Deliverable summary D2.4

Database with parameters for semi-mechanistic models for forest pest and pathogens risk assessment and management for use in decision support tools

Project acronym:	**HOMED**
Project full title:	**Holistic Management of Emerging forest pests and Diseases**
GA n°:	**771271**
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Duration:	**48 months**
Project coordinator:	**Herve Jactel (INRA)**
Planned delivery date:	**M42**
Actual submission date:	**M42 – A preliminary version of this deliverable was submitted at M36**
Work package:	**WP2**
WP leader:	**INRAE**
Lead beneficiary:	**WU**
Partners involved:	**INRAE and WUR (other contributors: ISA and USDA)**
Version:	**01**

Dissemination Level	
PU Public	**PU**
CI Classified, as referred to Commission Decision 2001/844/EC	
CO Confidential, only for members of the consortium (including the Commission Services)	

1. Summary

Models are indispensable tools in risk assessment and management of alien forest pests and pathogens (PnPs). In the previous deliverable of WP2 (D2.3), six different models or frameworks for risk assessment and management have been described that cover Tasks 2.1 to 2.3. This deliverable has two aims: 1) to refine and advance the methodology as published in D2.3; 2) to provide information, parameters and/or tools to be input for WP1.

Models presented in this deliverable are:

- Hotspot model for pest establishment (Chapter 3 and 4 of this document)
  - Chapter 3 and 4 of this deliverable are corresponding to tasks 2.1 and 2.2.
  - Partner leading this activity: WU with input from ISA and INRAE.
  - The method that was developed has been completed (Chapter 3) and the method has been applied to first establishment locations of invasive forest pests in Europe (Chapter 4).
  - Two draft interactive maps pointing out hotspots of forest pest establishment with and without correction for sampling bias have been provided for the WP1 toolbox. As an example of such a map, we refer to Figure 8 in Chapter 4.
- Data driven generic spread model
  - Chapter 5 of this deliverable is corresponding to task 2.2.
  - Partner leading this activity: WU.
  - Substantial progress has been made in data collection more than doubling the number of species to seventeen species.
  - Estimated mean spread rates will be provided to the knowledge hub. For an example see Table 3 in Chapter 5.
- Generic framework for emergence
  - Chapter 6 of this deliverable is corresponding to task 2.3.
  - Partner leading this activity: INRAE (URZF)
  - Progress has been made on the parametrisation of the generic outbreak model (insect profiles), and the methodology to assess the speed and direction of species potential spread has been refined. A paper on the outbreak model was submitted (see manuscript version presented in this deliverable, see section 6.1.2) and should be revised.
  - The Rscript of the outbreak model has been provided for the WP1 and a user-friendly interface to simulate the probability of outbreak is being implemented in the WP1 toolbox (see Section 6.1.1).
- Spread mitigation models
  - Chapter 7 of this deliverable is corresponding to task 2.2.
  - Partner leading this activity: INRAE (URZF) with input from ISA and USDA.
  - Progress has been made on the way to provide useful outputs for the WP1 toolbox. The most important parameters are being identified for each model and simulations will be conducted to provide an overview of the spread mitigation effectiveness when changing the value of these parameters.
  - Figures showing the effectiveness of various mitigation measures will be provided for the knowledge hub (see figures in the results of the draft article, section 7.2).
- Generic model for tree mortality with ash dieback as model system

- ○ Chapter 8 of this deliverable corresponding to task 2.2.
  - ○ Partner leading this activity: INRAE (IAM)
  - ○ Progress has been made on the drivers of host damage. An equation gives the proportion of crown dieback and ash mortality based on a number of stand parameters.
  - ○ We refer to section 8.4 for examples of the tables that will be provided to the knowledge hub.
- ● Modelling the effects of tree diversity on the evolution and propagation of tree cankers
  - ○ Chapter 9 of this deliverable – corresponding to task 2.2.
  - ○ Partner leading this activity: INRAE (BIOGECO)
  - ○ Progress has been made on model development, validation, and simulations. Two case-studies are explored to be presented in the knowledge hub: the deployment of resistant cultivars and the use of non-host trees in forest stands. See section 9.3 for the two case-studies
  - ○ Figures showing how the deployment of resistant trees and non-host trees impacts the development of emerging diseases caused by evolving fungal pathogens will be provided for the knowledge hub (see section 9.3).