TRANSCRIPTOMIC ANALYSIS OF GRAPEVINE INDUCED RESISTANCE BY RNA-Seq.

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Induced systemic resistance (ISR) is activated by selected strains of non-pathogenic microorganisms and provides protection against different types of pathogens. In grapevine, treatments with the biocontrol agent *Trichoderma harzianum* T39 (T39) induce resistance against downy mildew caused by *Plasmopara viticola*. ISR seems to be a promising strategy for controlling crop diseases, but scarce information is available on the molecular mechanisms in non-model plants. In order to identify key genes and processes activated by the plant against downy mildew we applied the RNA-Seq method based on next generation sequencing. Paired-end reads, 100 nucleotides in length, were sequenced and more than 15 million reads for each replicate were obtained, corresponding to a coverage greater than 32× the grapevine transcriptome. Filtered reads were mapped to the grapevine genome and the expression value of grapevine genes was calculated. A total of 7024 genes resulted as differentially expressed in at least one pairwise comparison. Their functional annotation revealed complex transcriptional reprogramming of grapevine leaves following treatments. T39 treatment directly affected the expression of genes related to protein metabolism, signal transduction and transcription. Moreover, a specific reaction against *P. viticola* inoculation was observed in T39-treated compared to control plants. Genes related to signal transduction and response to stress were mainly repressed by *P. viticola* in control plants. Conversely, genes related to transcription, signal transduction and response to stress were mainly induced by *P. viticola* in T39-treated plants, highlighting the specific defence reaction of T39-induced resistance.