IDENTIFICATION OF SPECIFIC GRAPEVINE BIOMARKERS TO SELECT EFFICIENT RESISTANCE INDUCERS

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Downy mildew, caused by *Plasmopara viticola*, is one of the most severe diseases of grapevine and is commonly controlled by fungicide treatments. The beneficial microorganism *Trichoderma harzianum* T39 (T39) has previously been shown to induce plant-mediated resistance and to reduce downy mildew symptoms in susceptible grapevines. Transcriptomic and proteomic analyses were used to study the global molecular changes associated with T39-induced resistance in grapevine leaves. By next generation RNA sequencing (RNA-Seq) approach, more than 14.8 million paired-end reads were obtained for each treatment and 7024 grapevine genes resulted as differentially expressed during resistance activation. Moreover, 800 unique proteins were identified and quantified by high-throughput eight-plex iTRAQ protocol and 218 proteins resulted as significantly changed in abundance during T39-induced resistance. The complex transcriptional and proteomic reprogramming of T39-induced resistance included the direct activation of the microbial recognition machinery after T39 treatment and the enhanced expression of defence-related processes after pathogen inoculation. We showed that T39-induced resistance partially inhibited some disease-related processes and specifically activated defence responses after pathogen inoculation. In particular, some defence processes known to be implicated in the reaction of resistant grapevines to downy mildew were partially activated by T39-induced resistance in the susceptible grapevine. Genes and proteins identified in this work are an important source of specific biomarkers to select novel resistance inducers and to better characterize the environmental conditions that might affect induced resistance mechanisms under field conditions. The final aim is the use of specific ISR biomarker to optimize the use of this biocontrol method for downy mildew control.