

**VOLATILES RELEASED BY *PINUS PINASTER* HALF-SIB GENETICALLY CONTRASTING FAMILIES FOR PINE WILT DISEASE SUSCEPTIBILITY BEFORE AND DURING *MONOCHAMUS GALLOPROVINCIALIS* INSECT-VECTOR FEEDING**

Elsa Gonçalves<sup>1</sup>, A. Cristina Figueiredo<sup>1</sup>, Isabel Carrasquinho<sup>2,3</sup>, José G. Barroso<sup>1</sup>,  
 Maria I. Inácio<sup>2</sup>, Joana Henriques<sup>2</sup>, Edmundo Sousa<sup>2</sup>, and Luís Bonifácio<sup>2</sup>

The pine wilt disease (pwd), caused by the pinewood nematode (PWN) *bursaphelenchus xylophilus*, is a major threat to conifer trees worldwide. The PWN is transmitted from infected to healthy trees by insect vectors in the cerambycid beetle genus *monochamus*. The PWD cycle involves the movement of the nematode between the insect vector and the host tree. PWN leaves the insect and enters the host through feeding wounds made by the insect. This study analyzed the volatiles released by genetically contrasting maritime pine half-sib families with susceptibility to PWD, before and during insect vector feeding activity, which can act as signals for the nematode to move into healthy trees. Thirty-eight pine trees from four half-sib families were selected among 96 different families. The canopy of each of the 7 year old pines was covered by a metallic net and foliage was enclosed in a plastic bag to collect the headspace volatiles, before and during 24 h exposure to feeding by a pair of newly emerged *m. galloprovincialis* males and females. Volatiles were collected by solid phase microextraction and analyzed by gas chromatography-mass spectrometry for component identification, and by gas chromatography for component quantification. For comparing the different families, the non-parametric kruskal-wallis test and dunn's test with bonferroni-type adjustment were used. Seventeen volatile compounds were detected both before and during feeding. Before insect feeding,  $\beta$ -pinene,  $\beta$ -myrcene,  $\beta$ -caryophyllene, phenethyl 2-methylbutyrate, and phenethyl 3-methylbutyrate showed significant differences among the contrasting families. During feeding, only  $\beta$ -myrcene and germacrene d showed different emission patterns among them. In this case, the most pwn susceptible family released significantly higher amounts of  $\beta$ -pinene and  $\beta$ -caryophyllene, and lower amounts of  $\beta$ -myrcene than the resistant cultivars.

<sup>1</sup>Centro de Estudos do Ambiente e do Mar (CESAM Lisboa), Faculdade de Ciências da Universidade de Lisboa (FCUL), Centro de Biotecnologia Vegetal (CBV), Departamento de Biologia Vegetal (DBV), C2, Campo Grande, 1749-016, Lisboa, Portugal.

<sup>2</sup>Instituto Nacional de Investigação Agrária e Veterinária (INIAV), Quinta do Marquês, 2780-159 Oeiras, Portugal, (isabel.carrasquinho@iniav.pt).

<sup>3</sup>Linking Landscape, Environment, Agriculture and Food (LEAF). Instituto Superior de Agronomia, Universidade de Lisboa, Tapada da Ajuda, 1349-017 Lisboa, Portugal.

Citation for proceedings: Nelson, C. Dana; Koch, Jennifer L.; Sniezko, Richard A., eds. 2020. Proceedings of the Sixth International Workshop on the Genetics of Host-Parasite Interactions in Forestry—Tree Resistance to Insects and Diseases: Putting Promise into Practice. e-Gen. Tech. Rep. SRS-252. Asheville, NC: U.S. Department of Agriculture Forest Service, Southern Research Station. 170 p.