DIFFERENTIAL RESISTANCE TO *PHYTOPHTHORA CINNAMOMI* IN TROJAN FIR

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RNA was sequenced from roots tissue samples of *Abies equi-trojani* that demonstrated differential susceptibility to dieback (root rot) when experimentally inoculated with the oomycete pathogen *Phytophthora cinnamomi*. Eight pooled RNA libraries of 10 inoculated individuals based on the progression of tree morbidity over the course of the inoculation experiment represented three conditions, uninoculated control (2 libraries), resistant (4 libraries), and susceptible (2 libraries). These data were used for differential expression (DE) analysis, which uncovered 12,680 instances of differential expression among the three groups; 326 upregulated and 1,219 downregulated in resistant relative to control, 5,955 upregulated and 343 downregulated in resistant relative to susceptible, and 4,722 upregulated and 115 downregulated in control relative to susceptible. Our analysis of DE genes leveraged a new functional annotation pipeline, Eukaryotic Non-Model Transcriptome Annotation Pipeline (EnTAP), which automates similarity searches across multiple databases and includes protein domain, gene ontology, and gene family assignment, Kyoto Encyclopedia of Genes and Genomes (KEGG) annotation and contaminant filtering. Functional annotation clustering of DE genes yielded patterns of increased expression of stress, metabolic and apoptosis related genes in resistant trees.

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