

Comparative transcriptome analysis of resistant and susceptible *Pinus thunbergii* infected with pine wood nematode using dual RNA-seq

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Pine Wilt Disease (PWD) caused by the Pine Wood Nematode (PWN) *Bursaphelenchus xylophilus*, is one of the most serious forest disease in East Asia and Europe. Japanese black pine *Pinus thunbergii* is highly susceptible to PWD and therefore resistant trees have been selected to cope with this disease. Several studies have assessed the histological responses or transcriptional changes in resistant and susceptible trees. However, the underlying mechanism of resistance of pine is still not fully understood. The purpose of this study was to identify mechanisms involved in the resistance of pine from a perspective of the host-pathogen relationships. Here, we identified multiplication of PWN in two resistant and one susceptible tree varieties inoculated PWN and then performed

the dual RNA-sequencing (RNA-seq) analysis. The susceptible trees showed wilting of leaves at 7 days post inoculations (dpi), and the number of PWN in trees was higher in the susceptible trees than the resistant trees at 14 dpi. RNA-seq performed on six cDNA libraries from two resistant trees and one susceptible tree at 1 and 3 dpi. A total number of 277,503,322 read pairs obtained from all cDNA libraries were mapped to the PWN genome. The percentages of reads mapped to PWN genome ranged from 0.11 to 0.36%, which indicated that we could reveal gene expressions of both hosts and pathogens simultaneously. Their expression profiles suggest that there is a difference in mechanism of resistance between resistant tree varieties against infection of PWN.