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► To cite this version:

Christelle Robinet, Jianghua Sun, Richard Baker, Hugh Evans, Alain Roques. A simulation model to predict the potential spread of the pine wood nematode, *Bursaphelenchus xylophilus* over a range of scales. 25. International Congress of Entomology, New Era in entomology, Jun 2012, Daegu, South Korea. 1 p. hal-02809033

HAL Id: hal-02809033

<https://hal.inrae.fr/hal-02809033>

Submitted on 6 Jun 2020

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XXIV International Congress of Entomology

'New Era in Entomology'

August 19-25, 2012 | Daegu, Korea



S1006M07

Integrated Pest Management

S1006

A simulation model to predict the potential spread of the pine wood nematode, *Bursaphelenchus xylophilus* over a range of scales

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The pine wood nematode, *Bursaphelenchus xylophilus*, is the causal agent of the pine wilt disease. The species is native to North America where it is only a minor pest, mainly on non-native tree species. It has been introduced to several Asian countries (Japan, China, Taiwan, Korea) and to Europe (Portugal with some records in Spain). In most cases, the nematode has spread very rapidly despite control measures, and caused extensive damage to forests. If tree species are susceptible and climate is suitable, then the pine wood nematode can cause pine wilt and trees can die within a few weeks. Within forests and woodlands, the nematode is carried from one tree to another by adult beetles of the genus *Monochamus* whereas it can spread over long distances as a result of accidental transportation of infested materials. It is therefore important to understand the dispersal mechanism of the nematode and to determine the areas at risk. Here we present a spread model which combines short distance spread (to describe the dispersal of the vector) and long distance spread (to describe human transportation). This model was successfully used to predict the potential range expansion of the pine wood nematode and pine wilt disease in China. It also provides indications of which European ports are the most at risk for nematode introduction arising from international trade. The potential spread in Europe from the present invaded area in Portugal will be determined more accurately in the frame of the EU project REPHRAME (2011-2014).

Keywords: *Pine wood nematode, Bursaphelenchus xylophilus, Biological invasion, Monochamus, Spread model, Potential range expansion*

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