Deliverable summary D2.3

Semi-mechanistic models for forest PnPs risk assessment and management

Project acronym:	**HOMED**
Project full title:	**Holistic Management of Emerging forest pests and Diseases**
GA n°:	**771271**
Start date of the project:	**October 1st 2018**
Duration:	**48 months**
Project coordinator:	**Herve Jactel (INRA)**
Planned delivery date:	**M30**
Actual submission date:	**M31**
Work package:	**WP2**
WP leader:	**INRAE**
Lead beneficiary:	**INRAE**
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). **This deliverable has the objective to report on six different models or frameworks that are considered useful for risk assessment and management.** HOMED aims to deliver approaches that are generic in the sense that they can be applied to novel, yet unknown species, and which can be readily parameterized to new species. Most models presented in this deliverable are generic of nature although in some cases particular species are chosen as model species**. The models that are presented are respectively: i) models to assess the effectiveness of pest control methods (chapter 2), ii) models of emergence to describe local outbreaks and potential spread (chapter 3), iii) a statistical model on crown dieback and ash mortality as a function of covariates derived from forest inventory data and climatic data (chapter 4), iv) a modelling framework to study the effects of control measures on the evolution of virulence and the propagation of tree fungal pathogens, v) a generic model to predict hotspots of pest establishment in Europe, and finally vi) a novel approach to estimate spread rates of invasive forest pests.**

Below we give a more extended summary of the six different model tools.

1) To assess the effectiveness of control methods of PnPs, we developed a model at local scale to describe respectively the effectiveness of: (1) pheromone trapping, (2) mating disruption, (3) host removal before PnPs dispersal (to prevent further host tree infestation and spread of PnPs), (4) host removal after PnPs dispersal (to remove potentially infested but not detected trees) and (5) classical biological control. These models are individual-based and stochastic models, they have been designed in a roughly similar way (same kind of inputs and outputs) and all of them provide an indication of the management success. They could be used later in the project to feed the modelling part related to the economic assessment of risk mitigation. *(Partner leading this activity: INRAE URZF; Contributors: INRAE Biogeco, ISA, USDA)*

2) A generic framework of emergence has been developed consisting of two parts: a model to describe local outbreaks (temporal dynamics) and a model to describe the potential spread across Europe (spatio-temporal dynamics). The first model is a probabilistic model. It has been built and parametrized on different types of PnPs. This parametrization allows obtaining species profiles that can be used as a baseline to make predictions even if poor data are available on the PnPs. However, the model also offers the possibility to easily include more data and also to add or remove drivers. This is to our knowledge the very first generic outbreak model that has been developed so far, and a user-friendly version using a shiny app was developed. Further refinements and parametrizations are ongoing. The second model describes the effect of the environment in a reaction-diffusion model to describe spread. It describes both the shift of the suitable area due to climate warming and the spread of the species within this suitable area. This generic model was used so far on virtual species to explore the model behaviour and should be parameterized soon on real case studies. *(Partner leading this activity: INRAE URZF)*

3) A Bayesian framework was developed to model crown dieback and ash mortality as a function of time of disease presence, including covariates derived from forest inventory data and climatic data, and including spatio-temporal effects. The development of models for crown dieback and ash mortality of Ash dieback (our model system) showed that the time of disease presence was a main variable to describe tree mortality of this fungal invader. Crown dieback at the stand level significantly increased from the third year after the first report of the pathogen in the stand. In turn,

the increase in ash mortality was significant after five years of disease presence. The main covariates in the models were the 5-year radial increment, ash density, and variables that approximated humidity conditions in the stand. Further, crown dieback was a good predictor of tree mortality. The applicability of this approach to other invasive diseases would depend on the definition of variable for disease severity and the selection of covariates that link to disease development. Coupling the models presented here with epidemiological models can be a great management tool to predict disease risk and damage cause by invasive diseases. *(Partners leading this activity: INRAE IAM)*

4) A new modelling framework was developed for studying the effects of control measures on the evolution of virulence and the propagation of tree fungal pathogens. The main control measures considered are resistant varieties deployment, and increase of inter-specific variability. The framework was also set to study, later on, the evolution of tree resistance in natural forests of ashes undergoing epidemics caused by *Hymenoscyphus fraxineus* (see link to above mentioned model). As an illustration of the framework and the simulation work realized, we report preliminary results about the efficiency of the deployment of quantitative resistances in a landscape of chestnuts mixing natural stands and orchards (case study 1). Preliminary analyses suggest that an intermediate proportion of resistant trees in chestnut orchards kept the highest number of hosts healthy over the medium term. Our results will help managers to recommend the most durable and efficient management practices for the targeted pathosystems, taking into account the evolutionary potential of pathogens. This may also contribute to theory on virulence evolution, adaptation to heterogeneous environment and co-evolution of hosts and pathogens. *(Partners leading this activity: INRAE Biogeco)*

5) The model to predict hotspots for pest establishments is a type of 'species distribution model'. However, instead of modelling the probability of establishment using a regression-like framework, the probability of establishment is derived from fitting probability distributions to individual spatial predictors. This method allows including sampling bias correction, and correlation between spatial predictors. We apply this new method to a dataset of invasive forest insects that established in Europe and we test which spatial predictors can predict the establishment of pests while correcting for sampling bias. The latter is important as forest pests are often not found in systematic surveys but in an ad-hoc fashion by observers. This method is highly flexible compared to existing methods. Further developments include: model testing and validation. A stakeholder feedback will be held to receive feedback on the approach. *(Partners leading this activity: WU with input from ISA and INRAE)*

6) A generic model is developed to examine the spread of PnPs in Europe. We show that the lognormal dispersal model performed best for the general model and for all species separately. Surprisingly, only gross domestic product per capita substantially improved the model fit. This research showed that commonalities do exist in the mechanisms of spread, which can be captured in a dispersal kernel model. However, more research is needed into mechanistic models that aim at estimating spread rate before it can be concluded that additional predictors help the spread rate prediction. Nonetheless, this study shows great potential for the inclusion of such external drivers to determine how fast an unknown species might invade a certain environment. *(Partners leading this activity: WU).*