Are there any *Pinus pinaster* trees resistant to *Bursaphelenchus xylophilus*?

Studies implemented in Portugal to address this question

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The Problem

The Pinewood nematode *Bursaphelenchus xylophilus* (Bx) was found to be responsible for maritime pine (*Pinus pinaster*) death for the first time in Europe in 1999, in a Portuguese stand in the South of Lisbon. It is the causal agent of the Pine Wilt Disease (PWD) and a quarantine organism in the European Union with approximately €80 million spent from 1999 – 2009 for attempting its eradication related with the control of the insect vector *Monochamus galloprovincialis*.

The Approach

Although PWN can cause devastating tree mortality, there is also evidence that some tree species such as *P. pinea* or individual trees within a species, are either tolerant (i.e. support the nematode, but are not killed immediately) or resistant to the nematodes. In order to investigate the susceptibility of *Pinus pinaster* to Bx, and as a first step for the establishment of methodologies for the improvement of its resistance, a research program was implemented recently in Portugal for this species, combining both genomic, transcriptomic and quantitative genetics approaches.

Results – Current stage of research

Selection strategy: About 500 trees were selected in highly infested areas with Pine Wilt Disease (PWD) for more than 10 years

| Progenies tests were established from 135 candidate trees and inoculation tests with Bx will be performed |
| Genotyping: A sample of 175 of the selected trees were genotyped with 6 SSRs markers and AFLPs (3 combinations) |

**Transcriptomics**: Suppression subtractive hybridization (SSH) detected differentially expressed genes between *P. pinea* and *P. pinaster*.

- 58% of the isolated sequences didn’t have a significant homology in the NCBI database;
- 40% of the expressed genes were related to defense mechanisms;
- Oxidative stress was found to be a very important defense mechanism triggered by the infection;
- Histone H4 was the differentially expressed gene by *P. pinea*, which might contribute to its apparent resistance to the disease;
- Pyrosequencing will allow further interpretation of data and generated novel sequences.