

## Hormonal and associated metabolic changes in susceptible harvest-ripe grapes under asymptomatic and symptomatic Esca disease

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**Abstract (250 words)** *Esca complex is a disease affecting grapevine trunks, characterized by the colonization of the wood by xylem-residing fungi (Phaeomoniella chlamydospora, Phaeoacremonium minimum and Fomitiporia mediterranea), and posing significant risks to vineyard longevity since no efficient treatment is available. Despite its prevalence, the mechanisms beyond symptomatic manifestations like interveinal chlorosis and leaf necrosis remain unclear. Preliminary findings indicated a more pronounced metabolic reprogramming in fruits compared to vegetative organs and a putative impact on wine quality by using fruits from symptomatic grapevines. Here, we conducted metabolic profiling and untargeted/ targeted metabolomics to gather more insights into the molecular and biochemical mechanisms responsible for the onset of symptoms. Ultra-High Performance Liquid Chromatography (UHPLC-qTOF-MS/MS), Gas Chromatograph-Quadrupole Time of Flight Mass Spectrometry (GC-qTOF-MS/MS), and Liquid Chromatography (LC-MS/MS) enabled the identification of putative markers of symptomatology regarding hormonal regulation, primary and secondary metabolisms. Abscisic acid, jasmonates, and specific amino acids and sugars decrease in harvest-stage fruits from symptomatic grapevines, in contrast with the accumulation of a wide variety of phenylpropanoids (e.g., procyanidin B1, caffeic acid, resveratrol) among others. Secondary metabolism was more strongly remodelled indicating a partitioning of carbon allocated to defence-related metabolism. RNA extraction and sequencing are being conducted to integrate these metabolic results with molecular data. This study may contribute to developing a model regarding the development of Esca symptoms in an attempt to mitigate the worldwide impact of this complex disease.*

**Keywords:** Esca disease, Hormonal profiling, Primary metabolism, Phenylpropanoid pathways, RNA sequencing.