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A comparative proteomics analysis on resistant provenance of *Pinus massoniana* inoculated with *Bursaphelenchus xylophilus*

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ABSTRACT:

Pine wilt disease caused by *B. xylophilus*, also known as the pine wood nematode (PWN), is the most devastating disease of pine trees. From different geographical provenance of *P. massoniana* were inoculated with nematodes, test results selected the provenance GD₅ which has strongly resistance to PWN. This article used resistant provenance GD₅ as the experimental material, and sensitive provenance SX₁ as comparison. Total proteins were extracted by using 2-DE and MALDI-TOF/TOF technology from the provenances pine needles respectively. Differentially expressed proteins in the provenance before and two weeks after inoculated with PWN, were analyzed. At last, 89 differentially expression proteins were successfully identified by MALDI-TOF–TOF. The test result also fund that there were five proteins involved in hydrogen peroxide scavenging capacity and protecting the redox homeostasis system from damaged. Their up-regulation may be the main cause of the provenance GD₅ resistant to PWN.

Keywords: *Pinus massoniana*, pine wilt disease, resistant provenance, proteomic, 2-DE, MALDI-TOF/TOF