

## Abstract

The Pine Wood Nematode (PWN) *Bursaphelenchus xylophilus* is a severe forest pathogen in countries where it has been introduced and is considered a worldwide quarantine organism. In this study, protein markers for differentiating populations of this nematode were identified by studying differences among four selected Iberian and one American population. These populations were compared by quantitative proteomics (iTRAQ). From a total of 2860 proteins identified using the public database from the *B. xylophilus* genome project, 216 were unambiguous and significantly differentially regulated in the studied populations. Comparisons of their pairwise ratio were statistically treated and supported in order to convert them into discrete character states, suggesting that 141 proteins were not informative as population specific markers. Application of the Character Compatibility methodology on the remaining 75 proteins (belonging to families with different biological functions) excludes 27 which are incompatible among them. Considering only the compatible proteins, the method selects a subset of 30 specific unique protein markers which allowed the compared classification of the Iberian isolates. This approach makes it easier search for diagnostic tools and phylogenetic inference within species and populations of a pathogen exhibiting a high level of genetic diversity. This article is protected by copyright. All rights reserved.