

***Bursaphelenchus xylophilus*: opportunities in comparative genomics and molecular host–parasite interactions.**

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Bursaphelenchus xylophilus, the pinewood nematode (PWN), is the causal agent of the pine wilt disease (PWD), which is a major threat to European and Far East forestlands. Knowledge concerning various aspects of the PWN ecology and interaction with different species of the insect-vector, a broad range of susceptibility/resistance of the tree hosts, coupled with associated bacteria, play a decisive role in the development of the disease. However, these mechanisms are not totally understood. The first insights into PWN genomics were based upon expressed sequence tags (EST) providing the identification of putative parasitism genes, or effectors. Moreover, the recent release of the whole-genome sequence of *B. xylophilus* will open new opportunities to further studies on nematode interactions, in particular with ecto-mutualistic bacteria that may contribute synergetically for PWN pathogenicity. A review of the current know-how on *B. xylophilus* is presented with recent developments in molecular biology of PWN which may bring new insights into its pathogenicity and interactions with the other factors governing PWD.