineyard of the Portuguese cultivar Aragonez (= Tempranillo) that had been monitored for five years. Collected samples were subjected to gene expression and metabolomic analyses using qPCR and GC-MS. Expression differences of the fatty acid metabolism and wax and tocopherol biosynthesis pathways were targeted while a wide range of soluble and volatile metabolites were quantified. Total phenolic content was also measured.

Principal component analysis of GC-MS data revealed that infected samples were clearly discriminated from control ones. The metabolic reprogramming due to infection was interestingly more evident in berries than in leaves. Several volatiles, fatty acids, triterpenoids and phenylpropanoids putatively involved in defense were present in significantly higher amounts in infected berries, making them strong candidates as Esca disease biomarkers of infection. Additionally, these results will contribute to predict the impact of infection on wine quality.

Keywords: Trunk disease, Esca complex, Metabolomic, Infection biomarkers