Comparison of gene expression profiles between resistance and susceptibility in *Pinus thunbergii* to pine wood nematode infection

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Pine wilt disease caused by the pine wood nematode (PWN) is a chronic problem in pine forests (*Pinus thunbergii* and *Pinus densiflora*) in Japan, where approximately 40,000,000 m^3 of pine forests have been blighted by the PWN. In the 40 years since the pathogen was identified, the physiological changes that occur as the disease progresses have been characterized using anatomical and biochemical methods, and resistant trees have been selected via breeding programs. However, there are few studies that have assessed the molecular genetics, e.g. transcriptional changes, associated with infection-induced physiological changes in resistant or susceptible trees. To understand the difference in the defense responses of resistant and susceptible individuals in *P. thunbergii*, we constructed seven subtractive suppression hybridization cDNA libraries using time-course sampling of resistant and susceptible trees inoculated with PWN, and we recovered 3,342 cDNAs. Among them, expression of putative pathogen-related (PR) genes (e.g., PR-1b, 2, 3, 4, 5, 6) and antimicrobial peptide was much higher in susceptible trees than in resistant ones at every time point. Whereas, expression of genes such as PR-9, PR-10, and cell wall-related genes (e.g., HRGPs and extensin) was higher in resistant trees than in susceptible trees. These results show that there were marked differences between resistant and susceptible trees in the timing and level of transcripts expressed in common following inoculation with PWN. The generated ESTs information in our study will certainly advance understanding of defense mechanism in transcriptional level of other varieties and/or other *Pinus* species against PWN.

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