RNA-Seq analysis of grapevine induced resistance

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Induced systemic resistance (ISR) is a mechanism of the plant immune system. ISR is activated by selected strains of non-pathogenic microorganisms and provide protection against different types of pathogens in several plant species. In grapevine, treatment with the biocontrol agent *Trichoderma harzianum* T39 (T39) induces 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.
Transcriptional changes associated with T39 treatment and subsequent inoculation with *P. viticola* were analyzed in grapevine by Illumina RNA-Seq method. Three biological replicates were analyzed for each condition. Each biological replicate was sequenced twice on separate lane and paired-end reads 100 nucleotides in length were obtained. More than 15 million reads 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 using TopHat tool, and the expression value of grapevine genes was calculated using Cufflinks tool. 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. Pearson correlations were greater than 0.97 and 0.95 between technical and biological replicates, respectively. Counts of technical replicates were summed to get better coverage, and 7024 genes resulted as differentially expressed in at least one comparison accordingly to DESeq statistical analysis. Functional annotation of differentially expressed genes by Argot2 tool highlighted a specific transcriptional reprogramming of T39-treated grapevines in response to pathogen inoculation.