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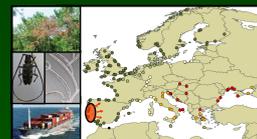
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Assessing the risk of invasion of the pine wood nematode and wilt disease expression in Europe: preliminary model and future directions

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1- INTRODUCTION

The pine wood nematode (PWN, Fig. 1a), *Bursaphelenchus xylophilus* (Steiner & Buhrer) Nickle, is the causal agent of the pine wilt disease (PWD). This pest originating in North America has invaded many countries in the world, especially in Asia and in Europe recently. In its native range it does not affect considerably *Pinus* health, whereas in the invaded range, it causes dramatic damage in pine stands (Fig. 1b). Transmission by insect vectors of the genus *Monochamus* (Fig. 1c) is the primary means of local dispersal but human mediated dispersal is suspected to play an important role in long distance jumps. Our objective is to develop a model that can simulate the spread of the vector beetles, the human-mediated spread and the disease expression based on climate conditions. Here we present: (1) the model initially developed to describe the invasion in China, (2) the model applied to Europe to determine the entry points from which the nematode and the disease could spread the most rapidly if it is introduced, and (3) the future directions within the EU project RE-PHFRAME.



Fig. 1: (a) pine wood nematode, (b) trees killed by the pinewilt disease, (c) carrier beetle, *M galloprovincialis*

2- MODELLING THE INVASION RISK IN CHINA

(A) Local spread of pinewilt disease

The pinewilt disease spread at a constant speed of 7.5 km/year around the first invaded site (Nanjing) during 5 years, and then the spread burst and no clear pattern was observed (Fig. 2; Robinet et al. 2009).

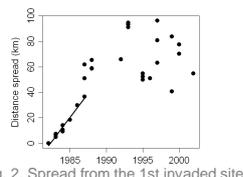


Fig. 2. Spread from the 1st invaded site

(B) Long distance dispersal of pinewilt disease

Infested sites located at more than 7.5 km from the nearest infested site were considered to be the result of a long-distance jump. The mean number of new infestations per year was equal to 3.4 during 1982-2000, and 18.2 during 2001-2005. The mean long-distance dispersal was estimated to 111-339 km. Railways, river ports and lakes had significant effects of the spread pattern, and human population density (indicator of the risk for accidental transportation) explained a large part of the invasion probability (Fig. 3; Robinet et al. 2009).

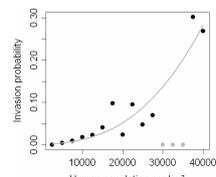


Fig. 3. Role of human population density of the invasion probability

(C) Climatic thresholds

Based on climatic thresholds for the carrier beetle (mean temperature in July above 21.3°C and mean temperature in January above -10°C; Ma et al. 2006), we determined the area where the climate was suitable (Fig. 4A). The potential area could expand by 40% with a 3°C warming (Fig. 4B).

(D) Combined spread model

Then we have developed a spread model combining climatic suitability, local dispersal and long-distance dispersal. This individual based model was stochastic and we made 300 replicate simulations to calculate the probability of invasion in each grid cell in 2025.

(E) Results

The model predicted an expansion of the potential invasion area (defined by $P > 0$) by 47% in 2025 under a stable climate (Fig. 4C), and by 55% under an increase of 0.03°C per year (Fig. 4D; Robinet et al. 2009).

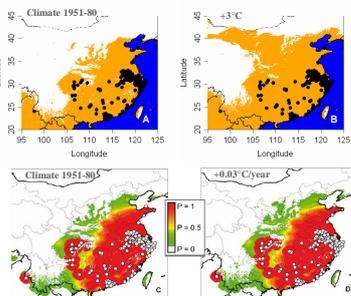


Fig. 4. Potential distribution of the pinewilt disease. A and B: orange color represents the area where the climate is suitable in case of a stable climate (A), and a 3°C warming (B). C and D: invasion risk in 2025 predicted by the spread model in case of a stable climate (C), or a warming (D).

3- MODELLING THE INVASION RISK IN EUROPE

The pinewilt disease was discovered in Portugal in 1999. Despite containment measures immediately applied, the disease has expanded over all the country and the European authorities are worried about the risk of expansion. To provide a first estimate of the invasion risk, we have applied the spread model initially developed for China and we simulated separate introductions of the nematode at 200 European ports under various climate change scenarios (Robinet et al. 2011).

(A) Potential spread of pine wood nematode

We combined the reaction-diffusion model to describe the vector spread and a stochastic model based on a dispersal kernel weighted by the human population density. In addition, we took into account the pine tree density in Europe. We made 200 replicate simulations to calculate the mean proportion of infested trees and infested area.

(B) Potential spread of pine wilt disease

The spread of the disease is considered to be the same as the spread of the nematode with the exception that the disease is expressed only where the mean temperature in July is above 20°C. We tested several scenarios: current climate (mean temperature in July for 1950-2000), and three HadCM3 climate change scenarios for 2020s (A1, A2, and B2).

(C) Results

Although it is not yet possible to adjust the model to the invasion pattern in Europe, these predictions can provide information about the relative risk of spread from European ports in addition to the natural spread from the Iberian Peninsula. The most important ports to control to prevent the invasion of the pine wood nematode are located in Eastern and Northern Europe (Fig. 5A; Robinet et al. 2011). For the pine wilt disease, they are located in Romania, Bulgaria, Croatia, Ukraine, Italy, Greece, Hungary, Slovakia and Slovenia (Fig. 5B-E). An introduction to ports located in the likely range expansion of the disease (Spain and Southern France) may have little additional influence on the invasion situation in 2030. The effects of climate warming will probably be more important in Europe than in China (+140% vs +40% for +3°C).

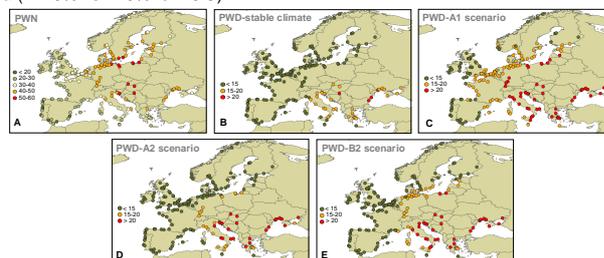


Fig. 5. Potential spread in case of a separate introduction at the 200 main ports in Europe. The symbol indicates the percentage of cells (10 km x 10 km) where the infested area is > 0 in 2030 if the nematode was introduced at the port located there. Spread of the pine wood nematode without climatic constraint (A), and spread of the pine wilt disease assuming: a stable climate (B), the A1 scenario (C), the A2 scenario (D) and the B2 scenario (E). Area in grey is the study area.

4- FUTURE DIRECTIONS

In the EU project RE-PHFRAME (2011-2014), predictions of the nematode spread in Europe and predictions of the wilt disease expression will be refined.



Fig. 6. Flight mill

(1) Spread model:

- the flight capacity of the European vector, *M. galloprovincialis* will be measured (flight mill, release-recapture experiment, and eventually radio-tracking)
- the history of invasion in Portugal will be analysed to detect possible patterns

(2) Disease expression:

- the mechanistic model (ForestETp) developed in a previous EU project (PHFRAME) will be refined and simplified to be applicable at larger scales
- a latency sub-model will be developed to describe more precisely the conditions for a delayed onset of wilt (latency) and non wilt (eco-climatic resistance).
- a correlative model will also be developed in Portugal

➔ All these improvements should help us to make more precise predictions of the potential spread of the pine wood nematode in Europe and the risk of wilt disease.

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