

TRANSCRIPTOMIC ANALYSIS OF GRAPEVINE INDUCED RESISTANCE AGAINST DOWNY MILDEW

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Downy mildew, caused by *Plasmopara viticola*, is one of the most destructive grapevine diseases, and its control is based on intense chemical treatments (Gessler et al., 2011). Enhancement of plant resistance by natural inducers seems to be a promising strategy for controlling crop diseases (Vallad and Goodman, 2004), but scarce information is available on the molecular mechanisms of induced resistance in non-model plants.

In grapevine, treatment with the biocontrol agent *Trichoderma harzianum* T39 (T39) induces resistance against downy mildew (Perazzolli et al., 2008). The mechanism is mediated by the plant and involves modulation of some defence-related genes (Perazzolli et al., 2011). Our aim is to characterize the resistance mechanisms activated in grapevine by the biocontrol agent T39, to identify key genes and processes activated against downy mildew.

Transcriptional changes associated with T39 treatment and subsequent inoculation with *P. viticola* were analyzed by Illumina RNA-Seq method. Three biological replicates were analyzed for each condition and each biological replicate was sequenced twice on separate lane. More than 15 million reads (paired-end, 100 nucleotides in length) were obtained for each biological replicate, corresponding to a coverage of at least 32x the grapevine transcriptome. Filtered reads were mapped to the grapevine genome and the expression value of grapevine genes was then calculated. Whereas exons comprise the 9% of the genome, 77% of mapped reads showed matches to predicted genes. From one to nine isoforms were recognized for each gene, and more than 3500 new expressed regions were identified. By statistical analysis, 7024 genes resulted as differentially expressed in at least one pairwise comparison, indicating a complex transcriptional reprogramming during T39-induced resistance.

T39 treatment induced the expression of grapevine genes in the absence of pathogen infection and reinforces the expression of other genes after *P. viticola* inoculation. Interestingly, T39-treated plants showed specific reaction against *P. viticola* inoculation compared to control plants. In control plants, genes related to signal transduction and response to stress are mainly repressed by *P. viticola* inoculation. Conversely, genes related to transcription and response to stress are mainly induced by *P. viticola* in T39-treated plants, demonstrating the specific reaction against pathogen infection during T39-induced resistance.

References

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