Virulence-related metabolism may be activated in *Botrytis cinerea* mostly in the interaction with tolerant green grapes that remain largely unaffected

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Abstract

Botrytis cinerea is responsible for the gray mold disease, severely affecting *Vitis vinifera* grapevine and hundreds of other economically important crops. However, many mechanisms of this fruitpathogen interaction remain unknown. The combined analysis of the transcriptome and metabolome of green fruits infected with *B. cinerea* from susceptible and tolerant genotypes was never performed in any fleshy fruit, mostly because green fruits are widely accepted to be resistant to this fungus.

In this work, peppercorn-sized fruits were infected in the field or mock-treated, and infected berries were collected at green (EL32) stage from a susceptible (Trincadeira) and a tolerant (Syrah) variety. RNAseq and GC-MS data suggested that Syrah exhibited a pre-activated/basal defense relying on specific signaling pathways (enrichment in protein kinases, transcription factors, Ca2+ signaling), hormonal regulation (jasmonates, and ethylene metabolism), and phenylpropanoid metabolism. In addition, putative defensive metabolites such as ursolic acid, trans-4-hydroxy cinnamic acid, and epigallocatechin were more present in Syrah than Trincadeira before infection. On the other hand, Trincadeira underwent a broad metabolism reprogramming upon infection but was unable to contain disease progression. RNA-seq analysis of the fungus in planta revealed an opposite scenario with higher gene expression activity in *B. cinerea* during infection of the tolerant cultivar and less activity in Trincadeira infected berries. The results suggested an active virulence state on the tolerant cultivar even without visible disease symptoms. Together, this study brings novel insights related to *B. cinerea* early infection strategies and the green berry defense involved in tolerance/susceptibility against necrotrophic fungi.

Keywords: Botrytis cinerea, fungus-plant interaction, transcriptome, metabolome, Vitis vinifera