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EXTERNAL SCIENTIFIC REPORT

Inventory and review of quantitative models for spread of plant pests for use in pest risk assessment for the EU territory[1]

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ABSTRACT

This report considers the prospects for increasing the use of quantitative models for plant pest spread and dispersal in EFSA Plant Health risk assessments. The agreed major aims were to provide an overview of current modelling approaches and their strengths and weaknesses for risk assessment, and to develop and test a system for risk assessors to select appropriate models for application. First, we conducted an extensive literature review, based on protocols developed for systematic reviews. The review located 468 models for plant pest spread and dispersal and these were entered into a searchable and secure Electronic Model Inventory database. A cluster analysis on how these models were formulated allowed us to identify eight distinct major modelling strategies that were differentiated by the types of pests they were used for and the ways in which they were parameterised and analysed. These strategies varied in their strengths and weaknesses, meaning that no single approach was the most useful for all elements of risk assessment. Therefore we developed a Decision Support Scheme (DSS) to guide model selection. The DSS identifies the most appropriate strategies by weighing up the goals of risk assessment and constraints imposed by lack of data or expertise. Searching and filtering the Electronic Model Inventory then allows the assessor to locate specific models within those strategies that can be applied. This DSS was tested in seven case studies covering a range of risk assessment scenarios, pest types and dispersal mechanisms. These demonstrate the effectiveness of the DSS for selecting models that can be applied to contribute to EFSA Plant Health risk assessments. Therefore, quantitative spread and dispersal modelling has potential to improve current risk assessment protocols and contribute to reducing the serious impacts of plant pests in Europe.

KEY WORDS

Plant pest, disease, invasion, dispersal, spread, model, simulation

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SUMMARY

Pests of plants cause major economic losses to the production of agricultural, forestry and ornamental plants in Europe and globally. Risk assessment for plant pests can target resources efficiently at managing the spread of current and novel pests. Such efforts would be enhanced by quantitative models for pest spread and dispersal. In principle, spread and dispersal models are able to predict the areas at risk of future spread, provide insights into the biological and abiotic factors facilitating spread, estimate pest impacts and experiment with different management strategies. However, a large number of spread and dispersal models have been developed and published in the scientific literature. It is the wish of the EFSA Panel on Plant Health to make a better and more tailored use of spread models in risk assessments. Therefore it is necessary to survey the range of different modelling techniques and evaluate their relative usefulness and limitations. Furthermore, a system for selecting the most appropriate models for application in risk assessment is required to guide potential users through the wide variety of modelling approaches available. Here we report on such an evaluation, to provide EFSA with guidance and case studies for future risk assessment.

The overall aims of this report are:

1. To conduct an extensive literature search of quantitative models of spread and dispersal of plant pests, and analyse the search results to identify distinct modelling strategies.

2. To produce a detailed electronic inventory of the spread and dispersal models located by the literature search.

3. To assess the fitness of different spread and dispersal model strategies for use in Plant Health risk assessment and develop a Decision Support Scheme (DSS) for choosing an appropriate model.

4. To present several risk assessment modelling case studies, including use of the DSS and practical application of the selected models.

The extensive literature search was based upon protocols for Systematic Reviews and Systematic Mapping, in order to provide as comprehensive, unbiased and reproducible a search as is possible. We searched for relevant literature within Web of Knowledge, Scopus, Google Scholar, EFSA Journal and the MOPEST, PESTCAST and CAMASE model inventories. The search was designed to locate generic terms for pests and host plants, as well as the names of 2381 important pest organisms and 282 crop plants. The pest organisms included insects, invasive, weedy and parasitic plants, fungi, oomycetes, viruses, viroids, bacteria, phytoplasmas, nematodes and mites listed in EC Directive 2000/29/EC, the EPPO Plant Quarantine Data Retrieval System, Q-Bank database of regulated pests and EU Emergency Control Measures. The search yielded nearly 14000 articles. We established clear criteria by which irrelevant results were screened out and discarded based on sequential examination of their titles, abstracts and full texts. After this process the extensive literature search resulted in 468 eligible papers containing models of pest spread or dispersal.

To identify the major modelling strategies, we performed a cluster analysis on the models located by the literature search. For clustering, we defined a set of 27 multiple-choice questions characterising the models' representation of space and time (e.g. continuous or discrete, scales, numbers of dimensions, heterogeneity, etc.) and representation of the pest and host organisms (e.g. generality, number of species, stochasticity, dispersal mechanisms, evolutionary processes, etc.). To cluster the models, we applied two different clustering algorithms – co-clustering based on the Bernoulli Latent Block Model and model-based clustering using the Gaussian Finite Mixture Model. Both algorithms indicated that the optimal clustering of the models was into eight separate strategies. However, the model-based

clustering gave a higher quality clustering than co-clustering, and so this model was retained for interpretation. Examination of the Clusters allowed us to identify the following major strategies:

- **Cluster A: Single-event pest dispersal**, generally dispersal kernel or disease gradient models for a single pest spreading over a fixed time period.
- **Cluster B: Large-scale simulation of pest dispersal events**, generally wind dispersal of the pest simulated through Lagrangian atmospheric dispersion, advection-diffusion, or wind trajectory models.
- **Cluster C: Pest spread or dispersal in continuous space and time**, generally reaction-diffusion and diffusion models without explicit modelling of the host plant.
- **Cluster D: Continuous-space pest spread in discrete time**, generally integrodifference models for pest spread through a homogeneous landscape with no explicit host representation.
- **Cluster E: Iterative colonisation of hosts at small scales**, generally simulation of spatial susceptible-infected epidemic models and network contact spread models.
- **Cluster F: Simulation of specific pest spread at large scales**, generally cellular automata or metapopulation models for pests without an explicit host plant model.
- **Cluster G: Simulation of specific pest and host dynamics**, generally cellular automata or individual-based models incorporating lots of biological detail on the focal pest and host.
- **Cluster H: Generic pest and host dynamics**, generally cellular automata or individual-based models for generic organisms.

Our ordering of Clusters begins with the dispersal-only strategies (A and B) and then covers the two most mathematically-based strategies for dispersal or spread (C and D). The next three strategies (E-G) primarily rely upon computer simulation of spread, and are ordered from the simplest to the most complex algorithms. The final strategy (H) combines both simulation and mathematical approximations.

After doing the clustering, we investigated differences between the resulting model strategies in terms of the ways in which they were applied and analysed. This used data not used in the clustering to ensure an independent evaluation and validation of the meaningfulness of the clusters. Some of the main findings were as follows.

- Although most clusters were applied to a range of pests and hosts and in a range of sectors, there were some significant differences. Some notable examples are:
    - Cluster A, which was mainly used for agricultural crop diseases;
    - Cluster F, which was mainly used for invasive plant competitors;
    - Cluster E, which was mostly used for plant diseases;
    - Cluster B, which was generally used in the agricultural sector;
    - Also, micro-organisms tended to feature in a narrower range of model clusters than insects or plants.
- The biological data used for parameterisation differed among Clusters. Parameters of Cluster A were most often fitted to spread data, while Clusters G and B generally relied upon independent empirically-determined parameterisation and Cluster H used arbitrary parameter values.

- Sensitivity analyses were commonly applied to determine the impacts of pest or host parameters on model outputs and investigate risk reduction options. The exceptions to this were Clusters A and B. Risk reduction analyses were most common within Clusters F and G.

The data from the extensive literature search and results of the cluster analysis were entered into a database providing a secure Electronic Model Inventory. Some of the key functionalities of the Electronic Model Inventory are the ability to search for records and to access and export the underlying data on their bibliography, formulation and usage. Therefore, the Electronic Model Inventory allows EFSA to identify and review quickly models for the spread and dispersal of plant pests. It should therefore provide a useful tool for rapidly determining whether models already exist for pests that are the subject of future Plant Health risk assessments.

To assess the pros and cons of the eight Clusters, we scored each strategy against 19 fitness criteria that assess the ability of the models to provide answers to the questions in the harmonised framework for EFSA risk assessments (EFSA Panel on Plant Health (PLH), 2010a). This revealed that there was no clear one-size-fits-all solution to using pest spread models in Plant Health risk assessment. All the strategies had their own strengths and weaknesses. However, Clusters A and E were clearly less useful than the other strategies, primarily due to their restriction to small spatial and temporal extents.

In general, we distinguished between strategies primarily based on a top-down approach (data-driven and more phenomenological, e.g. Clusters E and F) or a bottom-up approach (process-based equations parameterised empirically or arbitrarily, e.g. Clusters B, C and H). We considered that top-down approaches are most useful for predicting realistic spread dynamics and investigating spatial variation in control efforts. However, they are usually reliant on good distribution data for model parameterisation, which may be lacking for recently introduced pests. Bottom-up approaches were considered most useful for establishing general principles and biological scenario experiments, e.g. identifying the key life history stage to target for control. However, they rely on detailed biological information about the pest, which may not always be readily available.

Finally, some parts of the EFSA risk assessment protocol were not well addressed by the existing suite of published models that we reviewed. These included explicit modelling of pest entry, dynamic environmental heterogeneity (e.g. annual variation in weather), human-mediated dispersal (other than as a generic dispersal kernel) and multiple dispersal mechanisms.

Following the fitness assessment, we developed a Decision Support Scheme (DSS) that aids selection of the appropriate modelling strategy by weighing up the relevant goals and constraints on the modelling. The goals are the EFSA risk assessment questions and type of pest-host system towards which the modelling should provide evidence. The constraints include lack of data and lack of available software for modelling. The DSS gives relative scores to each modelling cluster's general suitability for the risk assessment task and its feasibility, given the constraints. As such, the DSS is best viewed as a method for the risk assessor to focus in on model types that should be most useful for guiding development of a model for the focal pest's risk assessment. We emphasise that because there was no general overall best modelling strategy following our fitness evaluation, the DSS will work best when the goals and constraints for modelling are well defined and limited.

Finally, we report upon seven case studies in which the DSS was used to select models for practical application. The case studies were based around four risk assessment scenarios:

1. A single outbreak (or small number of outbreaks) of a pest is detected. Modelling should be used to estimate the potential range of dispersal from the outbreak location.

2. Following an initial detection, a pest is documented dispersing to new locations. The dispersal range is to be characterised by using this information in a model.

3. A new pest is detected in the risk assessment area. Surveys quickly determine its current distribution but no information is available on its spread history, including the location or time of entry. Modelling should be used to estimate the potential rate at which the pest may spread.

4. Risk assessment is required for a pest that has been recorded spreading in the risk assessment area over a number of years. By using this information in a model, the future pest spread should be predicted.

The seven case studies addressed all four scenarios and additionally featured a range of pest taxonomic groups (fungi, bacteria, insect herbivores and invasive plant weeds), dispersal mechanisms (wind, insect vector, active movement and human, as well as generic models aggregating multiple mechanisms) and six of the eight clusters. For each case study, we successfully applied the DSS to select the appropriate model cluster and identify suitable models for application from the Electronic Model Inventory. Briefly, the case studies consisted of:

1. Risk assessment scenario (RAS) 1, Cluster B – Mechanistic modelling of the wind dispersal process for spores released from a hypothetical outbreak of the fungal pathogen *Phakopsora pachyrhizi*. The bottom-up HYSPLIT-WEB atmospheric model was parameterised from known traits of the spores. The modelling mapped the region at risk of spore dispersal from the hypothetical outbreak at a European scale, and suggested a potential for long-distance dispersal.

2. RAS 2, Cluster A – A generic anisotropic dispersal kernel model fitted to dispersal data inferred from a major spread event of the bacterial pathogen *Erwinia amylovora* in the Emilia-Romagna region of Italy. This top down model suggested highly directional spread, suggestive of important roles for directed dispersal mechanisms such as wind and humans. The fitted model can be overlain onto existing outbreak locations to model the region at risk of further dispersal.

3. RAS 3, Cluster C – A reaction-diffusion model applied to estimate the spread rate of the insect-vectored bacterium *Xylella fastidiosa* among olive trees in Apulia, Italy. The model is a bottom-up approach relying on estimates of the bacterial population growth rate and insect-vector diffusion rate from the literature to calculate a spread rate. However, the limited available evidence for parameterisation demonstrated major differences in its epidemiology in the risk assessment area compared to other regions in which it has spread. Therefore, we considered it was not possible to accurately predict the spread rate in this instance, because it would be highly uncertain and potentially misleading. This highlights the important need to understand the pest biology and data availability when selecting a model using the DSS.

4. RAS 3, Cluster D – Use of the generic Integro-difference equation for modelling spread of the invasive weed plant *Conyza canadensis* by wind dispersal. This bottom-up model predicts the rate of spread of the pest of based on demographic and dispersal traits that are commonly available in the literature. Sensitivity analysis of the parameterised model suggested that rapid spread of the weed is most dependent on high adult survival and fecundity. Therefore these demographic stages could be the most effective for targeting control efforts.

5. RAS 3, Cluster H – A stochastic simulation model for the spread of the insect-vectored bacterium *Xylella fastidiosa* among olive trees in Apulia, Italy. Although the DSS selected an existing generic model, we had to make substantial modifications to apply in this study. For example, we developed a computationally-efficient approximation to local population growth, and implemented

‘stratified’ dispersal with deterministic local diffusion and stochastic long-distance jumps. With reasonable parameter values, the model qualitatively reproduced similar distribution patterns as are observed in the affected region. We used the model to implemented a control scenario (roguing – removal of infected crops), which showed that roguing has little impact on spread, but has a significant impact on disease incidence.

6. RAS 4, Cluster F – A simulation model for spread of the bacterial pathogen *Erwinia amylovora* through a heterogeneous landscape. This top-down model was fitted to data on the pathogen spread over seven years in the Emilia-Romagna region of Italy. Land cover was used to represent heterogeneity, so that the model showed which land cover types were suitable or unsuitable for outbreaks. Furthermore, the model also indicated significant variability in spread rates between years. Stochastic simulations of the model allowed us to predict the region at risk of future spread of the pathogen.

7. RAS 4, Cluster F – A top-down simulation model for human-mediated spread of an invasive pest insect *Cameraria ohridella* in the UK. We investigated how well two alternative models for human dispersal fitted the spread pattern documented in the UK over 10 years. Both models were able to explain a large proportion of the observed spread, except for an apparent slow down in the invasion in the final years of the data. This suggests that the insect may have reached a climatic limit to invasion, not represented in the current model.

Together we consider that these case studies demonstrate the effectiveness of the DSS and Electronic Model Inventory for selecting models that could be applied to contribute to EFSA Plant Health risk assessments.

TABLE OF CONTENTS

BACKGROUND AS PROVIDED BY EFSA

The EFSA Scientific Panel on Plant Health (hereinafter, the PLH Panel) provides independent scientific advice on the risks posed by organisms which can cause harm to plants, plant products or plant biodiversity in the European Community. The PLH Panel reviews and assesses those risks with regard to the safety and security of the food chain to assist risk managers in taking effective and timely decisions on protective measures under the Council Directive 2000/29/EC to prevent the introduction and further spread of organisms considered harmful to plants or plants products in the European Community. On request, the PLH Panel prepares and evaluates pest risk assessments and identifies and/or evaluates the effectiveness of potential risk mitigation options in mitigating the risk of introduction and/or spread of a harmful organism. In general, these requests relate to the risk for the whole EU territory. The main components of plant health risk assessment, i.e. the assessment of the probabilities of entry, establishment and spread and of the potential consequences of plant pests, may be assessed by qualitative or quantitative approaches. Quantitative models to assess the probability of spread of plant pests[3] allow to dynamically estimate (in terms of space and time) the impact of plant pests, to conduct quantitative comparisons of the importance of different spread pathways and of different scenarios as well as to undertake a quantitative assessment of the effectiveness of different risk reduction options on reducing the probability of spread of a given plant pest. Spread models have been described in literature for specific plant pests or in some instances for certain plant pest categories as well as simple generic spread models which are less dependent on specific biological data of plant pests. An inventory and a comprehensive review of such models, particularly with regard to their fitness for use in pest risk assessment, are needed to support the assessment of the risks to plant health.

TERMS OF REFERENCE AS PROVIDED BY EFSA

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[3] A pest is defined here as any species, strain or biotype of plant, animal or pathogenic agent injurious to plants or plant products (FAO/IPPC, 2010. ISPM No. 5 Glossary of phytosanitary terms. Available at https://www.ippc.int/file_uploaded/1273490046_ISPM_05_2010_E.pdf). This definition includes plant pathogens as microorganisms causing diseases.

INTRODUCTION AND OBJECTIVES

Plant pests impose a major constraint on yields from agricultural, horticultural, forestry, forage, ornamental and other commercially important plants and their derived products (Waage et al., 2008). It has been estimated that 32% of global crop yield is lost to pests, with weeds, animal pests, pathogenic fungi and bacteria accounting for the majority of the loss (Oerke and Dehne, 2004). The same study calculated that the use of pesticides in Western Europe cost approximately US$100 per hectare of arable land in 1998. Other crop and plant protection measures, such as biological, mechanical and cultural control, undoubtedly add to this economic burden.

In addition to the harm caused by established pests, newly introduced non-native pests can quickly spread into available territory from points of entry. Indeed it has been estimated for several regions that 30-50% of the extant crop pest organisms are non-native (Pimentel, 2002). Increased trade has meant that rates of pest introduction to Europe increased throughout the 20th century (Waage et al., 2008). As globalisation of trade in commodities able to harbour plant pests continues it seems inevitable that many more novel pest introductions to Europe will occur in the future (Meyerson and Mooney, 2007; Hulme, 2009). Furthermore, changing climatic and other environmental conditions may lead to a greater propensity for introduced pests to establish, spread and cause impact than has been observed historically (Walther et al., 2009).

While it may be possible to develop control measures against plant pests once they are widespread, it is much more effective in terms of time, cost and ultimate success to take action before a pest becomes widespread (Wadsworth et al., 2000; Johnson and Turner, 2010; Kapustka, 2010; Travis et al., 2011). Therefore, risk assessment at an early stage in plant pest invasion forms a valuable weapon against their damaging impacts. By identifying emerging hazards, quantifying risks and recommending management strategies and risk reduction options, risk assessments have greatly reduced the long-term economic impacts (Keller et al., 2007).

The European Food Safety Authority (EFSA) Panel on Plant Health provides risk assessment on plant pests for the European Union territory. In response to requests for scientific opinions from the European Commission, the European Parliament, the Member States, or on its own initiative, the Panel provides independent scientific advice on issues related to organisms harmful to plants and plant products and biodiversity. EFSA Plant Health risk assessments follow harmonised protocols to ensure independence and transparency (EFSA, 2009; EFSA Panel on Plant Health (PLH), 2010a). This involves assessing the risk of entry, establishment and spread of the pest, and the consequences of this, to characterise the overall risk posed by the particular pest in question. In some cases, risk reduction or management options may also be considered (EFSA Panel on Plant Health (PLH), 2010b, 2011).

In the main, each of these Plant Health risk assessment components have been assessed qualitatively, while quantitative modelling of pest spread or dispersal has been used only rarely (e.g. EFSA Panel on Plant Health (PLH), 2010b, 2011). A greater use of quantitative spread and dispersal models may improve EU Plant Health risk assessment, because in principle modelling can identify the regions where a pest can persist, dynamically model its expansion from existing populations or points of entry and estimate the impacted areas for any given time period (Kehlenbeck et al., 2012; Parry et al., 2013). Since the population dynamics of pest organisms are expected to be strongly influenced by climate, the distribution of host plants, land cover, cultivation practices and risk reduction options, changes in these factors are likely to have a large impact on pest distributions and spread rates. Quantitative models can provide insights into these factors because of the ability to perform sensitivity analyses and scenario experiments that can be useful for understanding the biotic and abiotic factors contributing to spread and its successful management.

One of the main barriers to the application of quantitative spread models in EFSA Plant Health risk assessment is in understanding how to select appropriate models for different risk assessments from the great diversity of spread and dispersal models that have been developed over the last decades. Existing models are based on a diverse range of mathematical and computational methods (Parry et al., 2013). They range from very specific in location, pest and host (e.g. Calonnec et al., 2008; Harwood et al., 2009; Meentemeyer et al., 2011) to very generic and host- and pest-independent (e.g. Brewster and Allen, 1997; Kehlenbeck et al., 2012). Both types of model can be important for risk assessment. Specific approaches can include a lot of biological detail and make accurate predictions for the focal system but can require more data than are available for most species (Bullock et al., 2008). Generic models can be used in sensitivity analyses to identify pest traits favouring spread under alternative conditions, though their applicability may be limited by the degree of biological complexity built into the model (Kehlenbeck et al., 2012). Furthermore, spread and dispersal models have been developed across very different spatial and temporal scales (Parry et al., 2013). This variety in the formulation and use of pest spread models makes it difficult to assess which are most suited for the risk assessment protocols of EFSA, in particular for assessing of the probability of pest establishment and spread (EFSA, 2009; EFSA Panel on Plant Health, 2010a).

A framework for using quantitative modelling of spread and dispersal in plant pest risk assessment requires a critical appraisal of the range of modelling tools available, as well as a methodology for selecting appropriate models for different risk assessments. Previous attempts to do this have typically relied upon *a priori* definition of a small number of modelling strategies. For example Truscott and Ferguson (2012) and Kehlenbeck et al. (2012) consider four model types based upon all combinations of two factors – whether or not the pest is modelled as occupancy (i.e. presence/absence) or as population density and whether the model only has a temporal component or also includes a spatial component. In our opinion there is a far wider diversity of model strategies than are captured in this simple scheme.

In this report we appraise and evaluate the relative advantages and disadvantages of eight broad modelling strategies. We evaluated their fitness with regard to factors such as their data requirements, use of biological data, incorporation of landscape characteristics, taxonomic and functional group generalisation and capacity for experimentation with scenarios about land use and climate change or risk reduction options.

The overall aim of this report is to provide EFSA with an overview of existing spread and dispersal models for plant pests and a system for selecting an appropriate model for application in a risk assessment. Our main objectives are:

1. To review the scientific literature and produce a detailed electronic inventory of quantitative models for pest spread and dispersal.

2. To perform a clustering on the inventory database to identify distinct modelling strategies.

3. To appraise the fitness of each broad modelling strategy for different elements of Plant Health risk assessment.

4. To develop a Decision Support Scheme, allowing EFSA to identify the most suitable models for application in future risk assessments.

5. To use the Decision Support Scheme to select models for risk assessment case studies covering different taxonomic or functional pest groups and the most common European spread pathways for plant pests.

6. To apply those models to demonstrate their potential use in risk assessment.

Towards these objectives, the report is structured in four major project tasks:

1. Extensive literature search on quantitative models of spatial and temporal spread and dispersal of plant pests.

2. Electronic inventory of models of spread and dispersal of plant pests.

3. Assessment of the models of spread and dispersal of plant pests for their use in pest risk assessment.

4. Case studies of model selection and application.

TASK 1 - EXTENSIVE LITERATURE SEARCH ON QUANTITATIVE MODELS OF SPATIAL AND TEMPORAL SPREAD AND DISPERSAL OF PLANT PESTS

1. Objectives

The objectives of Task 1 are:

- To perform an extensive literature search, based on the principles of systematic reviewing and mapping (Bates et al., 2007; CEBC, 2010; EFSA, 2010; Randall and James, 2012), to sample the scientific literature and locate quantitative models of plant pest spread and dispersal, including both specific and generic models (see Glossary for our definitions of these terms).

- To perform a cluster analysis on the models located in the extensive literature search. Clustering will be based on the theoretical concepts used in the models and will allow us to identify discrete strategies used for modelling plant pest spread.

- To validate the clustering by testing whether there are differences in the functional or taxonomic groups of pest and host organisms or economic sectors in which the model clusters operate. Also, to test whether model clusters differ in their parameterisation and analysis.

2. Materials and Methods

The extensive literature search followed a protocol based on established guidelines for systematic reviews (CEBC, 2010; EFSA, 2010) and the newly emerging and related research technique of systematic mapping (Bates et al., 2007; Randall and James, 2012). Both are robust, repeatable, scientific methods for identifying and categorising the available literature on a particular topic.

The protocol considered the following areas:

- Research question

- Search terms

- Information sources

- Screening of the search results

- Reference management

- Quality assessment

Each are described in detail below, including results of feasibility testing performed during protocol development to ensure that the literature search followed a robust methodology.

2.1. Research question

In consultation with the EFSA Project Steering Committee, we defined the primary question for the extensive literature search as ‘How is the modelling of pest spread and dispersal done quantitatively?’. We identified the following question elements (CEBC, 2010; EFSA, 2010) relating to this (Table 1).

Table 1: Definitions of terms within the objective of the extensive literature search.

Question elements	Relevant elements for this study
Population	Quantitative models of the spread and dispersal of plant pests.
Intervention	Modelling strategies (assumptions, parameters and input data).
Comparators	Other modelling strategies. Comparison is based on the presence or absence of an assumption or use of an alternative model approach.
Outcomes	Prediction of pest spread or dispersal (e.g. rate of spread, dispersal distances, density or distribution at a particular time).

We considered that the research question was not strictly suited to systematic review as it cannot easily be converted into a simple closed framed-question, i.e. one with a well-formulated structure, presenting all relevant key elements and potentially answerable through a primary research study (CEBC, 2010; EFSA, 2010). Instead, the subject matter fell much more clearly under the remit of systematic mapping. Systematic mapping is used in the social sciences to give an overview of evidence within broad topic areas without attempting to answer a closed-framed question (Bates et al., 2007). The technique is now beginning to be used within the environmental sciences (Randall and James, 2012), where research questions are often more open-framed rather than closed-framed. In any case, systematic review and mapping guidelines for literature searching are very similar in nature so we developed the extensive literature search protocol drawing on methodologies from both fields.

2.2. Specification of search terms

The search terms were developed to ensure identification of as wide a range of relevant literature as possible, while excluding much of the irrelevant literature to increase the efficiency of the search. All searches included terms pertaining to the pest organism, host plant, spread and modelling. We selected a range of synonyms for each of these broad categories (Table 2). Wildcards were used where appropriate to pick up multiple suffixes and prefixes. A range of other search terms were considered but subsequently rejected (see Appendix A).

For pest organisms, we included generic terms for pests and the major groups of pests given in the project tender and also the recent and historical generic names of 2381 plant pests, or their common names where no binomial name is given (many viruses and phytoplasmas). These include all species listed in EC Directive 2000/29/EC, the EPPO Plant Quarantine data Retrieval system (EPPO, 2013), Q-Bank database of regulated pests (www.q-bank.eu), and the EU Emergency Control Measures by Species and Emergency Imports and Long Term Measures lists (http://ec.europa.eu/food/plant/plant_health_biosafety/legislation/index_en.htm). For insect pests we also specified the six orders of pest represented in the Q-Bank database, using both the scientific and common names of major pest taxa within each order. These were included as it is likely that some literature on insect pests would not necessarily include the term ‘insect’.

As synonyms for the plant hosts, we included both broad terms for groups of plants and English names for 282 crop groups and specific crops adapted from the Protected Crop classification of EC Regulation 178/2006. English names were considered acceptable as we were only able to review English-language literature.

Table 2: Synonyms for broad categories, selected for use as search terms in the extensive literature search.

Category	Synonyms used for search, including wildcards (*)
Generic plant pest	pest, disease, pathogen*, parasit*, herbivor*, weed*, competitor, alien, non*native, invasive, insect*, mite, acari*, nematod*, fung*, oomyc*, bacteri*, phytoplasm*, *virus*, *viroid, coleoptera*, beetle, diptera*, fly, hemiptera*, *bug, cicad*, aphid*, *hopper, hymenoptera*, sawfly, *wasp, lepidoptera*, moth, caterpillar, thysanoptera*, thrip, gastropod*, gasteropod*, snail, slug
Specific plant pest	[*1043 generic or common names of 2555 plant pests – see Appendix B for full list*]
Host plant	plant, crop, tree, shrub, herb, forb, grass*, gramin*, *berry, *corn, allspice, almond, angelica, anise, apple, apricot, arbutus, arrowroot, artichoke, asparagus, aubergine, avocado, azarole, balm, bamboo, banana, barley, basil, bay, bean, beet, beetroot, bergamot, bilimbi, borage, borecole, brassica*, broccoli, buckthorn, buckwheat, bulb, cabbage, cactus, calabrese, camomile, cane, canistel, caper, carambola, caraway, cardamom, cardoon, carob, carrot, cashew, cassava, cassia, cauliflower, celeriac, celery, cereal, cherimoya, cherry, chervil, chestnut, chickling*vetch, chickpea, chicory, chinotto, chive, chokeberry, cinnamon, citron, citrus, clementine, clove, cocoa, coconut, coffee, collard, coriander, corn, cornsalad, cotton, courgette, cowpea, cress, cucumber, cucurbit, cumin, curcuma, currant, damson, dasheen, date, dewberry, dill, durian, eddoe, eggplant, endive, fennel, fenugreek, fig, filbert, flageolet, flax, fruit, garlic, gherkin, ginger, ginseng, glasswort, gooseberry, grape, grapefruit, greengage, grumichama, guanabana, guava, hawthorn, hazelnut, hemp, hempseed, herb*, hibiscus, hops, horseradish, hyssop, jackfruit, jambolan, jasmine, juniper, kaki, kale, kapok, kiwano, kiwi, kohlrabi, kumquat, laurel, leek, legume, lemon, lentil, lettuce, lime, linden, linseed, liquorice, lollo*rosso, loquat, lovage, lupin, lychee, macadamia, mace, maize, mandarin, mangetout, mango, marjoram, marrow, mate, medlar, melon, millet, mint, mirabelle, mizuna, mountain*ash, mulberry, mustard, nectarine, nut, nutmeg, oat, oilfruit, oilseed, okra, olive, onion, orange, oregano, oysterplant, pak*choi, palm, palmfruit, palmoil, papaya, parsley, parsnip, passion*fruit, patisson, pea, peach, peanut, pear, pecan, pepino, pepper, peppermint, persimmon, pe-tsai, pine*nut, pineapple, pistachio, plantain, plum, pome, pomegranate, pomelo, pomerac, poppy, potato, pulasan, pulse, pumpkin, purslane, quince, radicchio, radish, rambutan, rape*seed, raspberry, rhubarb, rice, rocket, rooibos, root, rose*hip, rosemary, rye, safflower, saffron, sage, salad, sallowthorn, salsify, sapote, savory, scarole, scorzonera, seed, sesame, shaddock, shallot, sorghum, sorrel, soursop, soya, spelt, spice, spinach, sprout, squash, strawberry, sugar, sunflower, swede, sweet*cicely, sweetsop, tai*goo*choi, tamarind, tangelo, tangerine, tannia, taro, tarragon, tea, teff, thyme, tomato, treeberry, triticale, tuber, turmeric, turnip, ugli, valerian, vanilla, vegetable, vine, walnut, water*cress, watermelon, wheat, wineberry, witloof, yam
Spread	spread*, dispers*, invasion, colonis*, movement*, diffus*
Modelling	model*, simulat*

Initial testing of the search terms showed that these terms located many irrelevant results pertaining to human medicine or animal diseases. We therefore devised a set of exclusion search terms, to rule out automatically results unlikely to be relevant for models of plant pests (Table 3).

Table 3: Exclusion terms, used in the extensive literature search with a NOT qualifier, to automate the removal of highly irrelevant results.

Exclusion term	Reason for use
medic*	Results relating to human or animal medical treatments and medicines
clinic*	Results relating to clinical medicine and clinicians
veterinar*	Results relating to veterinary science and practice

2.3. Specification of information sources

Multiple information sources were searched to provide a comprehensive overview of the relevant literature. We principally focused on peer-reviewed scientific literature, as this was where we expected the most robust modelling studies to be reported, but some reliable grey literature, such as contract reports and postgraduate theses, was also included. The primary search engines for locating relevant and high-quality peer-reviewed results were ISI Web of Knowledge (WoK) and Scopus. We supplemented these with a Google Scholar search, articles in EFSA Journal and four other existing model databases on plant pest modelling. The methods for retrieving information from each source are described below.

2.3.1. Web of Knowledge

The ISI Web of Knowledge (WoK) incorporates ISI Web of Science, BIOSIS Citation Index (1969-present), BIOSIS previews (1969-2008 licensed by CEH), MEDLINE and Journal Citation Reports. On 12th April 2013 we searched WoK for literature containing at least one synonym from each category group (Tables 2 and 3), with the exception that no mention of the host is needed if one of the named specific pest organisms is given. For maximum efficiency, the entire search was encapsulated in a single search string. The full search string is given in Appendix C and was of the general form:

([(any generic pest synonym) AND (any generic host synonym)] OR [(any specific named pest)]) AND (any spread synonym) AND (any modelling synonym) NOT (any exclusion term)

The string was searched for within article WoK “Topics” (i.e. title, abstract and key-words). Results were restricted to English-language journal articles within the Science and Technology Research Domain. A set of required and excluded subject areas were established so that results were only obtained from relevant research areas (Table 4). Article citations and abstracts were exported directly to EndNote X5.

Table 4: Research areas used in refinement of the Web of Knowledge search results.

Included	Excluded	Neither included nor excluded
Agriculture, Biodiversity Conservation, Biotechnology Applied Microbiology, Computer Science, Entomology, Environmental Sciences Ecology, Evolutionary Biology, Forestry, Genetics Heredity, Infectious Diseases, Marine Freshwater Biology, Mathematical Computational Biology, Mathematics, Microbiology, Mycology, Parasitology, Pathology, Plant Sciences, Virology, Zoology	Acoustics, Anatomy Morphology, Anthropology, Astronomy Astrophysics, Automation Control Systems, Behavioral Sciences, Biochemistry Molecular Biology, Business Economics, Cardiovascular System Cardiology, Cell Biology, Chemistry, Communication, Criminology Penology, Critical Care Medicine, Dentistry Oral Surgery Medicine, Dermatology, Developmental Biology, Education Educational Research, Electrochemistry, Endocrinology Metabolism, Gastroenterology Hepatology, General Internal Medicine, Geology, Geriatrics Gerontology, Government Law, Health Care Sciences Services, Hematology, History, Imaging Science Photographic Technology, Immunology, Information Science Library Science, Instruments Instrumentation, Integrative Complementary Medicine, International Relations, Legal Medicine, Materials Science, Mathematical Methods In Social Sciences, Medical Informatics, Medical Laboratory Technology, Microscopy, Mining Mineral Processing, Neurosciences Neurology, Nuclear Science Technology, Obstetrics Gynecology, Oceanography, Oncology, Operations Research Management Science, Ophthalmology, Optics, Orthopedics, Otorhinolaryngology, Paleontology, Pediatrics, Pharmacology Pharmacy, Physical Geography, Physiology, Psychiatry, Psychology, Radiology Nuclear Medicine Medical Imaging, Research Experimental Medicine, Robotics, Social Issues, Social Sciences Other Topics, Sociology, Sport Sciences, Surgery, Telecommunications, Thermodynamics, Transplantation, Tropical Medicine, Urology Nephrology, Veterinary Sciences	Allergy, Biophysics, Demography, Energy Fuels, Engineering, Fisheries, Food Science Technology, Geography, Life Sciences Biomedicine Other Topics, Mechanics, Meteorology Atmospheric Sciences, Nutrition Dietetics, Physics, Public Environmental Occupational Health, Reproductive Biology, Respiratory System, Science Technology Other Topics, Toxicology, Urban Studies, Water Resources

2.3.2. Scopus

Scopus covers approximately 19,500 peer-reviewed journals and 400 trade publications, which were searched on 15th April 2013. We searched the titles, abstracts and key-words of published English-language journal articles and letters, limiting to the Agricultural and Biological Sciences, Computer Science, Environmental Science, Immunology and Microbiology, and Mathematics Subject Areas and excluding Arts and Humanities, Biochemistry, Business, Management and Accounting, Chemical Engineering, Chemistry, Decision Sciences, Earth and Planetary Sciences, Economics, Econometrics and Finance, Energy, Materials Science, Medicine, Neuroscience, Nursing, Psychology, Social Sciences, Veterinary, Dentistry and Health Professions.

To comply with limits on Scopus search string length, the full search string was broken into six independent blocks (see Appendix D). The first block was for generic plant pest and host plant terms, and was constructed as follows:

(any generic pest synonym) AND (any generic host synonym) AND (any spread synonym) AND (any modelling synonym) NOT (any exclusion term)

The remaining five searches were based on equal-length splits of the specific names of plant pests:

(any specific named pest) AND (any spread synonym) AND (any modelling synonym) NOT (any exclusion term)

For each of the six searches, article citations and abstracts were exported directly to EndNote X5 where automatic duplicate removal was performed to combine the results.

2.3.3. Google Scholar

Google Scholar was searched separately for each named pest on 15th April 2013. Google Scholar is slightly problematic in that it does not recognize operators such as parentheses or within-word wildcards, uses synonyms of the entered terms and searches within entire documents. Therefore, we increased the specificity of our search terms as far as possible.

Separate searches were conducted for each pest organism. Each search string consisted of the alternative names for the pest appended to the string “spread dispersal model” (Appendix E). Because of the large number of searches (1772), we wrote a web-scraping R script to automatically search for each pest and parse bibliographical information from the first page of Google Scholar results sorted by relevancy to the search terms (up to 20 results per pest as Google blocks larger multiple retrievals) into a spreadsheet.

Google Scholar’s page display meant that we often retrieved only partial strings for the article title, publication or author names (indicated by a “…” string). Also, this method does not import straightforwardly into EndNote or yield abstracts. Therefore, we performed a further rule-based automatically screening of the results, as follows:

- Exclude results from Google Books. We are only interested in journal articles and reports.

- Exclude results where the (possibly partial) author list and (possibly incomplete) title strings can be jointly matched in the WoK and Scopus results, ignoring letter case and allowing 10% string mismatch to accommodate typographic errors. This rule locates results duplicated from the peer-reviewed search.

- Exclude results where the (complete) journal name is present in the WoK and Scopus results. This rule locates results from journals thoroughly searched in WoK and Scopus.

As mentioned above, the remaining results were initially stored in the bibliographic data spreadsheet. From this spreadsheet we after screened out obviously irrelevant titles using the criteria set out fully in section 2.4.1. The screened results were then manually entered into EndNote X5 for examination of abstracts and full texts (see sections 2.4.2 and 2.4.3).

2.3.4. EFSA Journal

The EFSA Journal is an open-access, online scientific journal that publishes the scientific outputs of the European Food Safety Authority. EFSA Journal is not listed on WoK or Scopus and so was searched separately. References for all online articles within the Plant Health topic were manually copied into the bibliographic data spreadsheet on 5th March 2013. The automatic screening rules applied to Google Scholar were also applied to these results before manual import into EndNote X5.

2.3.5. MOPEST model inventory

The MOPEST project produced an inventory of models describing the establishment, development, and/or spread of plant pests on crops in Europe published between 1972 and 2009 (Rossi et al., 2009).

On 6th March 2013, we manually copied the primary references for all 174 models in the MOPEST web portal (http://31.171.244.105:8080/apex/f?p=112) to the bibliographic data spreadsheet for further examination and screening based on the automatic screening rules applied to Google Scholar. Primary references for the 174 listed models were copied from the MOPEST web portal on 6th March 2013.

2.3.6. PESTCAST model inventory

PESTCAST is a project of the University of California Statewide Integrated Pest Management Program and the California Environmental Protection Agency Department of Pesticide Regulation. Its goal is to expand the use of computer-based crop disease forecasting in California. Since California has a similar climate to parts of southern Europe, PESTCAST may be relevant for the EU. Literature references on models published between 1946 and 1999 are listed on the PESTCAST website (http://www.ipm.ucdavis.edu/MODELS/models_scientific.html). On 7th March 2013, these model references were copied to the bibliographic data spreadsheet for application of the screening rules applied to Google Scholar and then manual import to EndNote X5.

2.3.7. CAMASE model inventory

CAMASE (Concerted Action for the development and testing of quantitative Methods for research on Agricultural Systems and the Environment) is a register of published and unpublished agro-ecosystem models (http://library.wur.nl/camase/). We manually copied references and descriptions for each of the 211 models in the registry to the bibliographic data spreadsheet on 6th March 2013 and applied the same rules developed for Google Scholar before import to EndNote X5.

2.4. Screening the search results

To remove irrelevant results, search results were screened in a sequential three-phase process. Screening was conducted by three independent reviewers on random partitions of the search results. Screening phases involve sequential examination of: i) the titles, ii) then the abstracts, and iii) then the full texts. Only publications passing a phase were examined in the next phase. At each phase, we excluded search results only when we were confident to a high degree of certainty that they did not meet clearly described screening criteria for the current and all preceding screening phases. This minimised the chance of falsely rejecting relevant literature. The full screening criteria are given below.

2.4.1. Criteria for exclusion based on titles

- Exclude if confident that the paper is not about ecological spread and dispersal modelling (e.g. models of chemical reactions or biochemical processes, non-biological physics, population genetics, hydrology, pollutant dispersion modelling etc.).
- Exclude if confident that subject of paper is:
    - Not a member of the broad categories of plant pests listed in the database. Vertebrates were excluded but plants were not excluded at this stage as many plants may act as a weed pest in certain circumstances.
    - A member of these groups but specifically mentioned as not attacking plants (e.g. a predator, parasitoid, detritivore or animal disease).
- Exclude if confident the paper is a marine study.

2.4.2. Additional criteria for exclusion based on abstracts

- Exclude articles with no abstract. The search returned only a small proportion articles without abstracts (see section 1.3.8), many of which were old. They could not be assessed here.
- Exclude book chapters and conference proceedings.
- Exclude review papers.
- Exclude if confident that the paper does not contain a relevant model of pest spread or dispersal. Cases where papers may be excluded include:
    - Not a predictive model of spread or dispersal, e.g. a purely empirical study or statistical analysis of empirical spread or dispersal patterns without an attempt to develop a model.
    - The model does not explicitly include dispersal behaviour (e.g. a spatially implicit population model, a species distribution model or a weather-driven pest forecasting system or phenology model).
    - The model operates at spatial scales below the level of an individual plant. Models of pest spread within a single host plant or among harvested and stored crops were excluded.
    - The model represents only part of the dispersal process (e.g. a model for pest entry or introduction events, a model for patch emigration etc.).
    - Models for spread of novel forms of a species within an existing population (e.g. spread of pesticide-resistant genotypes through a non-expanding population, dispersal of sterile insect releases through a non-expanding population).

2.4.3. Additional criteria for exclusion based on full texts

- Exclude if the paper contains a spatial model but it is not used for population spread or dispersal (e.g. a model of spatial population dynamics within a region of space that is fully occupied by the species at varying density, such as a two-patch model). Valid models predict range expansion or dispersal distances.
- Exclude if the supposed spreading pest is a plant species but it is not mentioned as a pest of plants (i.e. not a weed, parasite or invasive).
- The host is modelled as a non-static organism (i.e. not a plant), excluding seed dispersal.
- Modelling of non-dispersive movements (e.g. foraging or mate-seeking using pheromone trails) except for organisms that vector plant diseases.

2.5. Reference management

References were primarily managed using EndNote X5 libraries, created and accessed from secure computer networks with automatic back up procedures to ensure the security of the references. As described above, results from WoK and Scopus were imported directly to EndNote. Results from the other sources (which do not integrate with EndNote automatically), were initially entered into a spreadsheet, and then manually imported to EndNote after the title screening phase.

For full text screening, we exported the EndNote bibliographic information into a Microsoft Access database, to which the full text PDF file was linked. The Access database allowed us to enter data for the model clustering analysis (see below) so that we were able to extract information from the papers passing the final stage of screening at the same time as reading them for screening.

2.6. Testing the quality of the search protocol

2.6.1. Performance of the search terms

Before running the full searches, we examined and tested the search strings and methods needed to extract results from each database. A more detailed initial scoping of the search terms was performed through WoK searches to validate the methodology and test search terms for sensitivity and specificity. This was done to estimate the relative volume of search results that would later be found in the full literature search and gave an approximation to the likely relevancy of the results.

To indicate the relative contribution of each search term to locating results, we searched the resulting WoK records for each term (except the individual pest names, of which there were too many), after export to EndNote. We note that since key-words are not exported from WoK into EndNote, the results of this exercise are not totally compatible with the WoK search process or results, but should still indicate the relative importance of the synonyms.

We next evaluated whether the search strategy was over-restrictive by conducting a broader WoK search for all English-language, scientific journal articles relating to a subset of 40 randomly selected pests from the database. The search string was:

“alternaria alternata” OR “bean golden mosaic virus” OR “boeremia exigua” OR “cacyreus marshalli” OR “cercoseptoria pini-densiflorae” OR “chrysanthemum stem necrosis virus” OR “clavibacter michiganensis” OR “colletotrichum cosmi” OR “dacus etiennellus” OR “ditylenchus dipsaci” OR “erwinia stewartii” OR “heliothis armigera” OR “heterodera ustinovi” OR “leptosphaeria rubefaciens” OR “leptosphaerulina argentinensis” OR “malacosoma castrense” OR “meloidogyne enterolobii” OR “meloidogyne fallax” OR “metamasius hemipterus” OR “mycosphaerella gregaria” OR “nigrograna mackinnonii” OR “paraconiothyrium flavescens” OR “paratrichodorus nanus” OR “peyronellaea pomorum” OR “peyronellaea subglomerata” OR “phoma longirostrata” OR “phoma omnivirens” OR “phytophthora brassicae” OR “phytophthora gonapodyides” OR “phytophthora hedraiandra” OR “phytophthora trifolii” OR “plenodomus lupini” OR “pleospora chenopodii” OR “pomacea” OR “popilia japonica” OR “pseudopityophthorus pruinosus” OR “raspberry leaf curl virus” OR “spodoptera exigua” OR “thaumetopoea pityocampa” OR “xanthomonas fragariae”

The titles and abstracts of WoK results arising from this search were inspected to identify results that may contain quantitative models of spread or dispersal. We then examined whether these results were found within the WoK results obtained using the full set of search terms.

2.6.2. Screening protocol testing

We performed initial testing of the title and abstract phases of the screening to trial the exclusion criteria and ensure consistent among the three independent reviewers. In this testing, we extracted a random 100 search results from the full database described above and each reviewer applied our proposed criteria to select potentially relevant results that should be selected for examination of the full text. Consistency among reviewers was estimated by calculating pairwise values of the Cohen’s kappa statistic.

2.7. Model clustering

2.7.1. Objective of the clustering

The clustering analysis aimed to classify the models in the studies found in the extensive literature search into a small number of discrete modelling strategies, based on the theoretical concepts upon which they were based. Cluster analysis is a generic term for a wide range of unsupervised statistical methods whereby multivariate data is grouped into clusters of observations that are similar to one another and separated from other observations. The ultimate aim was to gain a general oversight of the types of modelling used for plant pest spread and dispersal, which would aid interpretation, but also inform the choice of models to use in the case studies for later tasks of the project. Our specific objectives were:

- To collect data on the formulation of the models found in the extensive literature search.
- To partition the model formulation data into different numbers of clusters.
- To identify the optimal number of model clusters supported by the data.

2.7.2. Data for clustering

For each study passing the full text screening stage of the review, we examined the model or models within the paper and evaluated a number of questions in order to characterise the general model structure and the ways in which the pest and host were modelled (Table 5). Where the paper contained more than one unique model we answered questions for each unique model. The exception to this was if the paper presented several iterations of variations on the same model, in which case we examined the most complex model presented, which will have encompassed the more simplistic models as special cases of the complex model.

All questions yielded categorical answers, some of which being multiple choice. Therefore, categorical data were converted into binary dummy variables (also known as Boolean, indicator, design or qualitative variables) for cluster analysis. For single-choice fields the dummy variable for the first category was omitted as the variables for the remaining categories contain all the information needed to infer the value of the first.

Table 5: Data fields for model clustering.

Clustering field	Abbreviation	Options	Multiple choice?
Model structure			
How is space represented?	Sp	Continuous / discrete	No
How is time represented?	Time	Continuous / discrete / not explicitly modelled [(a)]	No
How many spatial dimensions are modelled?	SpDim	1 / 2 / 3 / other [(b)]	No
What spatial extent is spread modelled over?	SpExt	Small (single plot or field) / large (landscape or above) / all scales [(c)]	No
What is the model timestep?	TimeStep	Single event / continuous / sub-annual / annual / not specified	No
Is the model restricted to a single growing season, or does it model spread over multiple years?	TimeExt	Single / multiple / not specified	No
How is landscape heterogeneity represented with respect to abiotic, habitat or management factors?	SpHet	Uniform / categorical / smooth gradient / noisy gradient	Yes
Is temporal heterogeneity or forcing modelled?	TimeHet	Modelled / not modelled	No
Pest model			
Is the model specific to a particular pest or generic across broad groups of pests?	PestType	Specific / generic	Yes [(d)]
How many interacting pest species are modelled? [(e)]	PestNum	1 / 2 / 3	No
How are pests represented?	PestRep	Individual / population / occupancy / dispersal kernel [(f)]	No
How are pest temporal dynamics modelled?	PestDyn	Not modelled [(g)] / deterministic / stochastic	No
What broad types of pest dispersal mechanisms are represented?	PestMech	Active behaviour / ballistic release / biological vector / clonal growth / generic [(h)] / gravity [(i)] / human (short-distance) / human (long-distance) [(j)] / rain splash / water / wind	Yes
Is pest dispersal stochastic or deterministic?	PestDisp	Stochastic / deterministic	No
Is pest spread affected by natural enemies in the model?	PestEnemies	Yes / no	No
Does pest entry or introduction from outside the system occur at multiple times?	PestEntryTime	Yes / no	No

Clustering field	Abbreviation	Options	Multiple choice?
Does pest entry or introduction from outside the system occur at multiple locations?	PestEntrySp	Yes / no	No
Does the modelled pest evolve during spread	PestEvolve	Yes / no	No
Are pest control actions modelled?	PestControl	Yes / no	No
Host plant model ^(k)^			
How are host plants represented?	HostRep	Individual / population / occupancy / not modelled	No
Is the model specific to a particular host plant or generic across broad groups of host plants?	HostType	Specific / generic	Yes (d)
Are host plant temporal dynamics modelled?	HostDyn	Yes / no	No
Is the model a multi-host species model?	HostNum	0 / 1 / 2 / 3 / more	No
Is there temporal segregation of pest use of the host species?	HostSeg	Yes / no	No
Is host plant dispersal modelled?	HostDisp	Yes / no	No
Are negative effects of the pest on the host plant population dynamics or dispersal modelled?	HostImpact	Yes / no	No
Does the host plant evolve?	HostEvolve	Yes / no	No

(a): Time is not explicitly modelled in dispersal kernel or disease gradient models, which represent single spread events.
(b): ‘Other’ is for spread on a spatially-implicit contact network.
(c): ‘All scales’ is for continuous space models covering all space.
(d): Both options can be selected for a generic model applied to a specific species.
(e): If multiple species are modelled in the same landscape but without any interaction, this is counted as a single-species model.
(f): Dispersal kernels and disease gradient models can equally be considered as implicitly representing an individual or a population, so are given a separate category.
(g): ‘None’ is for single-event spread models without a specific time element (e.g. dispersal kernels or disease gradients).
(h): ‘Generic’ is where no specific mechanism is specified.
(i): ‘Gravity’ is for propagules with no specific adaptations for dispersal.
(j): ‘Human’ includes all forms of human-mediated dispersal, including spread by attachment of propagules to people and vehicles, and spread of propagules by trade-related activities. We judged whether the human-mediated dispersal was over relatively local or large scales.
(k): In this study host plant refers to the plant affected by the pest and so may include native species affected by an invasive plant or weed.

2.7.3. Clustering procedure

A large number of unsupervised clustering algorithms are available. We elected to use two state of the art approaches that have the advantage of using model log-likelihoods in their fitting, as likelihoods are more useful for selecting the optimal number of model clusters than heuristic measures of cluster quality that are used for fitting other clustering algorithms. The two chosen approaches are quite different to each other, and this allowed us to select the best algorithm and also check whether a clustering outcome was very specific to the approach used.

The first approach considered was co-clustering using the Bernoulli Latent Block Model (Govaert and Nadif, 2003) as implemented by the ‘blockcluster’ R library (Bhatia, 2012). This is specifically designed to accommodate high dimensional (i.e. many clustering fields, see Table 5) binary data. The algorithm organizes the data into homogeneous blocks of unequal size by sequentially permuting the rows and then the columns of the data matrix. In doing so, the algorithm identifies groups of similar observations and groups of similar clustering variables (see Figure 1). We fitted models for each combination of 2-12 row clusters and 2-12 column clusters. The software outputs a pseudo-log likelihood for the clustered configuration of the data matrix. We used this to select the optimal number of partitions.

The second approach was model-based clustering as implemented by the 'MClust' R package (Fraley et al., 2012). This assumes that the population consists of a defined number of subpopulations or clusters whose centres are located at some position in multi-dimensional space. The likelihood of observations belonging to each cluster decreases with increasing distance from the cluster centres allowing a maximum likelihood estimation of the model parameters defining cluster locations and assignments (Fraley and Raftery, 2002). Specifically we fitted the Gaussian finite mixture model with spherical, equal volume clusters by the EM algorithm (Fraley and Raftery, 2002; Fraley et al., 2012) (see Figure 2). Models with 2-12 clusters were fitted, and the optimal chosen on the basis of Bayesian Information Criteria (BIC). Since BIC penalises both model complexity and poor fit, it should be more robust than using the likelihood alone, as was done for co-clustering. Unfortunately we were not able to calculate BIC for the co-clustering models as the pseudo-log-likelihood provided by the software is not estimated per individual observation, but rather for the overall partitioning.

To select the best algorithm, the quality of their clustering was compared using the Dunn index and the mean silhouette width. The Dunn index is the ratio of the smallest multi-dimensional Euclidean distance between observations not in the same cluster to the largest within-cluster distance (Dunn, 1974). High values indicate better clustering. The silhouette width is calculated for each observation as $(b - a) / \max(b, a)$ where a is the average distance between the observation and others in the same cluster and b is the average distance between the observation and observations in the nearest other cluster (Rousseeuw, 1987). A mean across individuals is then calculated. As with the Dunn index, higher values indicate better clustering.

We also conducted three further tests of model reliability. First, we investigated the stability of the optimal clustering method, i.e. its dependence on the precise choice of clustering variables. To do this, the model was re-estimated with each of the variables dropped from the analysis. The proportion of data points assigned to a different cluster from the full clustering was calculated as a measure of instability. Second, we investigated whether simplifying some of the clustering fields would also affect the clustering. The most natural simplification was to reduce the options in the number of pests field (PestNum) to '1' and '>1' and the number of hosts field (HostNum) to '0', '1' and '>1'. The effect of this on cluster assignment was evaluated in the same way as for the stability test. Finally, we evaluated the statistical significance of the optimal clustering by comparing its log-likelihood with that generated by fitting the model to 1000 randomisations of the data matrix columns.

Figure 1: An example of co-clustering for simulated binary data, as implemented by the ‘blockcluster’ R library (Bhatia, 2012). The simulated data are plotted on the left, with 30 observations (rows) of 10 clustering variables (columns). The simulated data contain 3 clusters of observations and two clusters of variables. As shown in the right-hand column, the clustering algorithm repeatedly permutes the rows and then the columns of the data matrix to arrange it into homogeneous blocks. The red boxes illustrate the processing of one observation. Horizontal blue lines indicate the partitioning of observations into three clusters, while the vertical blue line shows the partitioning of variables into two clusters.

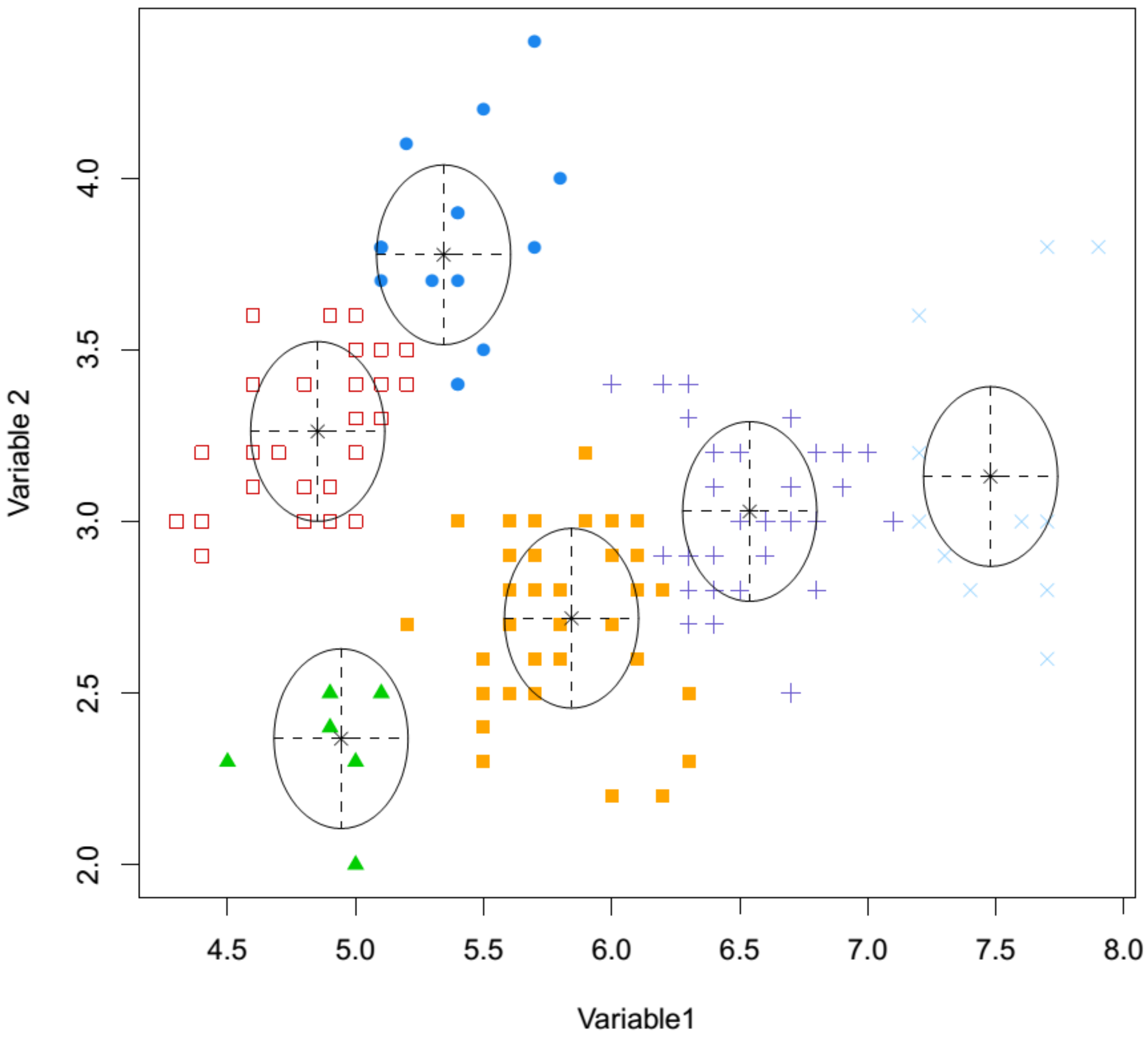

Figure 2: An example of model-based clustering using the Gaussian finite mixture model with spherical, equal volume clusters (Fraley and Raftery, 2002). Here, clustering is based on only two variables and six clusters are selected (ellipses). Data points are assigned to their nearest cluster.

2.7.4. Cluster interpretation

Independent data describing the way each model was applied and analysed were collected in order to interpret differences among the model types identified by the clustering. Significant differences between model clusters are not only useful in understanding the patterns detected in the clustering, but also provide an independent validation step in showing that the clusters exhibit meaningful differences.

As shown in Table 6, data on the taxonomic and functional group of the pest, functional group of the host, socio-economic sector for which the model was designed, model parameterisation and types of model analysis were collected. To test whether clusters differed in model usage, the frequency of each answer in each cluster was calculated and compared against the random expectation using standard χ^2 tests. We also recorded the name given to the modelling framework used in the paper.

Table 6: Additional data fields on model application for interpreting model clusters. All fields are multiple-choice for cases where more than one option applies.

Model application	Options
What taxonomic category is the pest?	Bacterium or phytoplasma / Fungus or oomycete/ generic / insect / mite / nematode / plant / protist / virus or viroid
What functional group category is the pest?	Competitor / disease vector / generic / herbivore / invasive species / macro-parasite / micro-parasite or disease
What functional group is the host plant?	Crop / generic / ornamental / wild plant
What is the socio-economic sector?	Agriculture / ecology [(a)] / forestry / horticulture
How do model parameters relate to observed data?	Arbitrary values / fitted to spread data / measured empirically in the paper or elsewhere
How is the model analysed?	Sensitivity analysis of pest or host parameters / validation of model predictions against independent data / scenario experiments for abiotic change / scenario experiments for risk reduction options

(a): 'Ecology' covers cases where a pest acts within natural ecosystems and also relates to less applied models that advance ecological theory.

3. Results

3.1. Testing the quality of the extensive literature search protocol

Preliminary tests of the search terms using WoK showed that the exclusion terms and subject area refinement were critical in efficiently distilling the search results and producing a manageable number of results. A total of 10,158 unique results were obtained from WoK (Table 7). Manual screening of this order of magnitude of results was possible with the resources available to the project, while the pre-refined number of results (69,968) would have been overwhelming.

Table 7: Overview of numbers of Web of Knowledge (WoK) results from the chosen search string during refinement and export to EndNote. Results are from a search conducted on 12th April 2013.

Search stage	Number of results
WoK search:	
Basic search, with no NOT terms	69,968[(a)]
After inclusion of NOT terms	54,385[(a)]
After restriction to English language results	52,906[(a)]
After restriction to Science and Technology Research Domain	52,424[(a)]
After restriction to document type Articles	47,945[(a)]
After positive refinement to relevant Subject Areas	35,511[(a)]
After exclusion of totally irrelevant Subject Areas	16,646[(a)]
Export to EndNote:	
After export	10,266
After automated removal of duplicates	10,178
After removal of book sections	10,158

(a): Overestimate because WoK includes duplicates within different searched databases in the reported result count.

Our preliminary testing also showed that nearly all of the individual search terms in Table 2 were found in the WoK results arising from the complete search string (Appendix F). The exception to this was for many of the specific crop names for less common crop plants in Europe. As expected, a general pattern was that the more generic the search term the more often it was found. Among pest terms, the most commonly located terms were weed*, fung*, aphid*, pathogen*, insect, bacteri* and pest (Appendix F). Among generic plant terms, the most common terms were herb*, plant, mate (referring to the crop plant maté *Ilex paraguariensis* but probably most commonly found in the broader sense of the word), pea, seed, tree and crop. The most common spread terms were dispers*, spread and invasion, while model* was more common than simulat* for the modelling terms.

Searching WoK using only the names of 40 individual pests returned 10,341 results from WoK. After inspection of their titles and abstracts, only 13 of the results (0.13%) were deemed potentially to contain models of spread or dispersal. Furthermore, only three of these results were WoK records including an abstract, while the remaining 10 results contained only the article title. Although this gives a small sample, the large effort required to screen so many WoK results meant we were unable to repeat the exercise with more species to increase the sample size. All three of the articles with abstracts were found within the results of the full WoK search. However, none of the 10 articles without abstracts were found in the full search. Therefore, this suggests that the search strategy is sufficient to find the vast proportion of relevant results, provided WoK (or the other sources of information) includes the study abstracts.

When the three literature reviewers independently applied the title and abstract screening criteria to 100 random search results, the consistency among the reviewers was high (pairwise Cohen's kappa = 0.901, 0.787 and 0.768). Where reviewers disagreed about selecting a particular paper, it was generally the case that the reviewer(s) selecting that particular study considered it unlikely that it would prove to be a useful study upon examination of the full text, but nevertheless considered it worth checking.

3.2. Results of the extensive literature search

As expected, the largest volumes of results were obtained from WoK, Google Scholar and Scopus (Figure 2) and results were disproportionately derived from more recent years (Figure 3). More results could have been taken from Google Scholar since we only took the first 20 results per species, but this was impractical. After title and abstract screening, a total of 1974 unique results remained in the database, of which we were able to retrieve full text PDFs for 1899 (96.2%). After examining these full texts, we considered 468 (24.6%) to contain relevant quantitative models of plant pest spread or dispersal. An EndNote library containing these references was developed.

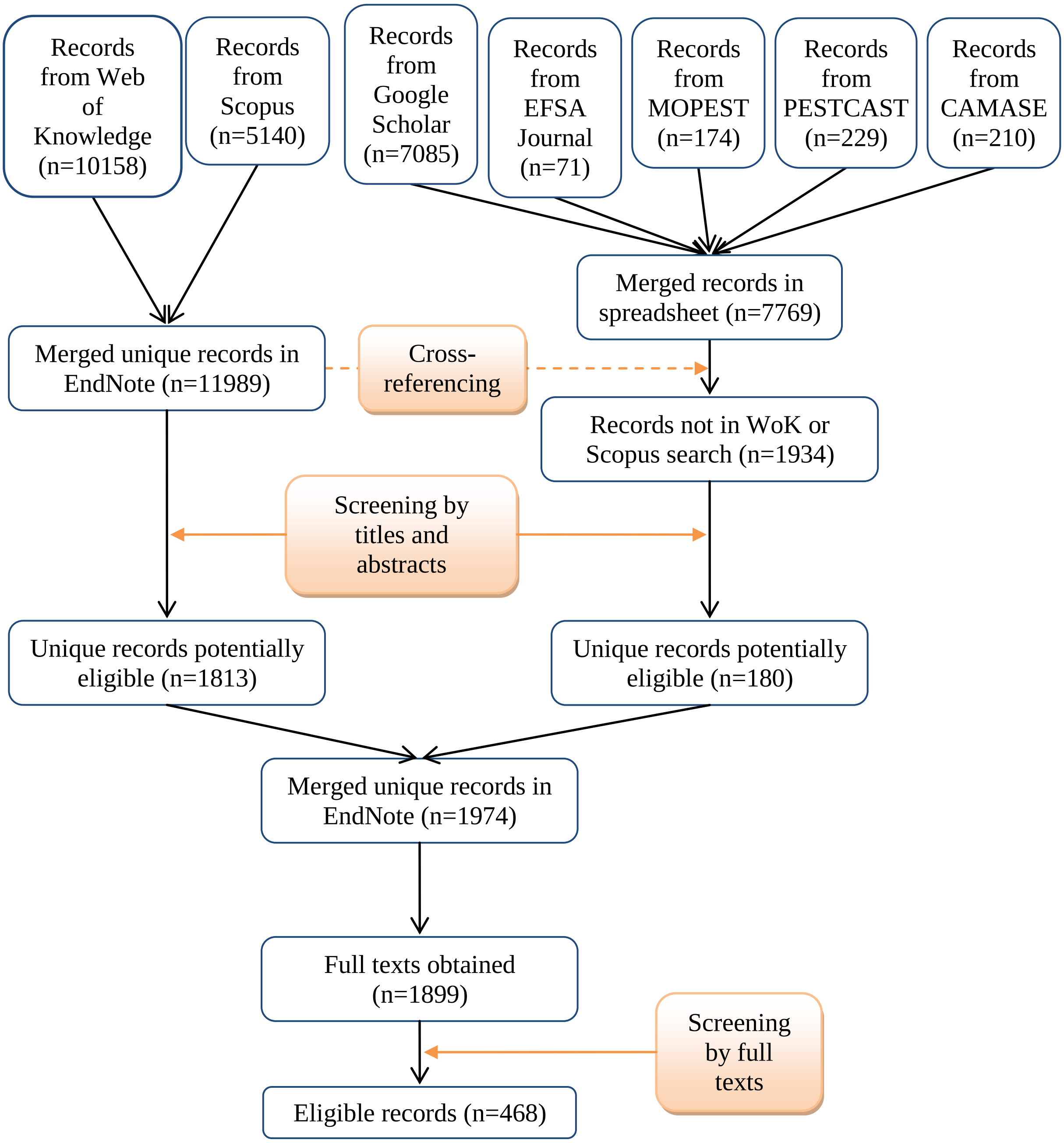

Figure 3: Flowchart showing the literature selection process of the extensive literature. The number of results (n) from each literature source and passing each stage in the process is given.

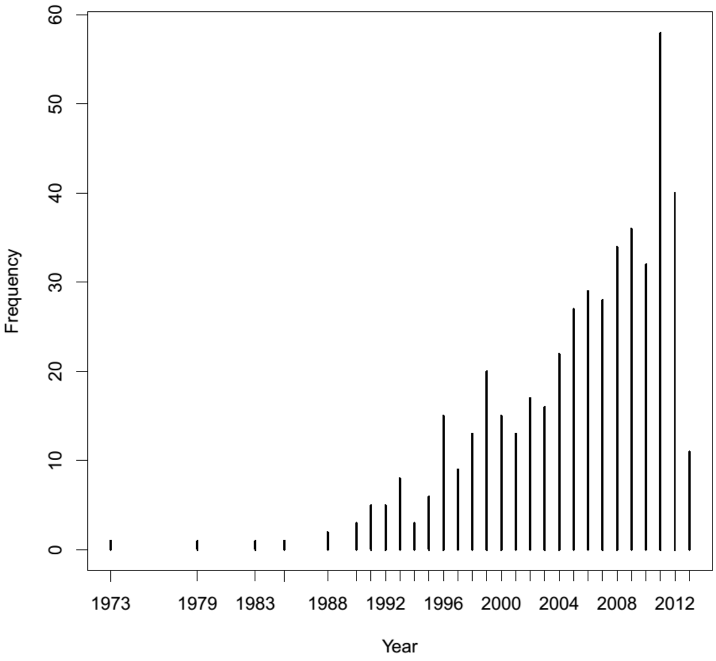

Figure 4: Distribution of publication years of the eligible studies selected in the extensive literature review.

3.3. Model clustering and analyses of between-cluster differences

Examination of the 468 papers resulting from the extensive literature search yielded data on 478 unique models, forming the basis of cluster analysis. Using the co-clustering algorithm, pseudo-log-likelihoods indicated that the data most strongly supported eight model clusters (equivalent to the grouped rows in Figure 1) and 11 variable clusters (equivalent to the grouped columns in Figure 1). The model-based clustering BICs also suggested eight model clusters were optimal. Visualisation of the clustering of both algorithms in two-dimensional ordination space (Figure 5) suggested that model-based clustering tended to produce more cleanly delineated partitions of the data and this was borne out by our more formal comparison. Compared to co-clustering, model-based clustering yielded a higher Dunn index (0.277 vs. 0.192) and a higher mean silhouette width (0.110 vs. 0.076). Therefore we selected model-based clustering into eight clusters as the optimal model (Table 8) and used this model for all further analysis and interpretation.

With this optimal model, only 30 of the 468 models (6.3%) had a cluster assignment probability of less than 0.95, showing that there were very few outlying models. Furthermore, the clustering was highly statistically significant as shown by every single clustering of 1000 randomised datasets having a lower log-likelihood than the model for the real data (decreases in log-likelihood of 4663-4913 units). Therefore, we can state that clustering of the real data was statistically significant at $P < 0.001$.

Dropping variables from the optimal model-based clustering generally had little effect on cluster assignment. Of the 27 clustering variables, individually dropping 22 of them caused <10% change in model cluster assignments (Table 9). This analysis showed that the variables most critical for the clustering were the spatial extent and time step of the model and the way in which the pest was represented. Repeating the clustering with simplified pest and host number variables, as described in the Methods, caused no change in model assignments.

As can be seen in Table 9, most of the clustering fields had a reasonable balance between answer categories. However, there were some notable exceptions. For example, we found very few models in which multiple pest or host species were modelled and it was rare to find models where natural enemies affected the pest, repeated pest entry events occurred or the modelled species evolved. It was also relatively rare for modelling to include host plant dispersal, even where the host's population dynamics were modelled. The most common specific dispersal vectors of the modelled pests were wind and active movement, although no specific mechanisms were mentioned in 27% of models. Models specifically examining some important mechanisms for long range species spread, such as water and human-mediated transport, were quite rare.

Summary data on model applications of the eight model clusters, based on the questions in Table 6 are presented in Table 10. The majority of models were for insect, plant and fungal pests of crop plants. There were very few models for bacteria, nematodes, mites or protists. We recorded 148 named model frameworks in the literature search, so for brevity these are not reported in Table 10.

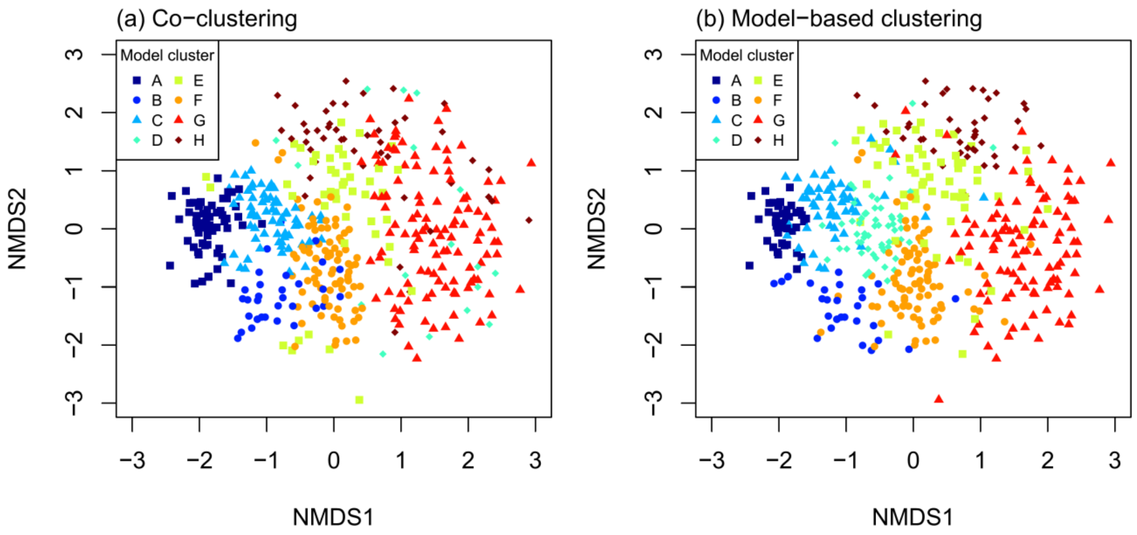

Figure 5: Illustration of the clustering of models into 8 partitions using (a) co-clustering and (b) model-based clustering. To visualise the proximity of the clustering data for each model, two axes of a nonmetric multidimensional scaling (NMDS) on the Euclidean distance between clustering variables are plotted. Each point represents a single model. The distance in NMDS space and Euclidean distance between models are strongly correlated ($r = 0.789$). Points are coloured according to the model clusters from both clustering analyses showing that both models give a similar, but not totally analogous, clustering. Also, models in the same cluster tend to be more similar than those in different clusters (so are close in NMDS space), although there is some overlap.

Table 8: Numbers of models assigned to each cluster by the model-based clustering.

Model cluster	A	B	C	D	E	F	G	H
Frequency	47	29	53	61	61	82	103	42

Table 9: Summary of the model-based clustering, giving the percentages of models satisfying each dummy variable across the whole dataset and within each model cluster. For single-choice fields, redundant dummy variables not used in the clustering are reported in italics for completeness. Over-representation of a variable within a cluster (percentage greater than for the whole dataset) is coloured orange, while under-representation is coloured blue. For example, Cluster H contains a slightly greater proportion of discrete space models than would be expected for a random division of the data. *P* values indicate significant differences in the frequencies of each dummy variable between clusters, as indicated by χ^2 tests. Instability is estimated as the percentage of models allocated to a different cluster if the focal group of variables are omitted from the model. See Table 5 for variable abbreviations.

Clustering variable	**% of all results**	**% of model cluster**								***P***	**Instability**
		A	**B**	**C**	**D**	**E**	**F**	**G**	**H**		
Model structure											
Sp == continuous	*40.0*	*98*	*38*	*94*	*70*	*11*	*2*	*18*	*31*	*<0.001*	7.5
Sp == discrete	60.0	2	62	6	30	89	98	82	69	<0.001	
Time == continuous	*20.3*	*0*	*14*	*100*	*0*	*10*	*5*	*13*	*40*	*<0.001*	10.9
Time == discrete	69.2	0	86	0	100	90	93	86	60	<0.001	
Time == none	10.5	100	0	0	0	0	2	1	0	<0.001	
SpDim == 1	*19.7*	*53*	*0*	*42*	*49*	*5*	*1*	*9*	*10*	*<0.001*	8.6
SpDim == 2	68.8	30	28	45	48	74	98	89	88	<0.001	
SpDim == 3	9.0	17	72	13	2	7	0	2	0	<0.001	
SpDim == other	2.5	0	0	0	2	15	1	0	2	<0.001	
SpExt == all scales	*16.3*	*21*	*3*	*34*	*33*	*13*	*5*	*2*	*36*	*<0.001*	21.1
SpExt == large	47.7	15	90	23	44	11	84	66	29	<0.001	
SpExt == small	36.0	64	7	43	23	75	11	32	36	<0.001	
TimeStep == annual	*34.5*	*0*	*0*	*0*	*67*	*8*	*72*	*50*	*19*	*<0.001*	17.8
TimeStep == continuous	22.2	0	14	100	8	10	5	17	40	<0.001	
TimeStep == single event	11.3	100	3	0	2	2	4	1	0	<0.001	
TimeStep == sub-annual	24.3	0	79	0	20	54	13	32	10	<0.001	
TimeStep == not specified	7.7	0	3	0	3	26	6	0	31	<0.001	
TimeExt == multiple seasons	*60.3*	*0*	*0*	*58*	*89*	*18*	*89*	*84*	*76*	*<0.001*	4.4
TimeExt == not specified	2.3	0	0	0	2	11	0	0	7	<0.001	
TimeExt == single season	37.4	100	100	42	10	70	11	16	17	<0.001	
SpHet == uniform	60.7	91	10	74	93	87	20	42	86	<0.001	10.9
SpHet == noisy gradient	19.7	6	90	8	3	3	39	23	2	<0.001	
SpHet == smooth gradient	2.3	0	0	4	3	0	2	3	5	0.638	
SpHet == categorical	20.7	4	0	15	2	10	46	40	7	<0.001	

Clustering variable	**% of all results**	**% of model cluster**								***P***	**Instability**
		A	**B**	**C**	**D**	**E**	**F**	**G**	**H**		
TimeHet == no	*73.4*	*98*	*7*	*89*	*75*	*84*	*65*	*64*	*95*	*<0.001*	1.9
TimeHet == yes	26.6	2	93	11	25	16	35	36	5	<0.001	
Pest model											
PestType == specific	71.1	83	79	60	80	46	78	99	7	<0.001	6.1
PestType == generic	52.3	57	59	75	57	75	41	9	100	<0.001	
PestNum == 1	*96.9*	*100*	*100*	*100*	*98*	*92*	*99*	*95*	*93*	*0.021*	4.2
PestNum == 2	2.9	0	0	0	2	8	0	5	7	0.021	
PestNum == 3	0.2	0	0	0	0	0	1	0	0	0.784	
PestRep == individual	*19.0*	*9*	*52*	*6*	*10*	*20*	*35*	*17*	*12*	*<0.001*	16.1
PestRep == kernel	8.6	57	17	11	2	0	1	1	0	<0.001	
PestRep == occupancy	23.4	6	7	8	7	70	24	18	40	<0.001	
PestRep == population	49.0	28	24	75	82	10	39	64	48	<0.001	
PestDyn == deterministic	*37.0*	*6*	*0*	*66*	*67*	*15*	*23*	*49*	*48*	*<0.001*	4.0
PestDyn == none	33.9	94	97	34	13	49	18	17	5	<0.001	
PestDyn == stochastic	29.1	0	3	0	20	36	59	35	48	<0.001	
PestMech == wind	34.9	64	93	40	43	16	24	32	0	<0.001	8.6
PestMech == movement	24.3	13	34	38	8	25	18	43	2	<0.001	
PestMech == vector	11.7	2	3	4	3	26	16	18	5	<0.001	
PestMech == generic	27.2	0	0	25	38	34	34	8	88	<0.001	
PestMech == gravity	4.8	2	3	8	3	0	13	4	0	0.005	
PestMech == human (short)	7.3	6	0	2	7	7	15	11	0	0.022	
PestMech == human (long)	8.6	2	0	4	10	3	22	11	2	<0.001	
PestMech == rain splash	4.4	15	3	4	2	2	2	7	0	0.010	
PestMech == clonal	4.2	0	0	0	7	5	4	7	7	0.225	
PestMech == water	3.8	0	0	2	2	0	18	1	0	<0.001	
PestMech == ballistic	1.5	0	3	4	2	0	2	1	0	0.571	
PestDisp == deterministic	*47.7*	*87*	*72*	*94*	*75*	*11*	*13*	*35*	*38*	*<0.001*	9.2
PestDisp == stochastic	52.3	13	28	6	25	89	87	65	62	<0.001	
PestEnemies == no	*92.7*	*98*	*100*	*87*	*92*	*98*	*94*	*89*	*88*	*0.069*	0.0
PestEnemies == yes	7.3	2	0	13	8	2	6	11	12	0.069	
PestEntryTime == multiple	*9.4*	*2*	*17*	*2*	*3*	*13*	*5*	*17*	*17*	*<0.001*	4.4
PestEntryTime == single	90.6	98	83	98	97	87	95	83	83	<0.001	
PestEntrySp == multiple	*40.0*	*2*	*48*	*11*	*15*	*44*	*60*	*58*	*60*	*0.002*	6.7
PestEntrySp == single	60.0	98	52	89	85	56	40	42	40	0.002	
PestEvolve == no	*96.4*	*100*	*100*	*100*	*97*	*98*	*94*	*95*	*90*	*0.100*	0.0
PestEvolve == yes	3.6	0	0	0	3	2	6	5	10	0.100	
PestControl == no	*75.7*	*96*	*97*	*87*	*77*	*92*	*65*	*55*	*71*	*<0.001*	2.1
PestControl == yes	24.3	4	3	13	23	8	35	45	29	<0.001	

Clustering variable	**% of all results**	**% of model cluster**								***P***	**Instability**
		A	**B**	**C**	**D**	**E**	**F**	**G**	**H**		
Host plant model											
HostRep == individual	*21.5*	***2***	***0***	***6***	***3***	***77***	***2***	***32***	***36***	*<0.001*	8.6
HostRep == none	52.3	**98**	**83**	**87**	**92**	**5**	**91**	**0**	**0**	<0.001	
HostRep == occupancy	9.8	**0**	**10**	**4**	**2**	**13**	**6**	**18**	**21**	<0.001	
HostRep == population	16.3	**0**	**7**	**4**	**3**	**5**	**0**	**50**	**43**	<0.001	
HostType == generic	80.5	**100**	**100**	**100**	**100**	**90**	**100**	**16**	**100**	<0.001	9.4
HostType == specific	22.2	**0**	**0**	**0**	**0**	**20**	**0**	**91**	**0**	<0.001	
HostDyn == no	*73.8*	***100***	***100***	***96***	***97***	***85***	***98***	***33***	***2***	*<0.001*	7.1
HostDyn == yes	26.2	**0**	**0**	**4**	**3**	**15**	**2**	**67**	**98**	<0.001	
HostNum == 0	*51.3*	***98***	***83***	***83***	***87***	***5***	***91***	***0***	***0***	*<0.001*	5.9
HostNum == 1	44.6	**2**	**17**	**17**	**10**	**92**	**5**	**92**	**88**	0.023	
HostNum == 2	2.9	**0**	**0**	**0**	**3**	**3**	**4**	**2**	**12**	0.023	
HostNum == 3	0.8	**0**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	0.051	
HostNum == more	0.4	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	0.354	
HostSeg == no	*99.6*	***100***	***100***	***100***	***98***	***100***	***100***	***99***	***100***	*0.927*	0.0
HostSeg == yes	0.4	**0**	**0**	**0**	**2**	**0**	**0**	**1**	**0**	0.927	
HostDisp == no	*92.7*	***100***	***100***	***100***	***100***	***100***	***99***	***87***	***50***	*<0.001*	4.4
HostDisp == yes	7.3	**0**	**0**	**0**	**0**	**0**	**1**	**13**	**50**	<0.001	
HostImpact == no	*77.8*	***100***	***100***	***98***	***97***	***85***	***98***	***49***	***7***	*<0.001*	4.4
HostImpact == yes	22.2	**0**	**0**	**2**	**3**	**15**	**2**	**51**	**93**	<0.001	
HostEvolve == no	*98.1*	***100***	***100***	***100***	***100***	***100***	***100***	***98***	***83***	*<0.001*	0.0
HostEvolve == yes	1.9	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**17**	<0.001	

Table 10: Between-cluster differences in model application and analysis, formatted as Table 9.

Model application	**% of all results**	**% of model cluster**								***P***
		A	**B**	**C**	**D**	**E**	**F**	**G**	**H**	
Pest taxonomic group										
Insect	31.6	13	45	40	26	26	30	50	5	<0.001
Plant	26.8	26	7	17	51	2	60	14	24	<0.001
Fungus or oomycete	22.6	49	55	25	15	25	1	27	7	<0.001
Virus or viroid	4.6	4	0	2	3	21	0	3	2	<0.001
Bacterium or phytoplasma	1.5	4	0	0	0	0	1	4	0	0.152
Nematode	1.3	0	0	0	2	2	0	4	0	0.228
Mite	0.8	4	0	4	0	0	0	0	0	0.042
Protist	0.4	0	0	0	0	2	0	1	0	0.926
Generic pest	14.4	0	0	17	10	31	9	0	67	<0.001
Pest functional group										
Micro-parasite or disease	40.2	57	55	34	20	77	4	40	67	<0.001
Invasive species	34.9	21	3	36	59	0	83	22	24	<0.001
Herbivore	31.8	15	45	43	26	26	28	49	10	<0.001
Competitor	26.2	26	7	19	49	2	60	11	24	<0.001
Disease vector	2.7	6	3	2	2	3	1	4	0	0.63
Macro-parasite	1.3	0	0	0	2	0	0	3	5	0.173
Generic pest	0.8	0	3	4	2	0	0	0	0	0.093
Host plant functional group										
Crop	60.9	81	86	64	54	70	37	74	29	<0.001
Wild plant	37.7	15	28	28	31	20	54	52	50	<0.001
Ornamental	8.6	6	14	6	8	5	6	17	2	0.052
Not specified	5.6	0	0	6	3	15	5	0	21	<0.001
Generic plant	9.6	6	3	19	23	0	22	0	0	<0.001
Sector										
Agriculture	48.3	81	76	51	48	66	28	40	26	<0.001
Ecology	44.6	19	24	45	54	30	72	33	69	<0.001
Forestry	18.4	11	14	11	16	8	16	41	7	<0.001
Horticulture	8.6	11	14	19	8	7	1	10	5	0.032
Parameterisation strategy										
Empirically determined	48.7	34	72	45	57	23	54	72	12	<0.001
Arbitrary values	38.9	9	28	43	39	61	37	21	90	<0.001
Fitted to spread patterns	31.2	70	17	32	30	31	37	24	5	<0.001
Model analysis										
Sensitivity analysis	66.9	32	17	72	77	75	72	68	95	<0.001
Validation	19.9	17	48	21	18	10	28	20	2	<0.001
Abiotic change scenarios	13.4	11	38	19	18	5	12	12	5	0.001
Risk mitigation scenarios	33.3	11	7	21	33	20	44	58	31	<0.001

4. Interpretation of the Clusters

In the sections below, the characteristics of each Cluster are elaborated, based on Tables 9 and 10. We also give a name to each Cluster which reflects the main distinguishing characteristics of their models. Three representative examples of each cluster are given, selected as the models with among the lowest uncertainty in their cluster assignment. We have tried to order the Clusters in a logical manner. This begins with the dispersal-only strategies (A and B) and then covers the two most mathematically-based strategies for dispersal or spread (C and D). The next three strategies (E-G) primarily rely upon computer simulation of spread, and are ordered from the most simple to the most complex algorithms. The final strategy (H) combines both simulation and mathematical approximations.

4.1. Cluster A: Single-event pest dispersal

Continuous space models with no time component, i.e. modelling single spread events. These are typically applied at the single-field scale (though they can calculate spread potential at all scales) and are restricted to a single growing season of spread from a single initial entry point or foci. Spatial and temporal heterogeneity are ignored, as are biological details such as interactions with natural enemies, pest evolution or pest control efforts. Host plants are not explicitly modelled. These models are most commonly applied for diseases of agricultural crop plants and are parameterised through fitting. Only rarely are the models used for sensitivity analysis, independent validation, or experimentation with scenarios of abiotic change or risk mitigation. Dispersal kernel and disease gradient models are strongly represented in Cluster A.

Example models:

- Septoria leaf spot lesion density on trap plants exposed at varying distances from infected tomatoes (Ferrandino and Elmer, 1996).
- Spore dispersal gradients and disease gradients of western gall rust (Blenis et al., 1993).
- Temporal and spatial dynamics of long-distance *Conyza canadensis* seed dispersal (Dauer et al., 2007).

4.2. Cluster B: Large-scale simulation of pest dispersal events:

Usually discrete in space and time, over three dimensions, large spatial scales and single growing seasons. Spatial and temporal heterogeneity in the wind drive deterministic dispersal of (generally) individual pests. Active behaviour of the pest may interact with the wind (e.g. insect flight). These are usually dispersal-only models with no pest population dynamics or representation of the host plants. There is a tendency for Cluster B to model dispersal from multiple points and at multiple times. These models are largely restricted to dispersal of insects and fungal spores that are most commonly agricultural pests. The physics of particle advection in the atmosphere plays a large role in these models and so parameters are generally empirically determined and predictions of the models validated against data on pest spread. Predictions under varying wind regimes are often made. Lagrangian atmospheric dispersion models, advection-diffusion models, and wind trajectory models are strongly represented in Cluster B.

Example models:

- Long-term prediction of soybean rust entry into the continental United States (Pan et al., 2006).

- Pest insect immigration warning by an atmospheric dispersion model, weather radars and traps (Leskinen et al., 2011).

- Real-time prediction system for migration of rice planthoppers *Sogatella furcifera* (Horváth) and *Nilaparvata lugens* (Stål) (Homoptera: Delphacidae).

4.3. Cluster C: Pest spread or dispersal in continuous space and time

These are generally models for deterministic models in continuous space and time. Spread may be over a single or multiple seasons. Population dynamics may or may not be modelled, so the models can either be for population spread or dispersal. One, two or three spatial dimensions are represented but they are not generally used at large spatial scales and typically ignore spatial and temporal heterogeneity. These are usually generic models applied to specific single pests and model spread from a single entry point via the wind or active movement. Host plant species are not usually modelled. Many of these models are used for insects or fungi, across a range of different host plant types and sectors. These models are parameterised and applied in diverse range of ways. Models in Cluster C are most often labelled as reaction-diffusion models for spatial population dynamics (Truscott and Ferguson, 2012) or diffusion models for dispersal behaviour (Pocock and Evans, 2014).

Example models:

- Beyond diffusion: Modelling local and long-distance dispersal for organisms exhibiting intensive and extensive search modes (Tyson et al., 2011).

- Local movement in herbivorous insects: applying a passive diffusion model to mark-recapture field experiments (Kareiva, 1983).

- Modeling population dynamics and dispersion of codling moth *Cydia pomonella* L.(Lepidoptera, Tortricidae) (Gharekhani, 2009).

4.4. Cluster D: Continuous-space pest spread in discrete time

These are discrete time models, usually in continuous space covering one or two dimensions. They generally model deterministic spread of a population through uniform environment over multiple years and at a range of spatial scales. The host plants are not generally modelled. Mostly, Cluster D has been applied to invasive plants and insects, across a range of host plant types and sectors. Parameters can readily be empirically determined, though often Cluster D uses arbitrary values or fitting. Sensitivity analyses predominate the use of such models, although there is also a tendency to examine scenarios of abiotic change (e.g. change in wind speed affecting the dispersal of the species). Integro-difference models (Katul et al., 2005) exemplify Cluster D.

Example models:

- Measuring and modelling anthropogenic secondary seed dispersal along roadverges for feral oilseed rape (Garnier et al., 2008).

- Prolonged diapause: A trait increasing invasion speed? (Mahdjoub and Menu, 2008).

- Temporally variable dispersal and demography can accelerate the spread of invading species (Ellner and Schreiber, 2012).

4.5. Cluster E: Iterative colonisation of hosts at small scales

Usually discrete space and time models for spread over a single season and at small spatial scales. Two-dimensional and spatially-implicit network models are included but spatio-temporal heterogeneity is not included. Pests are modelled as generic individuals or occupancies, and either one or two pests are modelled. Pest dynamics are often not modelled, so spread is an iterative colonisation process with no extinction or variation once colonised. Dispersal is stochastic and may be from single or multiple points of entry. Host plants are generally represented as generic individual units, but their dynamics or dispersal are rarely modelled. As a result, the pests rarely explicitly impact the hosts in these models. Cluster E is usually applied to crop diseases and the models are often arbitrarily parameterised but used for sensitivity analysis of spread rates. Cluster E models are most often referred to as individual-based or simulation models. The susceptible-infected class of epidemic models and network contact spread models (e.g. Zipf, 1946) are also mainly found in Cluster E.

Example models:

- A gravity model for the spread of a pollinator-borne plant pathogen (Ferrari et al., 2006).
- Analysis of spatiotemporal dynamics of virus spread in an Australian hop garden by stochastic modelling (Pethybridge and Madden, 2003).
- Examination of the effect of aphid vector population composition on the spatial dynamics of citrus tristeza virus spread by stochastic modelling (Gottwald et al., 1999).

4.6. Cluster F: Simulation of specific pest spread at large scales

These are similar to Cluster G in structure and pest representation. Differences include a greater propensity to model individual pests or their occupancy rather than population sizes, greater inclusion of stochasticity in dispersal and dynamics and a restriction to single-species models. Unlike Cluster G however, host plants are rarely modelled explicitly in Cluster F. These models are typically applied for invasive plants and insect pests that impact wild native plant species. As such they largely come under the ecological sector. Models are parameterised in a range of ways, often using sensitivity analysis and parameter validation. Risk mitigation experiments are also often included. Cluster F includes most of the individual-based models we found, but are also often referred to as simulation models, cellular automata and metapopulation models.

Example models:

- Potential geographic distribution of *Anoplophora glabripennis* (Coleoptera : Cerambycidae) in North America (Peterson et al., 2004).
- Predicting Argentine ant spread over the heterogeneous landscape using a spatially explicit stochastic model (Pitt et al., 2009).
- Temporal limits to simulating the future spread pattern of invasive species: *Buddleja davidii* in Europe and New Zealand (Pitt et al., 2011).

4.7. Cluster G: Simulation of specific pest and host dynamics

Generally discrete in space and time and modelling spread in two spatial dimensions over multiple seasons. These models typically represent landscape heterogeneity, but most do not include temporal heterogeneity in the landscape or other model parameters. Cluster G models are developed with a high degree of specificity to the focal system, which means they are quite diverse in terms of how the pest and its dynamics are represented and dispersal mechanisms. Biological details such as multiple pest entry, interactions with natural enemies, evolution and control efforts are included more often than most of the other clusters. Host plants are always explicitly represented, and as with the pests this is often done in a highly specific manner, leading to a diversity of host models. Generally, there are tendencies to include host population dynamics and pest impacts. These models are most commonly applied to pest insects or fungi attacking crops or wild plants across a range of sectors. Parameters are generally empirically determined and there is a strong focus on parameter sensitivity analysis and modelling of pest risk mitigation. These models are most often referred to very generally as simulations, but there are also many cellular automata, individual-based models and agent-based models.

Example models:

- Impact of scale on the effectiveness of disease control strategies for epidemics with cryptic infection in a dynamical landscape: an example for a crop disease' (Gilligan et al., 2007).

- Invasion of *Phytophthora infestans* at the landscape level: How do spatial scale and weather modulate the consequences of spatial heterogeneity in host resistance? (Skelsey et al., 2010).

- SIPPOM-WOSR: A Simulator for Integrated Pathogen POpulation Management of phoma stem canker on Winter OilSeed Rape. I. Description of the model (Lô-Pelzer et al., 2010).

4.8. Cluster H: Generic pest and host dynamics

These show a diversity of representations of space and time, but are generally two dimensional and modelling spread over multiple time seasons. Spatial and temporal heterogeneity are rarely modelled. Pests are typically modelled as generic population sizes or species occupancies with generic dispersal mechanisms, which may both be stochastic or deterministic. Though they are generic models of spread, this cluster shows an excess of biological details, similar to Cluster G. Generic host plant dynamics are also modelled and are generally impacted by the pest. Host plants may or may not disperse. Sometimes more than one host plant species or host plant evolution is modelled. Cluster H is mainly applied to generic diseases of wild or generic plants or crops. As a result, parameters are typically given arbitrary values and used for sensitivity analysis. These are often models strongly related to ecological theory and are referred to with similar terms as Cluster G.

Example models:

- Evolution of dispersal in metacommunities of interacting species (Chaianunporn and Hovestadt, 2012).

- Invasiveness in plant communities with feedbacks (Eppstein and Molofsky, 2007).

- Spatial dynamics of invasion: the geometry of introduced species (Korniss and Caraco, 2005).

TASK 2 - ELECTRONIC INVENTORY OF MODELS OF SPREAD AND DISPERSAL OF PLANT PESTS

5. Objective

The objective of this task was to develop an Electronic Model Inventory that captures the information gathered in the extensive literature review. This will aid EFSA in using the literature review results in future risk assessments by searching the inventory for suitable existing spread and dispersal models to apply in new risk assessment tasks. Here, we report on the design of the database and also provide a concise guide for users.

6. Development of the Electronic Model Inventory

The Electronic Model Inventory was developed as a Microsoft Access database[4]. The database stored details of each model included in the review and cluster analysis. Data fields were populated for each model including information on the paper in which it was described, the structure of the model (i.e. the data used for clustering analysis, see Table 5) and its usage (i.e. the data used for cluster interpretation, see Table 6).

A list of the data fields is given in Table 11, from where it can be seen that the bibliographic information was encoded so as to be compatible with the MOPEST database (Rossi et al., 2009). Categorical data fields used in the analyses were converted into binary dummy variables (also known as Boolean, indicator, design or qualitative variables), effectively representing a yes/no answer to each category of the variable. For single-choice fields the dummy variable for the first category was omitted as the variables for the remaining categories contain all the information needed to infer the value of the first.

The database was also designed to link to the PDF files of the EndNote library for a seamless integration of results of the literature search and model contents. Therefore, upon discovering a relevant looking paper in the Electronic Model Inventory, a user can open the full document with a single mouse click to examine the model in more detail.

The Electronic Model Inventory has been tested on Windows XP and Windows 7 operating systems. The EndNote library has been tested using EndNote X5 and the Access database has been tested using Microsoft Access 2007. We cannot guarantee that the library or database will be compatible with backward or forward versions of these software packages, but incompatibility is unlikely.

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[4] The Electronic Model Inventory database can be downloaded at http://www.efsa.europa.eu/en/supporting/doc/795eax1.zip

Table 11: Explanation of the data fields stored in the electronic model inventory (na = not applicable). The fields include the bibliographic information for the article in which the model was published, data on the model's formulation and use and results of the model-based cluster analysis defining eight major model strategies.

Field name in database	Meaning	Location in Inventory	MOPEST field?
ID	Unique identifier for each model	na	Yes
TITLE	Title of the article detailing the model	Overview	Yes
AUTHOR	Abbreviated names of the article author(s)	Overview	Yes
YEAR	Year of article publication	Overview	Yes
JOURNAL	Journal that the article is published in	Overview	Yes
VOLUME	Volume of the journal	Overview	Yes
ISSUE	Issue number of the journal	Overview	Yes
PAGES	Page range of the journal	Overview	Yes
DOI	Article Digital Object Identifier	Overview	No
LINK_PDF	Relative file location of the article document (PDF format)	Overview (Attachment string)	No
Sp	How is space represented?	General Model Structure	No
Time	How is time represented?	General Model Structure	No
SpDim	How many spatial dimensions are modelled?	General Model Structure	No
SpExt	What spatial extent is spread modelled over?	General Model Structure	No
TimeStep	What is the model timestep?	General Model Structure	No
TimeExt	Is the model restricted to a single growing season, or does it model spread over multiple years?	General Model Structure	No
SpHet	How is landscape heterogeneity represented with respect to abiotic, habitat or management factors?	General Model Structure	No
TimeHet	Is temporal heterogeneity or forcing modelled?	General Model Structure	No
PestType	Is the model specific to a particular pest or generic across broad groups of pests?	Pest Model	No
PestNum	How many interacting pest species are modelled?	Pest Model	No
PestRep	How are pests represented?	Pest Model	No
PestDyn	How are pest temporal dynamics modelled?	Pest Model	No
PestMech	What broad types of pest dispersal mechanisms are represented?	Pest Model	No
PestDisp	Is pest dispersal stochastic or deterministic?	Pest Model	No

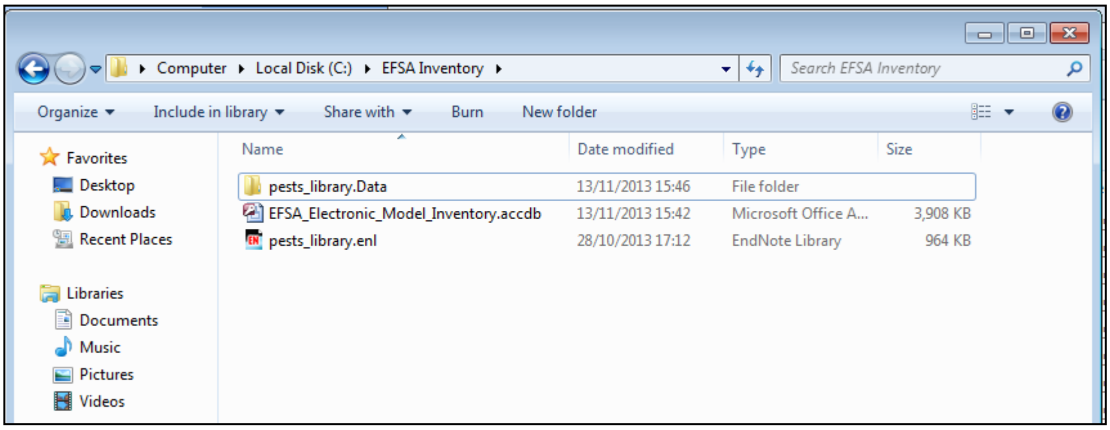
Field name in database	Meaning	Location in Inventory	MOPEST field?
PestEnemies	Is pest spread affected by natural enemies in the model?	Pest Model	No
PestEntryTime	Does pest entry or introduction from outside the system occur at multiple times?	Pest Model	No
PestEntrySp	Does pest entry or introduction from outside the system occur at multiple locations?	Pest Model	No
PestEvolve	Does the modelled pest evolve during spread	Pest Model	No
PestControl	Are pest control actions modelled?	Pest Model	No
HostRep	How are host plants represented?	Host Plant Model	No
HostType	Is the model specific to a particular host plant or generic across broad groups of host plants?	Host Plant Model	No
HostDyn	Are host plant temporal dynamics modelled?	Host Plant Model	No
HostNum	Is the model a multi-host species model?	Host Plant Model	No
HostSeg	Is there temporal segregation of pest use of the host species?	Host Plant Model	No
HostDisp	Is host plant dispersal modelled?	Host Plant Model	No
HostImpact	Are negative effects of the pest on the host plant population dynamics or dispersal modelled?	Host Plant Model	No
HostEvolve	Does the host plant evolve?	Host Plant Model	No
PestTaxGrp	What taxonomic category is the pest?	Model Use	No
PestFunGrp	What functional group category is the pest?	Model Use	No
HostFunGrp	What functional group is the host plant?	Model Use	No
Sector	What is the socio-economic sector?	Model Use	No
ParamStrat	How do model parameters relate to observed data?	Model Use	No
Validation	Validation of model predictions against independent data	Model Use	No
Sensitivity	Sensitivity analysis of pest or host parameters	Model Use	No
AbiotChg	Scenario experiments for abiotic change	Model Use	No
RiskMit	Scenario experiments for risk mitigation measures	Model Use	No
Framework	Names of modelling frameworks	Model Use	No
HostSpeciesName	Scientific name of the host plant(s)	Model Use	No
PestSpeciesName	Scientific name of the pest(s)	Model Use	No
Cluster	Model cluster to which the model is assigned	Cluster Analysis	No
PAssignment	Assignment probability for that cluster	Cluster Analysis	No
PClusterA	Assignment probability for Cluster A	Cluster Analysis	No
PClusterB	Assignment probability for Cluster B	Cluster Analysis	No
PClusterC	Assignment probability for Cluster C	Cluster Analysis	No
PClusterD	Assignment probability for Cluster D	Cluster Analysis	No

Field name in database	Meaning	Location in Inventory	MOPEST field?
PClusterE	Assignment probability for Cluster E	Cluster Analysis	No
PClusterF	Assignment probability for Cluster F	Cluster Analysis	No
PClusterG	Assignment probability for Cluster G	Cluster Analysis	No
PClusterH	Assignment probability for Cluster H	Cluster Analysis	No
ABSTRACT	The abstract of the article in which the model was published	Abstract	Yes

7. A guide to using the Electronic Model Inventory

7.1. Opening the Database

To ensure that document PDF files are properly linked between the EndNote library and the Access database, both files must be located in the same file path. That is, a copy of the EndNote library, the Access database and the data folder, are located in the same folder (see Figure 6). The exact location or name of the folder containing these three objects is not important and can be changed by the user. The file called "pests_library.enl" calls the EndNote library, "EFSA_Electronic_Model_Inventory.accdb" calls the Access database and the folder named "pests_library.Data" contains all of the PDF files associated with the EndNote library and Access database. Any changes to the file paths or names of the PDF files will result in the library and database being unable to open the relevant PDF articles.



Name	Date modified	Type	Size
pests_library.Data	13/11/2013 15:46	File folder	
EFSA_Electronic_Model_Inventory.accdb	13/11/2013 15:42	Microsoft Office A...	3,908 KB
pests_library.enl	28/10/2013 17:12	EndNote Library	964 KB

Figure 6: Screenshot of the required folder structure to link the electronic inventory ("EFSA_Electronic_Model_Inventory.accdb") to the articles describing the models in the EndNote library ("pest_library.enl"), with PDF documents in the folder ("pests_library.Data"). In the example shown, a folder called "EFSA Inventory" has been created on the C drive and the three items have been copied into the newly created the folder. However, correct linking does not require this exact folder name or location.

To open the database within Microsoft Access, double click on the "EFSA_Electronic_Model_Inventory.accdb" file. The user will be presented with the title screen as shown in Figure 7. This is the main starting point for using the database. To access the records within the database the user must click on the Enter Database button.

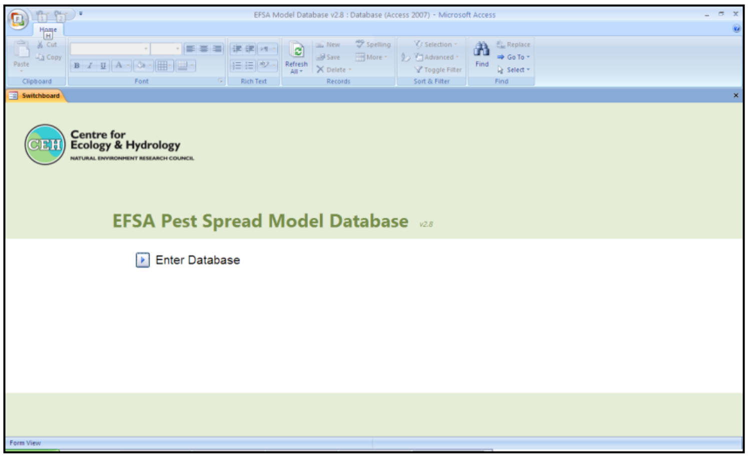
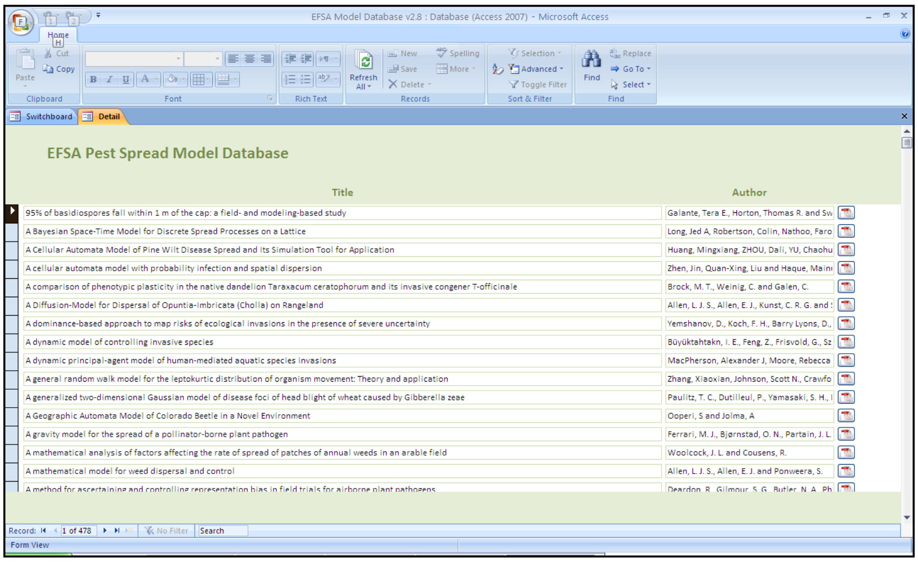


Figure 7: Screenshot of the initial Switchboard screen presented when opening the electronic model inventory. Clicking on the Enter Database box opens up a Detail tab allowing the user to view the data.

7.2. Viewing records

After entering the database the user will be presented with the entire list of the entries of the database (Figure 8). Each row contains the title, author and PDF link to the article. Clicking on the PDF link opens the relevant PDF file in the user's default PDF reader software. The Access database has a quick search feature, located at the bottom of the window (Figure 8). The user can simply type a search string into the text box and the title and author fields of the entire database will be searched. This allows quick access to all of the records in the database. To access any specific record, located by scrolling through the records or using the search box, the user can double click on the arrow on the left of the record row. This will then open a new window which contains the Article Details for this record (Figure 9).

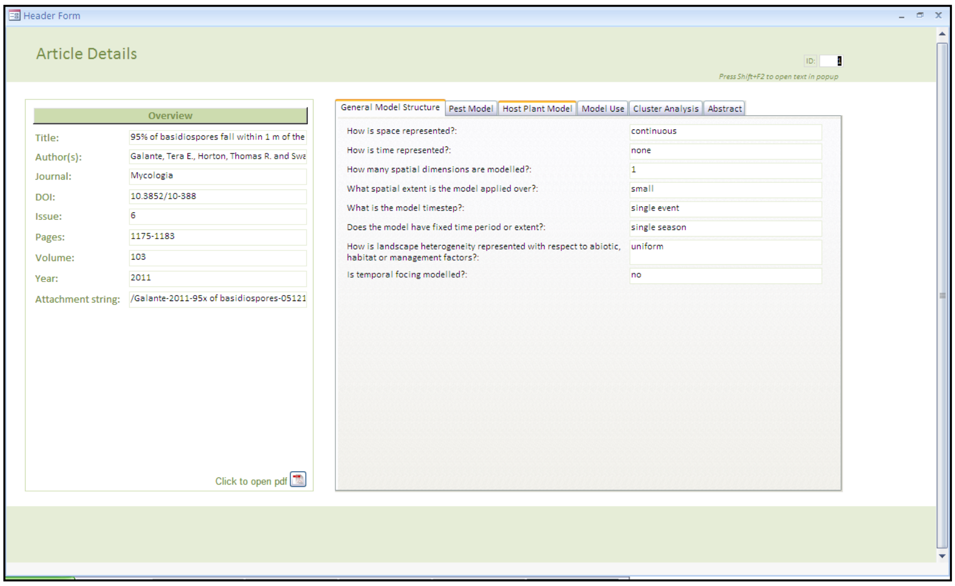
The Article Details page consists of two main areas: the overview on the left of the window and the model data on the right of the window (Figure 9). The overview contains the bibliographic information, such as the article title, authors, date published etc. Quick access to the PDF file can be obtained by clicking on the PDF button at the bottom of the overview section.



EFSA Pest Spread Model Database

Title	Author
95% of basidiospores fall within 1 m of the cap: a field- and modeling-based study	Galante, Tera E., Horton, Thomas R. and Sw
A Bayesian Space-Time Model for Discrete Spread Processes on a Lattice	Long, Jed A, Robertson, Colin, Nathoo, Faro
A Cellular Automata Model of Pine Wilt Disease Spread and Its Simulation Tool for Application	Huang, Mingxiang, ZHOU, Dali, YU, Chaohu
A cellular automata model with probability infection and spatial dispersion	Zhen, Jin, Quan-Xing, Liu and Haque, Main
A comparison of phenotypic plasticity in the native dandelion Taraxacum ceratophorum and its invasive congener T-officinale	Brock, M. T., Weinig, C. and Galen, C.
A Diffusion-Model for Dispersal of Opuntia-Imbricata (Cholla) on Rangeland	Allen, L. J. S., Allen, E. J., Kunst, C. R. G. and
A dominance-based approach to map risks of ecological invasions in the presence of severe uncertainty	Yemshanov, D., Koch, F. H., Barry Lyons, D.,
A dynamic model of controlling invasive species	Büyüktahtakn, I. E., Feng, Z., Frisvold, G., Sz
A dynamic principal-agent model of human-mediated aquatic species invasions	MacPherson, Alexander J, Moore, Rebecca
A general random walk model for the leptokurtic distribution of organism movement: Theory and application	Zhang, Xiaoxian, Johnson, Scott N., Crawfo
A generalized two-dimensional Gaussian model of disease foci of head blight of wheat caused by Gibberella zeae	Paulitz, T. C., Dutilleul, P., Yamasaki, S. H.,
A Geographic Automata Model of Colorado Beetle in a Novel Environment	Ooperi, S and Jolma, A
A gravity model for the spread of a pollinator-borne plant pathogen	Ferrari, M. J., Bjørnstad, O. N., Partain, J. L.
A mathematical analysis of factors affecting the rate of spread of patches of annual weeds in an arable field	Woolcock, J. L. and Cousens, R.
A mathematical model for weed dispersal and control	Allen, L. J. S., Allen, E. J. and Ponweera, S.
A method for ascertaining and controlling representation bias in field trials for airborne plant pathogens	Deardon, R., Gilmour, S. G., Butler, N. A., Ph

Figure 8: The Detail tab, listing the article titles and authors for each model, with a link to the PDF document. Double clicking the row links (column of blue boxes on the left) opens a header form showing the details for each model. The Search box at the bottom left of the screenshot allows the user to quickly search the titles and author names.



Article Details

ID: 1

Overview

Title:	95% of basidiospores fall within 1 m of the
Author(s):	Galante, Tera E., Horton, Thomas R. and Swa
Journal:	Mycologia
DOI:	10.3852/10-388
Issue:	6
Pages:	1175-1183
Volume:	103
Year:	2011
Attachment string:	/Galante-2011-95x of basidiospores-05121

How is space represented?:	continuous
How is time represented?:	none
How many spatial dimensions are modelled?:	1
What spatial extent is the model applied over?:	small
What is the model timestep?:	single event
Does the model have fixed time period or extent?:	single season
How is landscape heterogeneity represented with respect to abiotic, habitat or management factors?:	uniform
Is temporal focing modelled?:	no

Figure 9: Screenshot of the Article Details header form.

The record data in the tabbed area of the record window contains the collected information from the model described in the article. Within each tab are a series of questions relating to the data collected, described in Table 11. The tabs entitled “General Model Structure”, “Pest Model” and “Host Plant Model”, pertain to characteristics of the general model structure and the ways in which the pest and host were modelled. The questions in these tabs directly translate to the fields as described in Table 5, under the headings “Model structure”, “Pest model” and “Host plant model”. The tab “Model Use” corresponds to Table 6. The tab “Cluster Analysis” contains the results of the model-based clustering analysis, which is reported in the previous section of this report. The fields pertain to the cluster assignment and the assignment probabilities for each cluster. The final tab, “Abstract”, gives the abstract of the record.

To close the record, the user has to click the Microsoft close window icon at the top right of the record window. No information will be lost by closing the record. The database as delivered is locked, to prevent accidental changes to the fields and therefore no information can be added to the database. Fields may be copied and pasted into other documents as required. Once the record has been closed, another record can be opened as required. The Access database may be closed by clicking on the Microsoft close window icon at the top right of the database window.

7.3. Exporting data

To export data from the Access database it is necessary to view the Navigation Pane. If this is not visible as a box on the left of the screen, follow the instructions in Figure 10 to enable this option. The procedure for exporting to Excel spreadsheet format is then straightforward, as shown in Figure 11.

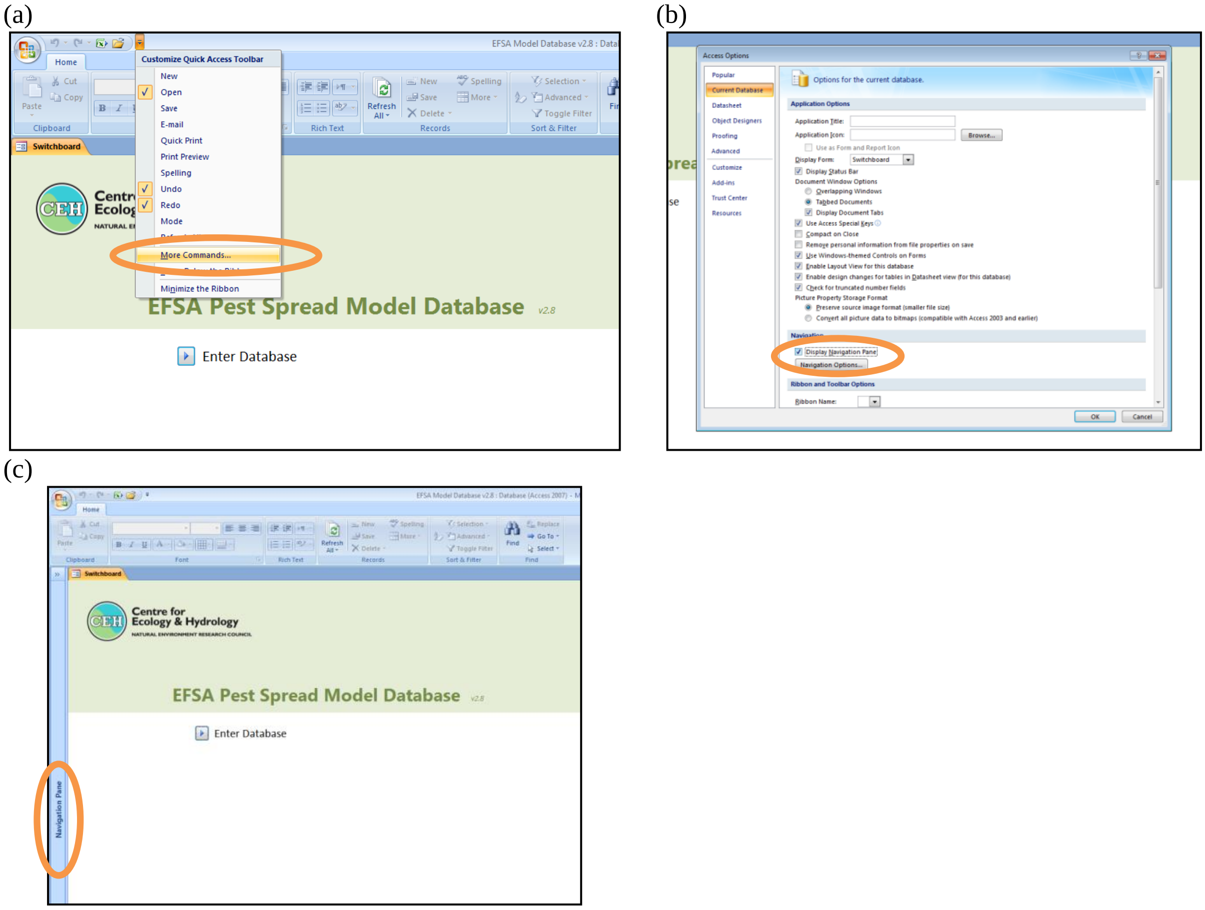
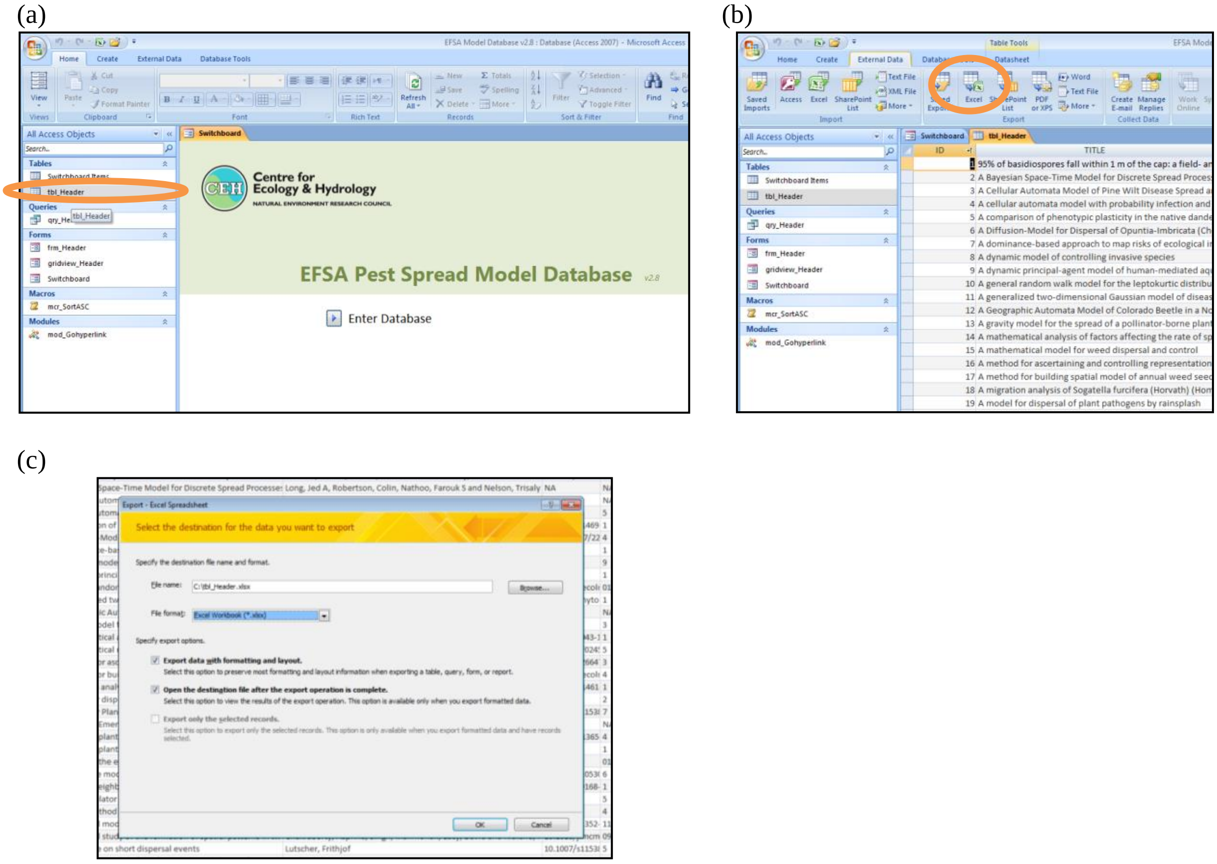


Figure 10: If the Navigation Pane does not display, (a) click on ‘More Commands’ in the Customise Quick Access Toolbar drop down menu and (b) make sure the Display Navigation Pane option is ticked. After clicking OK, the user will be prompted to re-open the database and (c) the Navigation Pane should be visible in the left of the screen.



ID	TITLE
1	95% of basidiospores fall within 1 m of the cap: a field- ar
2	A Bayesian Space-Time Model for Discrete Spread Proces
3	A Cellular Automata Model of Pine Wilt Disease Spread a
4	A cellular automata model with probability infection and
5	A comparison of phenotypic plasticity in the native dande
6	A Diffusion-Model for Dispersal of Opuntia-Imbricata (Ch
7	A dominance-based approach to map risks of ecological i
8	A dynamic model of controlling invasive species
9	A dynamic principal-agent model of human-mediated aq
10	A general random walk model for the leptokurtic distribu
11	A generalized two-dimensional Gaussian model of diseas
12	A Geographic Automata Model of Colorado Beetle in a No
13	A gravity model for the spread of a pollinator-borne plant
14	A mathematical analysis of factors affecting the rate of sp
15	A mathematical model for weed dispersal and control
16	A method for ascertaining and controlling representation
17	A method for building spatial model of annual weed seed
18	A migration analysis of Sogatella furcifera (Horvath) (Hom
19	A model for dispersal of plant pathogens by rainsplash

Export - Excel Spreadsheet

Select the destination for the data you want to export

Specify the destination file name and format.

File name: C:\tbl_Header.xlsx

File format: Excel Workbook (*.xlsx)

Specify export options.

☑ **Export data with formatting and layout.**
Select this option to preserve most formatting and layout information when exporting a table, query, form, or report.

☑ **Open the destination file after the export operation is complete.**
Select this option to view the results of the export operation. This option is available only when you export formatted data.

☐ **Export only the selected records.**
Select this option to export only the selected records. This option is only available when you export formatted data and have records selected.

Figure 11: A guide to exporting data from the Access database into Excel.

TASK 3 - ASSESSMENT OF THE MODELS OF SPREAD AND DISPERSAL OF PLANT PESTS FOR THEIR USE IN PEST RISK ASSESSMENT

8. Objectives

The overall aim of Task 3 is to evaluate the fitness of eight modelling strategies identified in Task 1 for use in EFSA Plant Health risk assessments, and to use this information to develop a Decision Support Scheme for assessing which strategies are most suitable for a given task. Our specific objectives were:

1. To develop a set of fitness criteria that assess the ability of spread and dispersal models to provide answers to the questions in the harmonised framework for EFSA risk assessments (Appendix C Stage 2B - Assessment of the probability of introduction and spread and of potential consequences; EFSA Panel on Plant Health (PLH), 2010a).

2. To assess each strategy as having low, medium or high fitness for the criteria. In assessing the fitness of the model strategies we principally considered the actual usage of models in the scientific literature, but where relevant and reasonable we considered the potential uses of the models for risk assessment.

3. To discuss the pros and cons of each strategy for use in risk assessment, based on the fitness scoring.

4. To establish protocols for a Decision Support Scheme (DSS) that identifies the model strategy most suited to a particular combination of risk assessment tasks for a particular pest species.

9. Model fitness criteria

Nineteen criteria for assessing the fitness of spread and dispersal models for various tasks of EFSA Plant Health risk assessment are defined in Table 12. In developing the fitness criteria, we considered the following.

9.1. Entry

EFSA risk assessments require detailed evaluation of entry, i.e. the economic or other dispersal pathways by which a pest may be introduced into the risk assessment area (questions 1.1-1.15 of EFSA Panel on Plant Health (PLH), 2010a). The aim is to determine how likely it is that a pest may enter the area. Bioeconomic models can use trade flows between economic units and relative infestation levels of source areas to estimate spatio-temporal variation in entry probabilities (Yemshanov et al., 2012). This was done in a recent EFSA risk assessment for silverleaf whitefly *Bemisia tabaci* and the viruses it vectors (EFSA Panel on Plant Health (PLH), 2013). As mentioned above, models solely predicting pest entry and not subsequent spread or dispersal were not included in our literature review, and so it is beyond the scope of this study to evaluate the fitness of the bioeconomic pest entry models themselves. Despite this, a minority of the reviewed spread models additionally modelled the entry process by incorporating multiple pest entry events in time and/or space (Table 9). Importantly, these are the only models capable of investigating the potential effect of phytosanitary measures (i.e. reductions in entry probabilities through better biosecurity) on pest introduction, spread and impacts for the risk assessment. Furthermore, repeated entry through traded commodities is common among invasions of many important plant pests, including common ragweed *Ambrosia artemisiifolia* (EFSA Panel on Plant Health, 2010a) and Mediterranean fruit fly *Ceratitis capitata* (Liebhold et al., 2006). Therefore the fitness criteria include evaluating the level of detail to which the model strategies represent the pest entry process and whether these models have the potential to incorporate mechanistic bioeconomic models for pest entry.

9.2. Establishment

EFSA risk assessments weigh up whether or not pest establishment is permitted or needs to be prevented through a variety of considerations. These considerations include the availability of host plants or habitat, the abiotic environment, competitors and natural enemies, land use or control measures and pest biological characteristics (questions 1.16-1.31 of EFSA Panel on Plant Health (PLH), 2010a). These parameters are highly relevant to spread modelling, since spread is a process of repeated dispersal and establishment (i.e. individual pest reproduction, colonisation or population growth). Therefore spread models could inform these parts of the risk assessment provided such effects are represented in the model dynamics. For example, a model for the spread of oriental chestnut gall wasp *Dryocosmus kuriphilus* only allowed establishment of the pest within the distribution of its host plant (EFSA Panel on Plant Health (PLH), 2010b). More complex models will include climatic and other effects on population growth parameters, as was done in the risk assessment for *Bemisia tabaci* (EFSA Panel on Plant Health (PLH), 2013). As with pest entry, models that only predict the region suitable for pest establishment but do not also feature dispersal and spread were outside of the scope of the extensive literature review. This was the case for the *B. tabaci* risk assessment (EFSA Panel on Plant Health (PLH), 2013), where the population dynamics model predicted the region where a favourable climate permitted a positive population growth rate and development of large pest populations, but dispersal and population spread through time were not modelled. Therefore, the fitness criteria appraise the population dynamics part of the model, with regard to spatio-temporal variation in the multiple factors identified as important for pest establishment by EFSA.

9.3. Spread

Pest spread is an area of EFSA risk assessments where the models considered in the extensive literature review can clearly provide important quantitative input. The key questions for risk assessment relate to the likelihood of rapid spread through ‘natural’ and human means, the likelihood that the pest will not be contained within the risk assessment area, and identifying the parts of the risk assessment area endangered by the pest (questions 1.32-1.36 of EFSA Panel on Plant Health (PLH), 2010a). The fitness for spread models to answer these questions is related to the discussion about establishment described above (e.g. where can the pest develop populations given habitat heterogeneity) but are also strongly affected by geographical restrictions on the pest’s range conferred by the dispersal part of the spread model. An example comes from the risk assessment for *Dryocosmus kuriphilus* (EFSA Panel on Plant Health (PLH), 2010b). In this, a population simulation model including both short-distance (‘natural’) and long-distance (human-mediated) dispersal was used to predict to where the pest might spread within its host plant range and from its current points of entry over a decadal time period. Other types of model that we reviewed may only provide partial answers, such as how far the pest can disperse in a single season via a single mechanism. An example of this is the Gaussian Plume Model for windborne dispersal of fungal spores used in the risk assessment for *Monilinia fructicola* (EFSA Panel on Plant Health (PLH), 2011). A further point is that for risk assessments to consider the possibility of spread beyond the risk assessment area, they are likely to require models that simulate spread or dispersal through realistically-represented spatial domains at landscape scales. Given these considerations, the fitness criteria score the ability of the models to include multiple dispersal mechanisms and predict the region invaded after a given amount of time.

9.4. Impact

The direct and indirect impacts of the pest and the possibilities for mitigating those impacts are considered in EFSA risk assessments (EFSA Panel on Plant Health (PLH), 2010a). Aspects of this for which spread models could provide input include estimating the impact on crop yield or quality (question 2.2), assessing how easily the pest could be controlled without phytosanitary measures (question 2.3), determining whether natural enemies might reduce pest populations (question 2.6) and identifying which parts of the risk assessment area may be most impacted (question 2.9). As with entry and establishment, non-spatial models for pest control within a single site were not captured in the extensive literature review. As such, the fitness criteria characterise whether the spread model strategies' predict pest impacts and capture processes that risk reduction options can affect.

9.5. Other considerations

The criteria also account for practical constraints on the development and application of the different strategies. The first of these is their data requirements. Some of the models make use of spatial data on factors that influence the spread of the pest. However, in most cases we consider these data needs can be met and so are unlikely to be a limiting factor on the modelling. High-resolution gridded European climate data for the recent past and projected future are readily available (e.g. E-OBS gridded climate data[5], Climatic Research Unit climate data[6], Climate Change, Agriculture and Food Security downscaling of Global Climate Model future predictions[7]). Likewise there are several freely-available sources of spatial land use or cover data (e.g. Corine land cover map[8], Global Agro-ecological Zones Data Portal[9]).

In our opinion, the data requirement that is most likely to limit modelling is biological information, such as accurate information on the distribution of the pest and host plants over time (in the risk assessment area and potentially also in the native range or other invaded regions) and experimental or observational data informing the demographic or population dynamic parameters of the model. Therefore the criteria assess the extent to which the modelling strategies rely on detailed biological knowledge about the pest.

The second extra consideration is the applicability of the models across taxonomic and functional groups and economic sectors. For this, the criteria assess how generically the pests, hosts and dispersal mechanisms are represented and which types of organisms and economic sectors the model strategies have been applied to.

9.6. Caveats

We did not include some potential criteria for which we do not expect much variation among model clusters. For example, it is straightforward to apply sensitivity analysis to all models (by varying parameter values according to certain criteria), even those in which this was not reported in the literature review. Therefore, although sensitivity analyses may be used in EFSA risk assessment it is not a useful criterion for comparing strategies.

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[5] http://eca.knmi.nl/download/ensembles/download.php
[6] http://www.cru.uea.ac.uk/cru/data/hrg/
[7] http://www.ccafs-climate.org/
[8] http://www.eea.europa.eu/data-and-maps/data/corine-land-cover-2006-raster-2
[9] http://gaez.fao.org/Main.html

Furthermore, the criteria cannot judge the accuracy with which the different model strategies predict outputs of interest for risk assessment – i.e. model 'validation'. Any model is only as good as its implicit or explicit assumptions and the quality of its input parameters and data. If for example two model types both incorporate multiple human and 'natural' dispersal mechanisms then they will necessarily be judged equally fit for predicting spread through both means, even if one includes a more accurate dispersal model than the other. Without having access to primary data with which to evaluate the reviewed models, we cannot judge their accuracy.

It is also important to note that the literature review focussed specifically on models of the spread or dispersal of plant pests – as per the project remit. Therefore, models that cover only certain aspects of risk assessment, such as pest entry, but do not also cover spread or dispersal will not have been included in our database.

Table 12: Criteria for assessing the fitness of the spread and dispersal modelling strategies for use in EFSA Plant Health risk assessment. Columns contain descriptions of their categorisations and the fields of the literature review database useful for assessment of each criterion. Note that the fitness categorisations can apply to both general model strategies and individual models. Where the medium categorisation is left blank, representative individual models will only be scored to either low or high, but the strategies may be assigned to medium if they contain a mixture of low and high-fitness individual models (see section 10. on methodology).

Fitness criterion	Fitness category			Relevant literature review fields
	Low	**Medium**	**High**	
1. Rate and extent of pest spread over the whole risk assessment area (the EU) can be predicted or hindcasted.	Constrained by small spatial extent or unrealistic spatial representation (e.g. one-dimension).		Model outputs landscape-scale maps of invaded areas through time.	SpExt, SpDim, TimeExt
2. The strategy can predict where environmental conditions are suitable for pest establishment and spread.	Spatial heterogeneity in climate/landscape is ignored and cannot easily be represented realistically.	Spatial heterogeneity in climate/landscape affects pest dispersal or dynamics, but is static in time.	Spatial and temporal heterogeneities in climate/landscape affect pest dispersal or dynamics.	SpHet, SpDim, TimeHet, Model analysis
3. The strategy can predict where the availability of host plants permits pest establishment and spread. (For invasive plants, 'host plants' are the invadable native communities.)	Host plants are never modelled.	Host plants often represented, but only as a static distribution.	Spatial dynamics of host plants and their interactions with the pest are often modelled.	HostRep, HostDyn, HostDisp, HostImpact
4. The strategy can assess whether competition or natural enemies might limit establishment and spread.	Pest competitors or natural enemies are never modelled.		Competitors or natural enemies are often modelled.	PestNum, PestEnemies
5. The strategy can predict the effects of phytosanitary measures to limit pest entry on subsequent spread and impacts.	The pest entry process is never modelled (entry points are only initial conditions).	Pest entry is often modelled, but as a simple stochastic process (fixed probability in space and time).	Pest entry processes are often modelled with a model of varying entry probabilities in space and time.	PestEntryTime, PestEntrySp

Fitness criterion	Fitness category			Relevant literature review fields
	Low	Medium	High	
6. The strategy can investigate whether risk reduction options (other than phytosanitary ones) would be effective at preventing establishment or spread.	Control efforts are never explicitly modelled.		Control efforts often explicitly modelled, including scenario experiments.	PestEnemies, PestControl, Model analysis
7. Impact of the pest on crop yield or quality is predicted.	No representation of the affected host plants, so impact cannot be predicted.	The model predicts where host plants are infested by the pest.	The region infested and level of damage to host plants is explicitly modelled.	PestEffects, HostRep, HostDyn
8. Spread rates through ‘natural’ dispersal mechanisms can be predicted.	‘Natural’ dispersal is never modelled.	‘Natural’ dispersal often modelled with a generic approach (e.g. kernel).	‘Natural’ dispersal is often modelled mechanistically (e.g. movement behaviour, water flow).	PestMech
9. Spread rates through human dispersal can be predicted.	Human-mediated dispersal is never modelled.	Human-mediated dispersal often modelled with a generic approach (e.g. kernel).	Human-mediated dispersal is often modelled mechanistically (e.g. trade model, gravity model).	PestMech
10. Spread rates through multiple dispersal mechanisms can be predicted.	Multiple mechanisms never modelled.		Multiple mechanisms are often modelled.	PestMech
11. The strategy can identify the key biological characteristics facilitating pest spread.	Parameters have little direct biological meaning (e.g. parameters of a habitat suitability model).		Parameters are biologically meaningful (e.g. propagule size, individual fecundity).	PestType, HostType, Parameterisation strategy
12. Parameterisation does not strongly depend on data on pest demography or population dynamics.	Large amounts of detailed demographic or population dynamic data needed.	Required information is widely-available (e.g. commonly-measured traits).	No use of demographic or population dynamic data for parameterisation.	PestType, PestDyn, Parameterisation strategy
13. Parameterisation does not strongly depend on pest distribution data.	Detailed pest distribution data in native or invaded range needed.	Coarse pest range maps are used in parameterisation.	No use of distribution data for parameterisation.	Parameterisation strategy

Fitness criterion	Fitness category			Relevant literature review fields
	Low	Medium	High	
14. Parameterisation does not strongly depend on data on pest dispersal.	Detailed pest dispersal data needed.	Dispersal model is based on widely-available information (e.g. commonly-measured traits).	No use of dispersal data for parameterisation.	Parameterisation strategy
15. The strategy is used for multiple pest taxonomic groups.	Application concentrated toward a small number of taxa.		Applied evenly across taxa.	Pest taxonomic group
16. The strategy is used for multiple pest functional groups.	Application concentrated toward a small number of functional groups.		Applied evenly across functional groups.	Pest functional group
17. The strategy is used for multiple host plant functional groups.	Application concentrated toward a small number of host functional groups.		Applied evenly across host functional groups.	Host functional group
18. The strategy is used across multiple sectors.	Application concentrated toward a small number of sectors.		Applied evenly across sectors.	Sector
19. Possibility of model application using existing software, assuming data and parameters are not limiting.	No software or model code is available. The model must be coded from the description in the paper.	Software is not available, but model algorithms are fully described (e.g. published online with the paper).	Specific model software is available that allows relatively straightforward application, regardless of the complexity of the model.	

10. Methodology for the fitness evaluation

The fitness of each modelling strategy to meet each fitness criterion was scored on a 3-point scale corresponding to low, medium or high fitness for each criterion (Table 12). The evaluation operated at the level of the modelling strategy, rather than the individual models within a strategy. However, information on individual models stored within the electronic model inventory was used to make our judgement on fitness of the strategies. To produce our overall score, we considered two sources of information: (1) examination of representative models from each cluster, and (2) evidence about each strategy already collected during the extensive literature review and model clustering as presented in Tables 9 and 10.

To examine representative models, the ten models with the highest assignment probabilities for each cluster were selected (Figure 12, see Appendix G). The advantage of re-examining a representative subset of models is that it reduced the effect of unusual models in the cluster and maximises the separation between the strategies (Figure 12). This means that fitness differences among the model strategies would be enhanced. The selected papers were re-read and individually scored for the fitness criteria in Table 12 by three independent reviewers, whose scores were then combined.

Because the criteria were developed for whole clusters, not all criteria apply directly to the individual models. This is very clearly the case for criteria 15-18, which could not be evaluated at all for individual models and so were omitted from the scoring of the representative models. For the other criteria, we assessed the fitness of the individual models and then summarised that across the cluster. When scoring individual models for criteria with no explicitly stated 'medium' category in Table 12, only high or low categories were assigned to the individual studies.

Evidence on model properties and their usage collected from the extensive literature review and model clustering was also useful in assessing the fitness criteria for each strategy. Table 12 defines the relevant clustering and usage fields (abbreviated as in Tables 5 and 6). Each of these fields was given a binary score for all models in the database, and so the percentages of models scored in the desired way are reported.

Criteria 15-18 examine whether the models are applied evenly across pest taxa, pest functional groups, host functional groups and economic sectors. To assess and compare this for the modelling clusters, we calculated an index of the divergence of each cluster from the overall pattern of application across the whole database. To ensure that the index was comparable across clusters with different numbers of studies, we used the Kullback-Leibler divergence (Morton et al., 2011), or classical relative entropy. The divergence for cluster k, D_k, is calculated as,

$$D_k = \sum_i \begin{cases} P_{k,i} \log_2 \left(\dfrac{P_{k,i}}{P_{all,i}} \right) \text{ if } P_{k,i} > 0 \\ 0 \text{ if } P_{k,i} = 0 \end{cases}$$

where $P_{k,i}$ is the proportion of models in cluster k assigned to category i (e.g. the categories of taxa, functional group or sector) and $P_{all,i}$ is the proportion of all models in the database assigned to category i. The divergence measure relies on the fact that $\sum_i P_{k,i} = 1$ and $\sum_i P_{all,i} = 1$. Lower values of D_k show that that cluster is applied more evenly across taxa, functional group or sector. Before calculating Kullback-Leibler divergences, we removed the categories of "generic" or "unspecified" taxa or functional group from the data. This ensured that we assessed the evenness of model application only where it was clearly stated.

A potential issue with the use of the divergence statistic is that commoner categories may appear more even because they make a greater contribution to P_{all}. For example, if one of the clusters represented 90% of the models, then P_k and P_{all} would necessarily be very similar and the very common cluster would appear evenly applied. However, we do not consider this to be a significant issue for our comparison because the most common cluster (Cluster G) accounted for only 22% of all models (Table 8).

The assessment was principally based upon the actual formulation and uses of the model strategies, drawing on the evidence above. However, where relevant we also considered whether there is unused potential for the strategies to meet the criteria. For example, Table 9 shows that only 9.4% of the reviewed models included multiple pest entry events in time (PestEntryTime). However, four of the clusters almost never modelled multiple pest entry, while the other four included it in 13-17% of models. Therefore the latter four clusters clearly have potential to model entry, despite it generally being omitted. We adjusted the fitness scores for these criteria accordingly for these strategies. The former four clusters may have some general features that prevent multiple entries being modelled and we therefore expect to score them as having low fitness for modelling pest entry.

Assigning the scores was a somewhat subjective process in which we aimed to find as natural a division of the Clusters as possible. We did not consider it would be possible to make the scoring more objective, e.g. by using fixed thresholds for the proportions of studies classed as high. This is because the decisions about each fitness criterion were based upon multiple considerations from the literature review and examination of the representative models. There was no obvious way to standardise comparisons across the criteria or their component considerations.

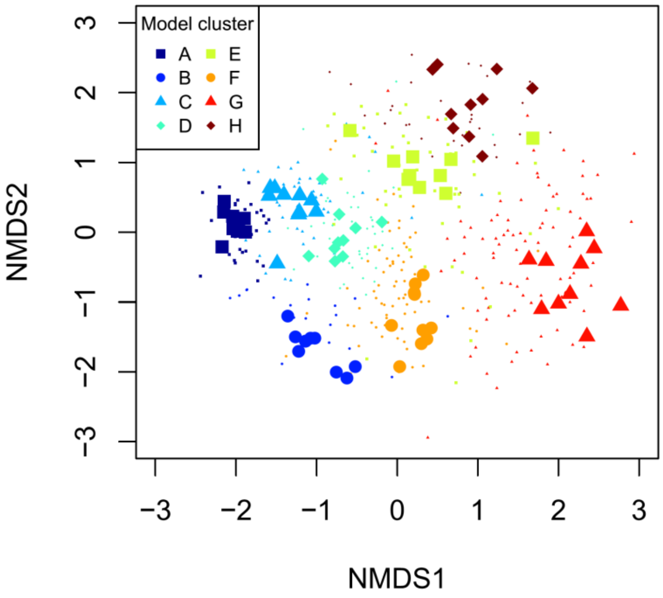

Figure 12: Illustration of the selection of ten representative models from each cluster for detailed scoring of the fitness criteria. The models are arranged in two-dimensional space using nonmetric multidimensional scaling (NMDS) on the Euclidean distance between clustering variables, as shown in Figure 5b. The large points show the positions of the ten selected models per cluster that had the highest assignment probabilities in the model-based clustering.

11. Results of the fitness evaluation

The scorings for each criterion are detailed in the sections below and summarised in Table 13. Values are given in orange if indicating higher fitness than the row median and blue otherwise. Footnotes are given to justify particular scoring decisions, where we considered this to be useful. Note that where a modelling activity is relatively rare, the representative models did not always capture that activity (as the association with a rare activity reduced the certainty of clustering). This caused occasional discrepancies between the evidence from the representative models and the literature review.

Criterion 1. Rate and extent of pest spread over the whole risk assessment area (the EU) can be predicted or hindcasted.

Evidence	**Cluster**							
	A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
Representative models								
% scored Low	**90**	**37**	**93**	**73**	**97**	**33**	**60**	**87**
% scored High	**10**	**63**	**7**	**27**	**3**	**67**	**40**	**13**
Literature review								
% at large scale (SpExt)	**15**	**90**	**23**	**44**	**11**	**84**	**66**	**29**
% with >1 dimension (SpDim)	**47**	**100**	**58**	**51**	**95**	**99**	**91**	**90**
% over multiple seasons (TimeExt)	**0**	**0**	**58**	**89**	**18**	**89**	**84**	**76**
Fitness rating (L=low, M=medium, H=high)	**L**	**M** (a)	**L**	**L**	**L**	**H**	**H**	**L**

(a): M instead of H because Cluster B models wind dispersal events within a single season. Therefore it is useful for EU-scale risk assessment only when the pest can disperse over the whole EU in a single year.

Criterion 2. The strategy can predict where environmental conditions are suitable for pest establishment and spread.

Evidence	**Cluster**							
	A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
Representative models								
% scored Low	**70**	**17**	**87**	**67**	**83**	**10**	**40**	**73**
% scored Medium	**23**	**13**	**3**	**10**	**7**	**67**	**43**	**13**
% scored High	**7**	**70**	**10**	**23**	**10**	**23**	**17**	**13**
Literature review								
% with landscape heterogeneity (SpHet)	**9**	**90**	**26**	**7**	**13**	**80**	**58**	**14**
% with >1 dimension (SpDim)	**47**	**100**	**58**	**51**	**95**	**99**	**91**	**90**
% with temporal forcing (TimeHet)	**2**	**93**	**11**	**25**	**16**	**35**	**36**	**5**
% reporting abiotic scenarios (Model Analysis)	**11**	**38**	**19**	**18**	**5**	**12**	**12**	**5**
Fitness rating (L=low, M=medium, H=high)	**L**	**M** (a)	**L**	**L**	**L**	**H**	**H**	**L**

(a): M because although atmospheric heterogeneity through the dispersal process is strongly represented, this will not necessarily show where the pest can or cannot establish.

Criterion 3. The strategy can predict where the availability of host plants permits pest establishment and spread. (For invasive plants, 'host plants' are the invadable native communities.)

Evidence	**Cluster**							
	A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
Representative models								
% scored Low	**63**	**60**	**87**	**80**	**27**	**60**	**30**	**23**
% scored Medium	**33**	**33**	**7**	**17**	**53**	**23**	**23**	**20**
% scored High	**3**	**7**	**7**	**3**	**20**	**17**	**47**	**57**
Literature review								
% representing hosts in model (HostRep)	**2**	**17**	**13**	**8**	**95**	**9**	**100**	**100**
% with host dynamics (HostDyn)	**0**	**0**	**4**	**3**	**15**	**2**	**67**	**98**
% with host dispersal (HostDisp)	**0**	**0**	**0**	**0**	**0**	**1**	**13**	**50**
% modelling impact on hosts (HostImpact)	**0**	**0**	**2**	**3**	**15**	**2**	**51**	**93**
Fitness rating (L=low, M=medium, H=high)	**L**	**L**	**L**	**L**	**M** (a)	**L**	**H**	**H**

(a): M because the host plant dynamics are rarely modelled.

Criterion 4. The strategy can assess whether competition or natural enemies might limit establishment and spread.

Evidence	**Cluster**							
	A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
Representative models								
% scored Low	**100**	**97**	**80**	**93**	**97**	**97**	**97**	**73**
% scored High	**0**	**3**	**20**	**7**	**3**	**3**	**3**	**27**
Literature review								
% with multiple interacting pests (PestNum)	**0**	**0**	**0**	**2**	**8**	**1**	**5**	**7**
% with pest natural enemies (PestEnemies)	**2**	**0**	**13**	**8**	**2**	**6**	**11**	**12**
% with multiple pests and/or natural enemies (PestNum and/or PestEnemies)	**2**	**0**	**13**	**10**	**8**	**7**	**16**	**19**
Fitness rating (L=low, M=medium, H=high)	**L**	**L**	**H** (a)	**M** (b)	**M** (b)	**L**	**M** (b)	**H** (a)

(a): H because high representation in representative studies show that these clusters have the highest potential for meeting the criteria.

(b): M because a relatively high proportion model competitors or natural enemies of the pest, despite this being rare among the ten most representative models.

Criterion 5. The strategy can predict the effects of phytosanitary measures to limit pest entry on subsequent spread and impacts.

Evidence	**Cluster**							
	A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
Representative models								
% scored Low	**93**	**90**	**100**	**93**	**83**	**93**	**80**	**77**
% scored Medium	**3**	**0**	**0**	**7**	**10**	**3**	**13**	**20**
% scored High	**3**	**10**	**0**	**0**	**7**	**3**	**7**	**3**
Literature review								
% with multiple pest entry in time (PestEntryTime)	**2**	**17**	**2**	**3**	**13**	**5**	**17**	**17**
% with multiple pest entry in space (PestEntrySp)	**2**	**48**	**11**	**15**	**44**	**60**	**58**	**60**
% with multiple pest entry in time and space (PestEntryTime and PestEntrySp)	**2**	**14**	**2**	**0**	**13**	**5**	**17**	**17**
Fitness rating (L=low, M=medium, H=high)	**L**	**L** (a)	**L**	**L**	**M** (b)	**M** (c)	**M** (b)	**M** (b)

(a): L because generally only dispersal by a natural mechanism is modelled.

(b): M because multiple entry is generally modelled as a simple stochastic process.

(c): M because the high representation of multiple entry in space means there is potential to model multiple entry in time, even if this is rarely done in in the representative models.

Criterion 6. The strategy can investigate whether risk reduction options (other than phytosanitary ones) would be effective at preventing establishment or spread.

Evidence	**Cluster**							
	A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
Representative models								
% scored Low	97	93	90	87	87	83	53	90
% scored High	3	7	10	13	13	17	47	10
Literature review								
% with pest natural enemies (Pest Enemies)	2	0	13	8	2	6	11	12
% with pest control measures modelled (PestControl)	4	3	13	23	8	35	45	29
% with risk reduction scenarios (Model Analysis)	11	7	21	33	20	44	58	31
Fitness rating (L=low, M=medium, H=high)	**L**	**L**	**M** (a)	**M** (a)	**L**	**H**	**H**	**M** (a)

(a): M because of potential to model pest control, even though it is rarely done in the representative models.

Criterion 7. Impact of the pest on crop yield or quality is predicted.

Evidence	**Cluster**							
	A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
Representative models								
% scored Low	60	57	73	60	37	40	27	10
% scored Medium	37	40	20	33	50	50	33	53
% scored High	3	3	7	7	13	10	40	37
Literature review								
% representing host plants (HostRep)	2	17	13	8	95	9	100	100
% modelling impact on hosts (PestEffects)	0	0	2	3	15	2	51	93
% with host dynamics (HostDyn)	0	0	4	3	15	2	67	98
Fitness rating (L=low, M=medium, H=high)	**L**	**M** (a)	**L**	**L** (b)	**M** (a)	**M** (a)	**H**	**H**

(a): M because models predict the areas infested by the pest, even though host plant impacts are not explicitly modelled within the infested area.
(b): L because although the population spread is generally modelled, it is usually in abstract space.

Criterion 8. Spread rates through ‘natural’ dispersal mechanisms can be predicted.

Evidence	**Cluster**							
	A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
Representative models								
% scored Low	3	7	13	3	10	13	10	27
% scored Medium	67	27	23	57	73	57	57	43
% scored High	30	67	63	40	17	30	33	30
Literature review								
% modelling ‘natural’ dispersal mechanisms (PestMech)	94	100	100	95	93	89	98	98
Fitness rating (L=low, M=medium, H=high)	**M** (a)	**H**	**H**	**M** (a)	**M (a)**	**M** (a)	**M** (a)	**M** (a)

(a): M because these mainly use non-mechanistic dispersal kernels. A caveat is when the kernel is derived from mechanistic models (e.g. the WALD kernel for wind dispersed seeds (Katul et al., 2005).

Criterion 9. Spread rates through human dispersal can be predicted.

Evidence	**Cluster**							
	A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
Representative models								
% scored Low	93	97	93	93	87	53	77	100
% scored Medium	7	3	3	7	10	17	13	0
% scored High	0	0	3	0	3	30	10	0
Literature review								
% modelling human dispersal mechanisms (PestMech)	6	0	6	13	7	26	16	2
Fitness rating (L=low, M=medium, H=high)	**L**	**L**	**L**	**M** (a)	**L**	**H** (b)	**M**	**L**

(a): M because it had a high representation of human dispersal across the cluster, even if not within the ten re-examined models.

(b): H because highest potential for modelling human-mediated pest dispersal.

Criterion 10. Spread rates through multiple dispersal mechanisms can be predicted.

Evidence	**Cluster**							
	A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
Representative models								
% scored Low	93	90	83	87	77	53	77	97
% scored High	7	10	17	13	23	47	23	3
Literature review								
% modelling multiple dispersal mechanisms (PestMech)	4	34	25	18	18	43	29	5
Fitness rating (L=low, M=medium, H=high)	**L**	**M** (a)	**M**	**L**	**M**	**H**	**M**	**L**

(a): M because many models feature multiple dispersal mechanisms, even if rare among the representative models.

Criterion 11. The strategy can identify the key biological characteristics facilitating pest spread.

Evidence	**Cluster**							
	A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
Representative models								
% scored Low	50	57	30	20	63	50	13	27
% scored High	50	43	70	80	37	50	87	73
Literature review								
% modelling a specific pest (PestType)	83	79	60	80	46	78	99	7
% modelling a specific host (HostType)	0	0	0	0	20	0	91	0
% using empirically determined parameters (Parameterisation strategy)	34	72	45	57	23	54	72	12
Fitness rating (L=low, M=medium, H=high)	**M**	**M**	**H**	**H**	**L**	**M**	**H**	**H**

Criterion 12. Parameterisation does not strongly depend on data on pest demography or population dynamics.

Evidence	**Cluster**							
	A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
Representative models								
% scored Low	13	17	20	47	27	20	47	13
% scored Medium	23	17	17	33	3	27	27	20
% scored High	63	67	63	20	70	53	27	67
Literature review								
% for generic pest species (PestType)	57	59	75	57	75	41	9	100
% with no pest population dynamics (PestDyn)	94	97	34	13	49	18	17	5
% not using empirical parameterisation (Parameterisation strategy)	66	28	55	43	77	46	28	88
% using arbitrary parameterisation (Parameterisation strategy)	9	28	43	39	61	37	21	90
Fitness rating (L=low, M=medium, H=high)	**H**	**H**	**L** (a)	**L**	**H**	**M** (b)	**L**	**H**

(a): L because Cluster C contains a mixture of about ≈ 30% dispersal-only models (which do not require pest dynamics parameters) and ≈ 70% population spread models (which do require dynamics parameters). The sample of models examined contained 80% dispersal-only models so gives a misleading impression of parameterisation needs.

(a): M because not as highly scoring as the other H clusters, and because of strong similarity to Cluster G.

Criterion 13. Parameterisation does not strongly depend on pest distribution data.

Evidence	**Cluster**							
	A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
Representative models								
% scored Low	20	27	7	10	40	53	20	7
% scored Medium	17	3	0	7	3	7	13	3
% scored High	63	70	93	83	57	40	67	90
Literature review								
% not fitted to spread or dispersal patterns (Parameterisation strategy)	30	83	68	70	69	63	76	95
% using arbitrary parameterisation (Parameterisation strategy)	9	28	43	39	61	37	21	90
Fitness rating (L=low, M=medium, H=high)	**M** (a)	**H** (b)	**H**	**H**	**M** (a)	**L**	**M** (a)	**H**

(a): M because not as highly scoring as the other H clusters

(b): H because the models are rarely fitted to distribution patterns.

Criterion 14. Parameterisation does not strongly depend on data on pest dispersal.

Evidence	Cluster							
	A	B	C	D	E	F	G	H
Representative models								
% scored Low	47	40	60	43	23	33	40	3
% scored Medium	27	7	3	20	10	27	37	17
% scored High	27	53	37	37	67	40	23	80
Literature review								
% not fitted to spread or dispersal patterns (Parameterisation strategy)	30	83	68	70	69	63	76	95
% using arbitrary parameterisation (Parameterisation strategy)	9	28	43	39	61	37	21	90
Fitness rating (L=low, M=medium, H=high)	**L**	**H** (a)	**L**	**L**	**H**	**M**	**L**	**H**

(a): H because the models are generally based on dispersal traits rather than data on dispersal distances (so they are very rarely fitted).

Criterion 15. The strategy is used for multiple pest taxonomic groups.

Evidence	Cluster							
	A	B	C	D	E	F	G	H
Literature review								
Kullback-Leibler divergence between observed proportions and null expected proportions, excluding the generic category	0.36	0.5	0.17	0.2	0.74	0.62	0.18	0.42
Fitness rating (L=low, M=medium, H=high)	**M**	**L**	**H**	**H**	**L**	**L**	**H**	**M**

(a): M because very rarely applied to plants (so χ^2 is high) even though it can be generically applied across other groups.

Criterion 16. The strategy is used for multiple pest functional groups.

Evidence	Cluster							
	A	B	C	D	E	F	G	H
Literature review								
Kullback-Leibler divergence between observed proportions and null expected proportions, excluding the generic category	0.17	0.48	0.05	0.19	0.89	0.53	0.15	0.29
Fitness rating (L=low, M=medium, H=high)	**M**	**L**	**H**	**M**	**L**	**L**	**M**	**L**

Criterion 17. The strategy is used for multiple host plant functional groups.

Evidence	Cluster							
	A	B	C	D	E	F	G	H
Literature review								
Kullback-Leibler divergence between observed proportions and null expected proportions, excluding the generic and unspecified categories	0.17	0.06	0.02	0	0.09	0.13	0.01	0.22
Fitness rating (L=low, M=medium, H=high)	**L**	**M**	**H**	**H**	**M**	**L**	**H**	**L**

Criterion 18. The strategy is used across multiple sectors.

Evidence	Cluster							
	A	B	C	D	E	F	G	H
Literature review								
Kullback-Leibler divergence between observed proportions and null expected proportions	0.24	0.16	0.07	0.01	0.12	0.21	0.15	0.22
Fitness rating (L=low, M=medium, H=high)	**L**	**M**	**H**	**H**	**M**	**L**	**M**	**L**

Criterion 19. Possibility of model application using existing software, assuming data and parameters are not limiting.

Evidence	Cluster							
	A	B	C	D	E	F	G	H
Representative models								
% scored Low	97	60	100	87	93	67	67	93
% scored Medium	0	0	0	3	0	13	17	3
% scored High	3	40	0	10	7	20	17	3
Fitness rating (L=low, M=medium, H=high)	**L**	**H**	**L**	**L**	**L**	**M**	**L** (a)	**L**

(a): L because although named model software is available for some of the models, the models are so specific and detailed that the chance of using the software for another pest is low.

Table 13: Summary of fitness scores given to each cluster and criteria (L=low, M=medium, H=high). are ordered according to our revised scheme, as described in the Introduction and Objectives section.

Fitness criterion	**Cluster**							
	A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
1. Rate and extent of pest spread over the whole risk assessment area (the EU) can be predicted or hindcasted.	L	M	L	L	L	H	H	L
2. The strategy can predict where environmental conditions are suitable for pest establishment and spread.	L	M	L	L	L	H	H	L
3. The strategy can predict where the availability of host plants permits pest establishment and spread. (For invasive plants, 'host plants' are the invadable native communities.)	L	L	L	L	M	L	H	H
4. The strategy can assess whether competition or natural enemies might limit establishment and spread.	L	L	H	M	M	L	M	H
5. The strategy can predict the effects of phytosanitary measures to limit pest entry on subsequent spread and impacts.	L	L	L	L	M	M	M	M
6. The strategy can investigate whether risk reduction options (other than phytosanitary ones) would be effective at preventing establishment or spread.	L	L	M	M	L	H	H	M
7. Impact of the pest on crop yield or quality is predicted.	L	M	L	L	M	M	H	H
8. Spread rates through 'natural' dispersal mechanisms can be predicted.	M	H	H	M	M	M	M	M
9. Spread rates through human dispersal can be predicted.	L	L	L	M	L	H	M	L
10. Spread rates through multiple dispersal mechanisms can be predicted.	L	M	M	L	M	H	M	L
11. The strategy can identify the key biological characteristics facilitating pest spread.	M	M	H	H	L	M	H	H
12. Parameterisation does not strongly depend on data on pest demography or population dynamics.	H	H	L	L	H	M	L	H
13. Parameterisation does not strongly depend on pest distribution data.	M	H	H	H	M	L	M	H
14. Parameterisation does not strongly depend on data on pest dispersal.	L	H	L	L	H	M	L	H
15. The strategy is used for multiple pest taxonomic groups.	M	L	H	H	L	L	H	M
16. The strategy is used for multiple pest functional groups.	M	L	H	M	L	L	M	L
17. The strategy is used for multiple host plant functional groups.	L	M	H	H	M	L	H	L
18. The strategy is used across multiple sectors.	L	M	H	H	M	L	M	L
19. Possibility of model application using existing software, assuming data and parameters are not limiting.	L	H	L	L	L	M	L	L
Total number of Low scores	13	6	9	9	8	7	3	8
Total number of Medium scores	5	8	2	5	9	7	8	4
Total number of High scores	1	5	8	5	2	5	8	7

12. Pros and cons of the model strategies

In the following section, we synthesise the data presenting in Table 13, to appraise the advantages and disadvantages associated with using each of the model strategies in Plant Health risk assessment. In particular, we focus on the ways in which the models may provide evidence to EFSA answer risk assessment questions (EFSA Panel on Plant Health (PLH), 2010a) and the potential barriers to applying the models. Statements about model usage refer to percentages given above and in Tables 9 and 10.

12.1. Cluster A: Single-event pest dispersal

The major advantage of Cluster A is its simplicity. These models are dispersal kernels or disease gradients, representing the probability distribution for dispersal or disease spread over different distances over a fixed period of time. They typically feature a single, relatively simple equation with only a small number of parameters. However, our scoring revealed that the extreme simplicity of these models made them the least suited to risk assessment tasks. Cluster A had the fewest number of High scores and greatest number of Low scores across the fitness criteria (Table 13).

In the main, Cluster A models represent spread at small spatial scales, have no temporal population dynamics or interactions among pest or host species. They also do not capture environmental heterogeneity in space or time. The positive side of this is that detailed biological knowledge about the pest (beyond its dispersal traits or distances) is not needed. However, the negative side is that the models are of little use for risk assessment tasks such as predicting spread across the heterogeneous environment of the EU or modelling pest impacts and risk reduction measures.

In most cases Cluster A models are applied to ‘natural’ rather than human-mediated dispersal mechanisms. In some cases the kernels are derived mechanistically for a particular dispersal mechanism and can be parameterised from common traits. Mainly this has been done for wind dispersal, as in the WALD dispersal kernel (e.g. Stephenson et al., 2007; Skarpaas et al., 2011) and the Gaussian Plume Model (e.g. EFSA Panel on Plant Health (PLH), 2011). These predict the distribution of dispersal distances from an interaction between propagule traits (e.g. terminal velocity and release height) and local environmental conditions (e.g. wind and land surface properties). This approach is potentially useful for determining the most suitable environments and biological characteristics for dispersal and therefore potentially spread of the pest, although this was not usually done.

However, in most cases Cluster A models are more phenomenological, i.e. 70% of models fit generic functions to describe the decay in dispersal probability with increasing distance to empirical data (e.g. Blenis et al., 1993). One drawback with this is that it is difficult to transfer the fitted dispersal pattern in space or time for prediction of spread. This is perhaps especially so for dispersal mechanisms relying on abiotic conditions such as the wind that vary strongly. For example, anisotropic two-dimensional kernels can capture preferential dispersal in the direction of the prevailing wind very well for a particular location (e.g. Paulitz et al., 1999) but the model may be of little predictive value outside of the location where it was fitted if the direction and strength of the wind differ.

We consider that the principal way in which models from Cluster A could be used in risk assessment is to estimate the likely zone of dispersal from points of current pest outbreak. This is potentially useful for indicating the risk of spread over single dispersal event (e.g. a single growing season) at relatively local scales. For example a kernel derived from the Gaussian Plume Model for particle dispersion on prevailing winds was used to estimate that conidia of the fungus *Monilinia fructicola* are virtually all are deposited within 500 m of an infected source tree (EFSA Panel on Plant Health (PLH), 2011).

12.2. Cluster B: Large-scale simulation of pest dispersal events

Models in Cluster B mainly represent wind dispersal events at large spatial scales. Because of this restriction to wind dispersal, Cluster B is not very useful in risk assessment for human-dispersed pests and is not very evenly applied across pest groups. Indeed these models are largely used for fungal crop diseases and migrating insect crop pests (see Table 10).

Wind dispersal is simulated using atmospheric models to replicate the passage and deposition of dispersing propagules. The simplest of these use numerical weather prediction models to estimate the forward trajectories of airflows from pest source locations or backward air trajectories from locations where the pests have been detected (e.g. Hopkinson and Soroka, 2010). The aim is to estimate where the pest might disperse to or where it might have dispersed from. Essentially no biological information is required for these trajectory analyses, which might be seen as advantageous. However, this also means they are of no use for determining the biological characteristics promoting pest spread.

The more complex models in Cluster B couple the outputs of numerical weather prediction models to models for the transport and deposition of particles in the airflow (e.g. Isard et al., 2007; Aylor et al., 2011). Furthermore, in some models for wind-assisted insect dispersal, aspects of the insects' flight behaviour are modelled alongside the atmospheric transport. For example, Leskinen et al. (2011) used specific insect flight take-off times in their transport model and Furuno et al. (2005) incorporated more complex flight behaviours such as the insects stopping actively hovering when the temperature falls below 16.5 °C. A key advantage of these is that simulated dispersal is strongly dependent on biological traits such as propagule release heights and terminal velocities. This subset of models within Cluster B can therefore be considered to have high ability to identify the biological characteristics promoting pest spread. This is despite our judgement across the whole cluster being for medium fitness because of the non-biological trajectory models mentioned above. Since the key traits of these models are generally simple to measure or estimate, we scored Cluster B as not being strongly limited by data availability.

Because models in Cluster B rely on numerical weather prediction, they nearly always capture the effects of spatial and temporal heterogeneity in the atmospheric environment on dispersal. However, we considered that this only gave medium fitness for predicting where environmental conditions favour pest establishment and spread. Although Cluster B is useful for showing where pests might or might not disperse to, establishment success is more likely to be determined by pest population dynamics and habitat conditions at the land surface. These are generally not represented in the models in Cluster B (e.g. 97% have no pest dynamics). An exception might occur if the models could identify areas where wind patterns mean immigration of the pest is very unlikely such that dispersal constrains establishment.

As with Cluster A, the lack of pest dynamics within Cluster B confers disadvantages such as low suitability for modelling pest impacts or interactions with other species. Furthermore, because large-scale wind dispersal is effectively outside of human control, Cluster B has low ability to investigate risk reduction options including phytosanitary actions.

A key advantage of this cluster is that many of these models have published software, for example HYSPLIT4 (Draxler et al., 1999; http://ready.arl.noaa.gov/HYSPLIT.php) or SILAM (Beaumont, 2010; http://silam.fmi.fi/). However, using the software will generally require expertise in atmospheric science.

In our opinion the most useful role for Cluster B models in pest risk assessment would be to estimate dispersal and deposition patterns of propagules from a newly established wind-dispersed pest from a small number of entry points. As with Cluster A, this would inform on the likely zone of dispersal from the current pest outbreak, but results from Cluster B are more likely to show dispersal at landscape scales. It could also be possible to use climate change scenario outputs from the weather prediction models to determine whether or not the pest is likely to become more or less dispersive in future conditions.

12.3. Cluster C: Pest spread or dispersal in continuous space and time

Cluster C contains models such as diffusion and reaction-diffusion where a pest population either disperses (diffusion) or spreads (reaction-diffusion) in a continuous representation of space and time. These models are highly mathematical and abstract representations of pest invasions using partial differential equations (PDEs). These comprise a function depicting the pest population density across space, whose instantaneous rate of change in time is characterised. A disadvantage of this is that significant mathematical expertise is therefore required to apply the models.

However, an advantage is that these mathematical frameworks are based on well-known equations derived from an established body of research in theoretical ecology (Skellam, 1951; Truscott and Ferguson, 2012). As such, the models can be clearly communicated and used across many different species. Indeed we found that Cluster C was among the most evenly applied across taxa, functional groups and sectors. Moreover, the equations underlying dispersal and spread are well known, thoroughly investigated and have standardised frameworks for analysis. The well-developed theory provides the tools to calculate important quantities such as the rate of pest spread.

Some of the dispersal-only diffusion models allow extension of the basic theory to include particularities of pest movement behaviour. For example, Tyson et al. (2011) present a model where the pest population comprises a subpopulation moving by pure diffusion and a subpopulation moving by advection (i.e. carried by a flow of air or water). It is suggested that this model can produce more realistic movement patterns than models of a homogeneous population. Because of this mechanistic representation of dispersal as a diffusion process, we scored Cluster C highly for ability to represent natural dispersal. However, we scored it low for human-mediated dispersal because human behaviour is often expected to deviate from simple random diffusion and only 6% of models in Cluster C refer to human-dispersal.

However, the basic and most commonly applied form of the population spread reaction-diffusion models are restricted to simple diffusive movement, resulting in a constant rate of population expansion and linear increase in the radius of the invaded area over time. This may be seen as a disadvantage because it does not accommodate the leptokurtic or ‘fat-tailed’ dispersal patterns characteristic of many species. Therefore pest spread promoted by rare long-distance dispersal may be poorly represented by Cluster C.

There are also well-developed mathematical methods for identifying the model parameters most important for governing pest spread in the reaction-diffusion equations. For simple models, with low levels of non-linearity, it is often possible to conduct mathematical analysis of the long-term behaviour of the model, such as steady state calculations, stability analysis, asymptotic techniques and wavespeed calculations. These analyses give explicit relationships between the biological parameter values and the model behaviour, and so are powerful highly mathematical tools for ecological theory. For example, analysis of the basic model shows that the spread rate depends on the diffusion rate and maximum population growth rate (Truscott and Ferguson, 2012). However, for more complex non-linear models, solutions to the model’s partial differential equations are calculated via simulation, where a broader set of parameter values is required.

Since the model parameters have direct biological meaning, we considered Cluster C to have high fitness for identifying the biological characteristics facilitating spread. However, despite their direct meaning these parameters may not be straightforward to estimate when applying the models to a particular species. Therefore we considered that application of Cluster C was disadvantaged by a reliance on biological knowledge about dynamics and dispersal.

To aid mathematical tractability, models in Cluster C often represent space in one dimension (42% of models), usually ignore environmental heterogeneity (74% with a uniform environment, 89% with a static environment) and rarely explicitly represent landscape-scale spread (23% at large scale). Because of this abstract spatial representation, we scored Cluster C as having low fitness for assessing spread at EU-scales and predicting how environmental heterogeneity affects spread. This also meant we considered Cluster C to have limited potential for modelling the effect of phytosanitary measures. Most of the models initiate spread from a single entry point in space (89%) and time (98%).

A further disadvantage of this cluster is a lack of representation of host plant dynamics affecting spread of the pest. 87% of Cluster C's constituent models had no representation of the host plant, and 98% had no representation of its dynamics. For this reason, we scored Cluster C low for showing where host plants limit pest spread or for predicting yield losses to the pests. By contrast the effects of natural enemies on pest spread are relatively well represented in this cluster (e.g. Harrison et al., 2005). As such, we scored it as highly for showing where competition or natural enemies might limit spread and for modelling biocontrol.

Because Cluster C models are quite abstract, we suggest their most appropriate use in risk assessment would be to ask fairly general questions. For example, the diffusion models may be used similarly to the other dispersal-only models in Clusters A and B to determine the likely range of dispersal in a single year or dispersal period. Similarly, the reaction-diffusion model could be parameterised for the focal pest to estimate the rate at which it might spread. The reaction-diffusion models could also be used for estimating the potential of biocontrol to limit spread of the pest. After parameterising the model for the focal pest, one could add a generic natural enemy to the model (e.g. Harrison et al., 2005) and investigate the properties that the enemy would need to have in order to limit the spread of the pest.

12.4. Cluster D: Continuous-space pest spread in discrete time

All but one of the ten representative models for Cluster D were integro-difference equation (IDE) models (Kot et al., 1996) and so our discussion here concentrates on that modelling framework. In overview, IDEs couple a discrete-time population dynamics model to a dispersal kernel. IDEs predict spread by representing population density over continuous space and how this changes in discrete time steps because of local population growth and redistribution (Kot et al., 1996). IDEs are firmly rooted in ecological theory and have been informed by the earlier theoretical development of reaction-diffusion models (Cluster C). It could be that because of this historical sequential dependency, our fitness scoring for Cluster D was very similar to the scoring for Cluster C (Table 13).

An advantage that IDEs have over reaction-diffusion (Cluster C) is that the dispersal kernel can accommodate rare long-distance dispersal through use of a leptokurtic function. In these cases, the pest may not spread at a constant rate, but might accelerate its invasion over time (Kot et al., 1996). Therefore the ability to represent both constant and accelerating pest invasions should be seen as an advantage of Cluster D. Furthermore, the chosen dispersal kernel can take on a range of different forms that are straightforwardly fitted to dispersal data or derived mechanistically (such as for wind – see discussion for Cluster A). Because of this flexibility, and the fact that a comparatively high 13% of the models in Cluster D referred to human dispersal, we scored the cluster as having a medium ability to represent human dispersal.

The population dynamics model can be chosen as a relatively simple difference equation (e.g. the logistic, Beverton-Holt or Ricker models; Kot et al., 1996). Alternatively the population dynamics can be modelled using a stage-structured population matrix, which contains values for age or stage-specific fecundity, survival and transitions between stages (Beaumont, 2010). Examples where the structured IDEs are used for modelling invasive plant spread can be found in Bullock et al. (2012) and Caplat et al. (2012). A particular advantage of the latter approach is that it is firmly based in biologically-meaningful and measurable demographic parameters, which for many species may be found in the literature. Also, standard mathematical methods are available to estimate the dependence of spread rates on each of the model parameters. For example, elasticity analysis of the structured IDEs characterises the change in spread rate for a small change in each demographic and dispersal parameter (Beaumont, 2010). Based on this, and the above discussion on dispersal kernels, we judged Cluster D to have high fitness for identifying the pest characteristics important for spread, but of course the corollary of this that Cluster D models are highly reliant on data on pest demography or population dynamics and dispersal.

As with Cluster C, many applications of IDEs use quite abstract spatial representations. Cluster D has 49% of models in one spatial dimension, 93% uniform in space and 75% uniform in time. In none of the reviewed studies was pest spread modelled with multiple entry events in space and time. Furthermore host plant dynamics are generally not represented (92% have no host representation). Therefore, we scored Cluster D as not being very suitable for estimating effects of environmental and host plant variation on spread, yield impacts or effectiveness of phytosanitary measures.

However, IDEs do have interesting potential for investigating control of invasive species, evidenced by a comparatively high proportion of reviewed models in Cluster D investigating risk reduction scenarios (33%) or pest natural enemies or competitors (10%). For example, Shea et al. (2010) present a structured IDE for the invasive thistle *Carduus nutans*, which is used to assess the effectiveness of alternative control measures targeting different stages in the species' life cycle. Therefore Cluster D was scored as being of medium fitness for both investigating risk reduction and natural enemy or biocontrol effects on pest spread. A caveat to this, relevant to this discussion, is that of the five models in Cluster D including natural enemies none were actually IDEs (though they shared sufficient properties with them to be grouped into this cluster).

Our conclusion is that models from Cluster D could be used in risk assessment in similar ways to the related reaction-diffusion approaches in Cluster C. However, the fact that the structured IDEs are very firmly based in the demographics of the pest means that an additional usage is to identify the optimal life history stages to target for effective control measures.

12.5. Cluster E: Iterative colonisation of hosts at small scales

Models in Cluster E mainly comprise computer simulations of pest spread between individual host plants at small spatial scales and over a single growing season, often referred to as contact models. Spread is modelled as an iterative process of repeated stochastic colonisation events arising from dispersal into the local neighbourhood of already infected plants. Application is mostly concentrated towards diseases (77% of models), and so Cluster E scored poorly for being evenly applied across pest taxonomic or functional groups.

Overall, Cluster E was one of the lowest rated strategies, receiving only two High scores. Mainly this was because most of the models had very limited spatial and temporal extent, lacked environmental heterogeneity and did not model the dynamics of the host population. However, one advantage of Cluster E is that it uses a simplified and generic representation of the pest. Indeed this is as simple as the presence/absence of the pest on each host plant in 70% of the models. As such, application is not strongly reliant on detailed knowledge of the pest population dynamics. Information on dispersal is clearly needed, but this is generally estimated not with direct observation of dispersal distances, but inferred from the within-field distribution pattern of the disease over time. Often, sophisticated statistical methods are used to fit the models to multiple distribution snapshots (e.g. Marion et al., 2003).

A relatively high proportion of models in Cluster E include both ‘secondary’ spread by localised dispersal around infested host plants and ‘primary’ infestation stochastically arising anywhere in the modelled landscape at a fixed background rate (e.g. Gottwald et al., 1999; Pethybridge and Madden, 2003). To the extent that the primary infestations can be considered to represent multiple entry events, Cluster E was judged to be one of the better groups of models for assessing the effectiveness of phytosanitary measures. However, it should be borne in mind that multiple entry of a pest within the same field is a less likely scenario than multiple entry events occurring over a larger spatial domain.

Models from Cluster E could be used similarly to Cluster A for risk assessment, to predict the spread distance per year or growing season. An advantage of using Cluster E over Cluster A is that the estimate of the range of spread can be made from a more mechanistic perspective. For example, spread patterns arising from non-random foraging movement behaviours of insect vectors can be predicted (e.g. Ferrari et al., 2006; Sisterson, 2008).

12.6. Cluster F: Simulation of specific pest spread at large scales

Cluster F represents computer simulations for single pest species. Most of the models simulate spread over multiple years (89% of models) and large spatial scales (84%). They typically operate over a discrete gridded landscape. Therefore, they are highly suited to inputting gridded climate or land use maps and using these to influence the population dynamics or dispersal of the pest. As a result, we scored Cluster F as having high fitness for predicting spread over the whole risk assessment area. Furthermore a comparatively large proportion of models factored in temporal changes in the landscape (35%) and in some cases this was used for simulations of spread under climate change scenarios (Fennell et al., 2012). Therefore we scored Cluster F as very useful for assessing where the environment permits pest establishment and spread.

Although many of the models in Cluster F use similar design concepts, the algorithms vary considerably from application to application depending on the biological processes affecting spread and the data available. For example, the representation of pests was fairly evenly divided between individuals, populations and occupancies, in contrast to the predomination of a particular representation seen in most other clusters (see Table 9). Therefore, we considered the models in Cluster F to be more specific and *ad hoc* than, for example the more mathematically-oriented and generic models in Clusters C and D. Perhaps because of this, Cluster F was applied more unevenly than the other Clusters. Nearly all the examples in this cluster were for invasive plants and insects, and very few models in this Cluster tackled spread of pathogens.

Models in Cluster F were rated as the most suited to modelling human-assisted dispersal. For example, Niggemann et al. (2009) used sociological data that quantified rates of human movement between a network of settlements to weight dispersal pathways for invasive plant spread. Where such detailed information is not known, gravity models (based on Newton’s Law of Universal Gravitation) are a promising approach to represent human dispersal that are often employed in Cluster F (e.g.Carrasco et al., 2010b; Iverson et al., 2010; Rothlisberger and Lodge, 2011; Stanaway et al., 2011). The basic gravity model specifies that the dispersal rate between two locations decays with distance but also depends on the product of the ‘mass’ of the two locations. To represent human-dispersal, ‘mass’ is replaced with a measure of human usage, such as population density. As a result more dispersal occurs between two ‘massive’ locations (e.g. large towns) than between less ‘massive’ locations. The gravity model can also be used for dispersal of pathogens by insect vectors that actively seek out host plants rather than randomly diffuse. In this case, ‘mass’ is a measure of the host plant attractiveness to the insect (e.g. Ferrari et al., 2006). Rothlisberger and Lodge (2011) present a more complex producer-constrained gravity model for spread of an invasive plant between waterways. This accounts for the density of dispersal vectors (boats) kept in the vicinity of each waterway and the likelihood that boaters prefer to sail on larger waterways.

Cluster F also had the greatest potential for representing multiple dispersal mechanisms, because separate algorithms for different dispersal processes can readily be coded into the simulation models. In the most basic applications, a dispersal kernel for local dispersal is combined with a second dispersal kernel for long-distance dispersal (Peterson et al., 2004; Pitt et al., 2009; Pitt et al., 2011). The long-distance component can be as simple as global dispersal that is independent of distance (Pergl et al., 2011; Hester and Cacho, 2012). More advanced approaches use mechanistic simulation algorithms for the long-distance dispersal. For example, in modelling the spread of *Agrilus planipennis*, Muirhead et al. (2006) combine a basic exponential decay function to represent local diffusion of the insects with a gravity model for long-distance human-mediated dispersal.

Despite this flexibility to include multiple dispersal mechanisms, only a very small minority of models (5%) included multiple pest entry events in time. However, we still scored Cluster F as being of medium suitability for investigating the effectiveness of phytosanitary measures because the flexibility to include multiple dispersal mechanisms means there should be potential to model dispersal through trade. For example, Epanchin-Niell et al. (2012) present a model in which new populations enter from outside the modelled domain randomly in both space and time, which bears strong similarity to the models using global dispersal for long-distance spread (Pergl et al., 2011; Hester and Cacho, 2012).

By contrast, other risk reduction options were relatively commonly modelled within Cluster F, and so we rated it to have high fitness in this regard. As with dispersal, the flexibility of simulation algorithms can simulate the practices of management regimes. For example Richter et al. (2012) compared alternative spatial strategies for targeting eradication effort for the invasive plant *Ambrosia artemisiifolia*. There is also potential to replicate actual management regimes within the algorithms, as was demonstrated by Carrasco et al. (2010a) who compared actual buffer zones and eradication or containment measures for the beetle *Diabrotica virgifera* in use in Europe.

A disadvantage of the models in Cluster F is that they rarely represent host plants (only 9% of models) or other species affecting the pest. As such, we considered Cluster F was not very useful for assessing where host plants, competitors or natural enemies affect spread. Partly this reflects their concentration towards modelling spread of invasive insects and plants based on general habitat characteristics rather than biotic interactions.

Finally, we considered Cluster F to be more reliant on data than many other clusters, especially since the models are commonly fitted to snapshots of the distribution through time (e.g. Cook et al., 2007; Stanaway et al., 2011; Richter et al., 2012). In addition to good data, considerable statistical expertise is required to fit these models.

We consider that there are two major ways in which models in Cluster F could be used in risk assessment. First, simulation of spread from the initial entry to the current distribution and from the current distribution into the future can be used to assess invasion of the risk assessment area and show where the suitable environments occur. Second, the simulations can be used to experiment with risk reduction options, either through phytosanitary action (that prevents pest entry) or other control practices (that target the pest populations or dispersal once it is established).

12.7. Cluster G: Simulation of specific pest and host dynamics

Cluster G had by far the fewest Low scores in our fitness assessment (Table 13) indicating that its constituent models could be applied for most risk assessment tasks. In general, the model properties and representation of the pest organisms in Cluster G were very similar to those of Cluster F (Table 9). Both were highly flexible but species-specific computer simulation approaches. As a result, both clusters were scored fairly similarly (Table 13) and have similar pros and cons.

However, our conclusion was that the models in Cluster G specified more biological detail and complexity than Cluster F. This additional complexity could have two important drawbacks for using Cluster G in risk assessment. First, because the Cluster G models are so specific, it is unlikely that one of the existing models will be directly applicable in a new risk assessment. Second, it may often be difficult to understand exactly how the models were constructed or operate because the simulations typically comprise numerous *ad hoc* algorithms that can be difficult to communicate in a scientific paper.

Following the reasoning for Cluster F, we considered models in Cluster G to be especially suitable for assessing spread across the EU risk assessment area, modelling landscape heterogeneity and experimenting with risk reduction measures. Models in Cluster G often comprised extremely detailed representations of management activities. For example the management algorithms of the model in Lô-Pelzer et al. (2010) detail the sowing density, sowing date, fungicide application, fertiliser use, tillage types and harvesting. In other cases direct management responses to pest infestation such as tree removal and girdling can be directly modelled (Mercader et al., 2011). Therefore realistic risk reduction measures can be simulated for risk assessments.

As with Cluster F, a major disadvantage was a reliance on data. This was even more restricting for Cluster G because of the additional complexity of the simulations and the fact that the models were more likely parameterised from empirical knowledge (72%) than through by fitting model outputs (24%).

A major departure from Cluster F was that in Cluster G 100% of the models had some representation of the host plants (versus 9% in Cluster F). The level to which host plants were represented varied across the cluster. For example, although all models contained some representation, host plant dynamics featured in 67% of the models, while host dispersal was modelled in just 13%. The fact that hosts were represented meant that we scored Cluster G as being highly suitable for assessing impacts of the pest and effects of the host on spread. A second departure from Cluster F was that Cluster G was much more evenly applied across pest and host types and sectors.

Because of the high specificity of models in Cluster G and the difficulty of accurately re-coding their complex algorithms, it is unlikely that a suitable model can be taken directly from Cluster G and applied for a new pest in Europe. It seems likely that the range of approaches in Cluster G should be used as inspiration for development of a new model for the specific assessment. A barrier to doing this is likely to be a lack of detailed knowledge, especially for the behaviour of a novel pest that has recently entered Europe. However, if it can be done, then the model can be put to work for a range of risk assessment tasks.

12.8. Cluster H: Generic pest and host dynamics

Cluster H is a grouping of models characterised as being highly generalised (100% classed as generic pests and hosts, 88% refer to no specific dispersal mechanism) and incorporating both the dynamics of the pest and the host plant (98% of models have host dynamics, 50% have host dispersal). Models in Cluster H are often constructed and analysed as a combination of two-dimensional spatial simulations and mathematical analyses such as spatially-implicit mean field approximation (Park et al., 2001; Eppstein and Molofsky, 2007), moment closure (Bolker and Pacala, 1999; Filipe et al., 2004a) or pair approximation (Brown and Hastings, 2003; Filipe et al., 2004b).

Being developed for generic systems, Cluster H models show a strong link to ecological and evolutionary theory and are usually used to establish general principles rather than predict spread of a particular pest. For example, Brown and Hastings (2003) construct a model for a pathogen of two competing host species to demonstrate the conditions required for evolution of reduced resistance in the host plant. These include localised disease dispersal and high disease-damage to the competitor plant.

As a result of this generality, models in Cluster H tend to ignore heterogeneity in the landscape (86% are uniform) and are not clearly tied to a particular spatial scale (see Table 9). Because of this, we classified Cluster H as being poorly-suited to assessing spread over the EU risk assessment area or showing where environmental conditions favour spread. However, the generality also meant Cluster H had the advantage of not being overly reliant on data. Models in Cluster H were typically arbitrarily parameterised (90%) and subjected to sensitivity analysis (95%) rather than given realistic values for a species estimated from data.

Another major advantage of Cluster H is that the models capture the effects of biological interactions and processes on pest spread. We considered that this gave high fitness for elucidating the pest and host characteristics promoting spread. For example, Cluster H has explicit representation of pest-host interactions and comparatively high representation of other species interactions of the pest (19% of models). Therefore, we considered Cluster H to be potentially well-suited for estimating the effects of host plants and pest enemies on spread, notwithstanding issues applying the generic models to specific species. Evolutionary models were also relatively common in Cluster H (10% of models included pest evolution) so important eco-evolutionary dynamics could be represented. For example, Sapoukhina et al. (2009) showed that the spatial arrangement of host genotypes has a critical effect on evolution of pathogen virulence and spread.

Similarly the generality of Cluster H and flexibility of the simulation approaches employed within it also gave potential for establishing general effects of realistic management strategies. For example, Sisterson and Stenger (2013) develop a generic simulation model for spread of orchard pathogens among and between farms. They used the model to investigate rouging – replacement of infected plants with healthy ones – showing that efficient and coordinated management can slow spread of the pathogen.

Despite being generic, the models in Cluster H were not evenly applied. In the main they were used for pathogens of wild plants. This probably results from the fact that explicitly modelling the host dynamics is more appropriate to the spread of pests of wild plants than crops – whose populations are strongly controlled by farmers.

We suggest that models from Cluster H could be used in risk assessment in similar ways to Clusters C and D, i.e. to establish general answers to risk assessment questions rather than produce specific predictions of where the pest will spread to.

13. Use of the fitness criteria in a Decision Support Scheme (DSS)

From the results of the fitness evaluation, we have developed a Decision Support Scheme (DSS) to assist selection of the most appropriate spread models for risk assessment. Our aim is to provide a DSS that selects a relatively small group of models with properties that lend themselves to providing useful information for a specific pest risk assessment. In some cases, one or more of the selected models may be directly implemented for the aims of the focal species' risk assessment, following re-parameterisation for the new pest's biological characteristics. However, in most cases we expect that there would not be the possibility of direct application because existing models are likely to have features not applicable for the pest. However, the group of selected models should provide a guiding framework for the risk assessor in constructing a bespoke model for the focal pest based on the example elements provided by the DSS-selected studies.

In developing the DSS, we have accounted for the fact that there is a great deal of heterogeneity within each of the model clusters (see Figure 1). Therefore, while the fitness scoring may indicate that the typical model within a cluster is not especially suited to a particular task, there may be still models within that cluster that could be useful. To address this, we have developed the DSS to both rank the criteria by appropriateness, but also ensure consideration of models within unfavoured criteria.

13.1. Steps prior to using the Decision Support Scheme

Prior to using the DSS, the risk assessor should conduct a thorough review of the scientific literature and available data on the pest species. Much of this information is already collected during the Initiation Stage of EFSA risk assessments (EFSA Panel on Plant Health (PLH), 2010a). The review should consist of the following non-hierarchical elements:

1. The key features of the biology of the pest that may require consideration for modelling. For example, what are the main entry pathways and dispersal mechanisms and what are the key climate or habitat variables important for limiting the species? If little is known about the specific pest species, are there general features of its broader taxonomic or functional group relevant for generic modelling?

2. Values for parameters likely to be useful for modelling spread. This will include reports of the dispersal range of the species, population growth rates and individual demographic parameters or characterisations of responses to temperature, moisture etc.

3. Existing "non-spread" models that could still be useful for developing a model that includes spread. For example, if there is an existing model for the local population dynamics of the pest, then it may be possible to couple this to a dispersal model to estimate spread. Importantly, models that did not explicitly include dispersal were not assessed in our review, and so the inventory will not necessarily contain all useful models for the species.

4. Sources of high resolution spread distribution data. Online sources such as the Global Biodiversity Information Forum[10] and the Global Invasive Species Information Network[11] should be consulted. Plant protection organisations at regional, national and European level may also provide high quality data.

Following this review, the risk assessor should then appraise potential constraints on the spread modelling in terms of the following:

1. Lack of information on demographic, dynamic or dispersal parameters or the distribution of the pest.

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[10] www.gbif.org
[11] http://www.gisin.org/

2. Expertise of the modeller. For example, is the modeller proficient in mathematical analysis, computer simulation or any existing modelling software platforms?

Third, the risk assessor should consider the risk assessment tasks that the modelling needs to address and identify any possible constraints on which models can be applied. This can be done using subsets of the fitness criteria. Specifically, Criteria 1-11 directly relate to risk assessment tasks, as shown in Table 14, while Criteria 12-14 and 19 relate to constraints presented in Table 15. Fitness Criteria 15-18 relate to the diversity of model application – which is not strictly relevant for selecting a model. Since our previous discussion emphasised the fact that no single cluster is highly suited to addressing all the tasks of risk assessment, it is preferable to restrict the choice of criteria from Table 14 to a small number that are focused on a particular knowledge gap in the assessment. Otherwise, several model clusters will appear to perform similarly, but none will perform very well.

Table 14: Possible (non-exhaustive) list of links between the fitness criteria and the aims of spread or dispersal modelling in Plant Health risk assessment. The aims include both the actual EFSA risk assessment questions from Stage 2B of EFSA risk assessment of (EFSA Panel on Plant Health (PLH), 2010a) and modelling activities that might contribute to answering the questions.

Fitness criterion to be weighted by relevance	Relevant risk assessment aims
1. Rate and extent of pest spread over the whole risk assessment area (the EU) can be predicted or hindcasted.	• To answer Question 1.35 to identify the part of the assessment area vulnerable to pest spread. • To estimate potential spread at regional, national or continental scales.
2. The strategy can predict where environmental conditions are suitable for pest establishment and spread.	• To answer Questions 1.19-1.20 on the suitability of the environment for pest establishment. • To estimate the effects of climate or landscape heterogeneity on pest spread. • To investigate potential spread under climate change or land use change scenarios.
3. The strategy can predict where the availability of host plants permits pest establishment and spread.	• To answer Questions 1.17-1.18 on the availability of host plants for establishment. • To assess the effect of the host plant distribution on pest spread. • To model joint dynamics of the host pest and its plant.
4. The strategy can assess whether competition or natural enemies might limit establishment and spread.	• To answer Questions 1.22-1.23 on the probability of establishment despite competition or natural enemies. • To answer Question 2.6 on probability of control through natural enemies. • To predict limitation of pest spread through natural enemies or competitors. • To investigate the potential for biocontrol organisms to restrict spread.
5. The strategy can predict the effects of phytosanitary measures to limit pest entry on subsequent spread and impacts.	• To answer Questions 1.1-1.15 on the probability of entry. • To answer Questions 1.30-1.31 on the dependence of establishment on repeated pest introduction. • To predict spread dynamics driven by repeated pest introduction or entry. • To investigate whether stronger phytosanitary measures would restrict spread.
6. The strategy can investigate whether risk mitigation measures (other than phytosanitary ones) would be effective at preventing establishment or spread.	• To answer Questions 1.24-1.26 on the effects of management on probability of establishment. • To answer Question 2.3 and 2.6 on the ease of control in the risk assessment area. • To estimate the level of mitigation from control efforts compared to unrestricted spread. • To identify the optimal control strategy for restricting pest spread and impacts.

Fitness criterion to be weighted by relevance	Relevant risk assessment aims
7. Impact of the pest on crop yield or quality is predicted.	• To answer Question 2.2 and 2.5 on potential damage in the risk assessment area. • To predict the level of damage caused by the pest invasion.
8. Spread rates through 'natural' dispersal mechanisms can be predicted.	• To answer Question 1.32 on the likelihood of rapid spread by natural means. • To model spread of a pest for which 'natural' dispersal mechanisms are identified as important.
9. Spread rates through human dispersal can be predicted.	• To answer Question 1.32 on the likelihood of rapid spread by human assistance. • To model spread of a pest for which human dispersal is identified as important.
10. Spread rates through multiple dispersal mechanisms can be predicted.	• To answer Question 1.31-1.32 on the likelihood of rapid spread by natural and human assistance. • To model spread of a pest for which several dispersal mechanisms are identified as important.
11. The strategy can identify the key biological characteristics facilitating pest spread.	• To answer Questions 1.26-29 on the effects of pest characteristics on probability of establishment. • To answer Questions 1.34 on whether biological characteristics favour containment. • To identify the key demographic or life history stages that are most important for spread. • To compare control efforts that target different life history stages.

Table 15: Possible (non-exhaustive) list of links between the fitness criteria and constraints on spread or dispersal modelling for Plant Health risk assessment.

Fitness criterion to be weighted by relevance	Relevant constraints for modelling
12. Parameterisation does not strongly depend on data on pest demography or population dynamics.	Little information on pest population biology prevents application of models that rely on missing parameter values.
13. Parameterisation does not strongly depend on pest distribution data.	Little information on pest distribution over time prevents application of models that are fitted to spread patterns.
14. Parameterisation does not strongly depend on data on pest dispersal.	Little information on dispersal prevents application of models that require input of dispersal parameters.
19. Possibility of model application using existing software, assuming data and parameters are not limiting.	Lack of existing software means model must be coded and/or analysed for the risk assessment.

13.2. An application guide for the Decision Support Scheme

13.2.1. DSS Step 1: Identify any existing spread models for the focal species

It is worth considering first whether any spread models exist for the focal species, or for closely related species. This is because an existing model may be directly applicable in the risk assessment, or at least provide parameter values for an alternative or bespoke model. To do this it is straightforward to search the EndNote library from the extensive literature search for the pests' species, genus and family name. We consider that searching the EndNote library is more suitable for this purpose than searching the electronic model inventory database, which is more suited for filtering information about model usage, for instance by cluster or sector.

The most comprehensive approach is to search within the EndNote data and the attached PDF document. In some cases the pest may not be mentioned in the data fields stored by EndNote, so searching the PDF will minimise the chance of missing relevant papers. This could be especially true where generic models are developed with a specific group of pests in mind, but they are not mentioned in the title, abstract or key-words stored by EndNote.

To search within EndNote (version X5) click 'Tools' and select 'Search library', or press ctrl+F, to bring up the search window. From the left-hand drop down menu, which specifies the field to search, select 'Any Field + PDF with Notes', then make sure the central drop down menu is set to 'Contains' and type the search term in the right-hand dialogue window. It is necessary to check that the default options of searching the whole library and ignoring search term case are in place before clicking 'Search' to show the results. We recommend conducting searches for several terms relating to the pest since not all results may be given by a single term, as in the example for *Xylella fastidiosa* shown in Table 16. To do this, multiple search term lines, linked with OR statements can be specified.

The results can then be examined to determine whether they are suitable for use in the current risk assessment. If the search provides only a small number of models from the inventory, we recommend also conducting a wider literature search for models of the species (e.g. search Web of Science, Google Scholar etc. for the pest name and examine the first 100 results returned) because newer models might have been published after completion of the inventory, sources may not have been available online earlier or in case our literature search protocols did not capture all relevant models for the species. Even if a likely model is found at this stage, we suggest it is worthwhile proceeding to the next steps to determine whether it fits with the most suitable types of models for the current risk assessment.

Table 16: An example of EndNote searches within the literature review database for existing models pertaining to *Xylella fastidiosa*, the causal pathogen of Citrus Variegated Chlorosis Disease, Pierce's disease, bacterial leaf scorch, oleander leaf scorch and phoney peach disease. Seven different search terms were used and seven unique results were returned. Including the attached PDF document in the search was far superior to only using the EndNote fields.

Search term	Results from searching in 'Any Field' [(a)]	Results from searching in 'Any Field + PDF with Notes'
xylella	Blackmer et al. (2006)	Blackmer et al. (2004); Blackmer et al. (2006); Sisterson (2008); Sisterson and Stenger (2013).
fastidiosa	Blackmer et al. (2006)	Blackmer et al. (2004); Blackmer et al. (2006); Sisterson (2008); Sisterson and Stenger (2013)
citrus variegated chlorosis	-	Blackmer et al. (2004); Laranjeira et al. (2006); Zhen et al. (2007)
pierce's	Blackmer et al. (2004)	-
pierces	-	Blackmer et al. (2006)
leaf scorch	-	Ntahimpera et al. (1998); Blackmer et al. (2004); Blackmer et al. (2006); Sisterson and Stenger (2013)
phoney peach	-	-
xylella OR fastidiosa OR citrus variegated chlorosis OR pierce's OR pierces OR leaf scorch OR phoney peach	Blackmer et al. (2004); Blackmer et al. (2006)	Ntahimpera et al. (1998); Blackmer et al. (2004); Blackmer et al. (2006); Laranjeira et al. (2006); Zhen et al. (2007); Sisterson (2008); Sisterson and Stenger (2013)

(a): Equivalent to searching in the 'Quick Search' dialogue box.

13.2.2. DSS Step 2: Assess which modelling clusters best address the aims and constraints of the risk assessment

The second step is to weigh up the suitability of the Clusters for achieving the required risk assessment tasks (identified from the initial consideration of Table 14) and the feasibility of using each cluster, given any constraints on the modelling (Table 15).

First the risk assessor assigns an importance weighting to each row in Table 17. The weightings could be as simple as a binary scoring of criteria as relevant (weighting = 1) or not relevant (weighting = 0). The most sophisticated weighting might involve grading the criteria on a continuous scale from most important to least important. The entries of Table 17 contain the fitness criteria reflecting Cluster suitability for risk assessment tasks, important features of the pest being assessed and the fitness criteria reflecting Cluster feasibility. Features of the pest were included in order to further guide the DSS towards the more relevant modelling clusters. The selected features are the pest taxonomic and functional group and dispersal mechanism(s), the host plant functional group, and the appropriate time scales for the pest spread or dispersal. The latter was selected because the time scale on which the model should represent dispersal will generally be known by the assessor and is important in differentiating models. For example, if the goal is to predict dispersal patterns from existing pest outbreaks then models for single dispersal events, or those with short timesteps (continuous or subannual) will be most relevant.

Once the weightings in Table 17 are populated, they should be multiplied by each Cluster's scorings for the suitability and feasibility criteria in Table 18. The scorings in Table 18 were assigned in two ways. Where rows of Table 18 were taken from the fitness criteria, we used the fitness evaluation scores in Table 13, converted to a numeric scale (Low = 0, Medium = 0.5, High = 1). For the entries representing pest features, we considered two options – the proportion of models in the cluster meeting the criteria, and the proportion of models meeting the criteria that are in the cluster. For instance, the proportion the focal cluster that is for pest insects, vs. the proportion of models for pest insects that are in the cluster. The former measure will direct the decision towards clusters where there is a high proportion of suitable models (but not necessarily a high number), while the latter will direct towards clusters where there are a high number of suitable models (but not necessarily a high proportion). To balance these two extremes, we decided to use the average of both measures in Table 18.

Following the multiplication, overall suitability and feasibility scores for each Cluster can be obtained by summing the results for all the suitability criteria and all the feasibility criteria. For convenience, we have provided an Excel spreadsheet allowing simple calculation of the suitability and feasibility scores[12].

More formally, the overall suitability S_k and feasibility F_k for modelling Cluster k can be calculated as,

$$S_k = \sum_i w_i s_{k,i}$$
$$F_k = \sum_j w_j f_{k,j}$$

where i iterates over the weightings for the modelling goals and j iterates over the weightings for modelling constraints. The values of w represent the weightings assigned in Table 17. The values of s and f are given in Table 18.

The ordering of S and F will rank the Clusters from highest fitness to the lowest, allowing the user to compare and select strategies that perform well on both metrics for closer inspection.

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[12] The Decision Support Scheme scoring Excel spreadsheet can be downloaded at http://www.efsa.europa.eu/en/supporting/doc/795eax1.zip

Table 17: The Decision Support Scheme weighting table. The risk assessor would fill in the weightings to reflect the relative importance of each factor to the current risk assessment. The weightings will then be used to direct to the risk assessor towards appropriate model clusters.

Modelling goals and application (Suitability)		Importance Weighting
To model pest spread or dispersal at a large scale (Fitness criteria 1)		
To model pest spread or dispersal in a heterogeneous landscape (Fitness criteria 2)		
To model how pest spread or dispersal is affected by the distribution/dynamics of host crops (Fitness criteria 3)		
To model how pest spread or dispersal is affected by competitors or natural enemies (Fitness criteria 4)		
To model the effectiveness of phytosanitary measures as a risk reduction option (Fitness criteria 5)		
To model the effectiveness of other management measures as a risk reduction option (Fitness criteria 6)		
To model the impacts of the pest on crop yield or quality (Fitness criteria 7)		
To model 'natural' pest dispersal mechanisms (Fitness criteria 8)		
To model 'human' pest dispersal mechanisms (Fitness criteria 9)		
To model multiple pest dispersal mechanisms (Fitness criteria 10)		
To use sensitivity analyses to identify the key pest characteristics facilitating spread or dispersal (Fitness criteria 11)		
What taxonomic groups of pests are to be modelled?	Bacterium or phytoplasma	
	Fungus or oomycete	
	Insect	
	Mite	
	Nematode	
	Plant	
	Protest	
	Virus	
	Generic	
What functional groups of pests are to be modelled?	Competitor	
	Disease vector	
	Herbivore	
	Invasive species	
	Macroparasite	
	Microparasite or disease	
	Generic	
What pest dispersal mechanisms are to be modelled?	Active movement	
	Ballistic	
	Clonal	
	Gravity	
	Human (long distance)	
	Human (short distance)	
	Rain splash	
	Vector	

Modelling goals and application (Suitability)		Importance Weighting
	Water Wind Generic	
What functional groups of host plants are to be modelled?	Crop Ornamental Wild plant Generic Not modelled [(a)]	
What are the most appropriate time scales for the model, considering the processes and data?	Single event Continuous Subannual Annual Generic [(a)]	

Constraints on modelling (Feasibility)	Importance Weighting
There is a lack of data on pest demography or dynamics (Fitness criteria 12)	
There is a lack of data on pest distribution (Fitness criteria 13)	
There is a lack of data on pest dispersal (Fitness criteria 14)	
There is a need to use existing software to run the model (Fitness criteria 19)	

(a): originally classed as ‘unspecified’.

Table 18: The scores given to each model cluster, considering their suitability for different risk assessment goals and the feasibility of their application under different constraints. These scores are multiplied by the chosen importance weightings entered into Table 17 to appraise the overall suitability and applicability of each model cluster.

Modelling goals and application (Suitability)		**Suitability score for cluster (*s*)**							
		A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
To model pest spread or dispersal at a large scale (Fitness criteria 1)		0	0.5	0	0	0	1	1	0
To model pest spread or dispersal in a heterogeneous landscape (Fitness criteria 2)		0	0.5	0	0	0	1	1	0
To model how pest spread or dispersal is affected by the distribution/dynamics of host crops (Fitness criteria 3)		0	0	0	0	0.5	0	1	1
To model how pest spread or dispersal is affected by competitors or natural enemies (Fitness criteria 4)		0	0	1	0.5	0.5	0	0.5	1
To model the effectiveness of phytosanitary measures as a risk reduction option (Fitness criteria 5)		0	0	0	0	0.5	0.5	0.5	0.5
To model the effectiveness of other management measures as a risk reduction option (Fitness criteria 6)		0	0	0.5	0.5	0	1	1	0.5
To model the impacts of the pest on crop yield or quality (Fitness criteria 7)		0	0.5	0	0	0.5	0.5	1	1
To model 'natural' pest dispersal mechanisms (Fitness criteria 8)		0.5	1	1	0.5	0.5	0.5	0.5	0.5
To model 'human' pest dispersal mechanisms (Fitness criteria 9)		0	0	0	0.5	0	1	0.5	0
To model multiple pest dispersal mechanisms (Fitness criteria 10)		0	0.5	0.5	0	0.5	1	0.5	0
To use sensitivity analyses to identify the key pest characteristics facilitating spread or dispersal (Fitness criteria 11)		0.5	0.5	1	1	0	0.5	1	1
What taxonomic groups of pests are to be modelled?	Bacterium or phytoplasma	0.164	0.000	0.000	0.000	0.000	0.077	0.305	0.000
	Fungus or oomycete	0.351	0.332	0.178	0.111	0.183	0.011	0.262	0.048
	Insect	0.084	0.253	0.260	0.176	0.174	0.233	0.417	0.029
	Mite	0.271	0.000	0.268	0.000	0.000	0.000	0.000	0.000
	Nematode	0.000	0.000	0.000	0.091	0.091	0.000	0.352	0.000
	Plant	0.175	0.040	0.117	0.360	0.011	0.487	0.121	0.153
	Protest	0.000	0.000	0.000	0.000	0.258	0.000	0.255	0.000
	Virus	0.067	0.000	0.032	0.061	0.394	0.000	0.082	0.034

Modelling goals and application (Suitability)		**Suitability score for cluster (*s*)**							
		A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
	Generic	0.000	0.000	0.147	0.090	0.282	0.093	0.000	0.521
What functional groups of pests are to be modelled?	Competitor	0.150	0.037	0.108	0.275	0.012	0.366	0.086	0.133
	Disease vector	0.141	0.053	0.045	0.044	0.092	0.042	0.169	0.000
	Herbivore	0.082	0.234	0.233	0.135	0.174	0.156	0.354	0.050
	Invasive species	0.115	0.018	0.187	0.293	0.000	0.440	0.156	0.123
	Macroparasite	0.000	0.000	0.000	0.088	0.000	0.000	0.261	0.185
	Microparasite or disease	0.299	0.277	0.170	0.093	0.478	0.018	0.262	0.332
	Generic	0.000	0.140	0.264	0.130	0.000	0.000	0.000	0.000
What pest dispersal mechanisms are to be modelled?	Active movement	0.087	0.165	0.233	0.055	0.169	0.119	0.340	0.016
	Ballistic	0.000	0.084	0.158	0.078	0.000	0.150	0.075	0.000
	Clonal	0.000	0.000	0.000	0.127	0.096	0.086	0.199	0.109
	Gravity	0.032	0.034	0.116	0.057	0.000	0.279	0.101	0.000
	Human (long distance)	0.022	0.000	0.039	0.113	0.038	0.284	0.172	0.024
	Human (short distance)	0.073	0.000	0.022	0.084	0.085	0.215	0.195	0.000
	Rain splash	0.238	0.036	0.062	0.030	0.031	0.055	0.191	0.000
	Vector	0.019	0.021	0.033	0.031	0.254	0.163	0.235	0.041
	Water	0.000	0.000	0.035	0.034	0.000	0.471	0.031	0.000
	Wind	0.396	0.410	0.217	0.251	0.099	0.132	0.212	0.000
	Generic	0.000	0.000	0.146	0.242	0.227	0.208	0.058	0.563
What functional groups of host plants are to be modelled?	Crop	0.438	0.372	0.320	0.283	0.395	0.200	0.389	0.160
	Ornamental	0.066	0.101	0.060	0.095	0.059	0.086	0.265	0.024
	Wild plant	0.088	0.127	0.157	0.183	0.123	0.340	0.334	0.303
	Generic	0.000	0.000	0.079	0.051	0.234	0.094	0.000	0.271
	Not modelled	0.062	0.024	0.186	0.248	0.000	0.285	0.000	0.000

Modelling goals and application (Suitability)		**Suitability score for cluster (*s*)**							
		A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
What are the most appropriate time scales for the model, considering the processes and data?	Single event	0.935	0.027	0.000	0.017	0.017	0.046	0.014	0.000
	Continuous	0.000	0.088	0.750	0.065	0.077	0.043	0.163	0.283
	Subannual	0.000	0.496	0.000	0.150	0.413	0.114	0.302	0.065
	Annual	0.000	0.000	0.000	0.460	0.056	0.539	0.410	0.119
	Generic	0.000	0.031	0.000	0.043	0.347	0.098	0.000	0.330

Constraints on modelling (Feasibility)	**Feasibility score for cluster (*f*)**							
	A	**B**	**C**	**D**	**E**	**F**	**G**	**H**
There is a lack of data on pest demography or dynamics (Fitness criteria 12)	1	1	0	0	1	0.5	0	1
There is a lack of data on pest distribution (Fitness criteria 13)	0.5	1	1	1	0.5	0	0.5	1
There is a lack of data on pest dispersal (Fitness criteria 14)	0	1	0	0	1	0.5	0	1
There is a need to use existing software to run the model (Fitness criteria 19)	0	1	0	0	0	0.5	0	0

13.2.3. DSS Step 3: Within the most appropriate clusters, identify models that are most likely to help in designing a model for the focal species

The next step is to review the models assigned to the selected clusters to identify those that have properties that align to the expertise of the modeller and requirements of the modelling. For example, if the risk assessment requires prediction of climatic effects on spread, then a discrete-space, discrete-time model may be considered desirable because climate data are usually available as discrete grids for discrete time periods. Such a model lends itself readily to computer simulation of spread on a lattice, provided the modeller has sufficient expertise in coding these kinds of models.

To perform this assessment, one can make use of the data on individual model properties stored within the electronic model inventory. This can be filtered appropriately to identify models within the selected cluster that have desirable characteristics for designing the model for the focal pest. A convenient way to perform the filtering is to open the inventory database in Access, then from the 'Navigation Pane' double click the 'tbl_header' option listed under 'Tables'. This will open a spreadsheet-like view of the database. Filters can be applied to the individual data columns by opening their drop-down menus and selecting particular values. Sequential application of multiple filters results in a subset of modelling papers that can be examined individually.

13.2.4. DSS Step 4: Identify similar models from other clusters

Since there is a large amount of heterogeneity within each cluster, atypical models within a mainly unsuitable cluster may provide useful information for constructing a model for the focal pest. Therefore, it may also prove useful to apply Step 4 across the whole database of models. Step 4 is probably most sensible in cases where the preceding steps have resulted in quite a small number of models or if they have proved not especially useful. The simplest way to do this, is to remove the filter on the Cluster data field in the electronic model inventory (or reverse it to exclude the chosen clusters).

TASK 4 - CASE STUDIES OF MODEL SELECTION AND GUIDES FOR PRACTICAL APPLICATION

14. Objective

The objective of Task 4 was to apply case studies for using the DSS to select and then practically apply models for the spread or dispersal of plant pests. This tests the ability of the model inventory, clustering and Decision Support Scheme to support a greater use of spread or dispersal modelling in EFSA Plant Health risk assessment.

15. Summary of the case studies

In developing the case studies, we considered four general scenarios that EFSA may be faced with when attempting to use spread or dispersal modelling in plant pest risk assessments (Table 19). The first covers the modelling of dispersal from a single pest outbreak to identify the area at risk of spread. An example from EFSA risk assessment is the Gaussian Plume Model of *Monilinia fructicola* wind dispersal (EFSA Panel on Plant Health (PLH), 2011). The second is where data on spread or dispersal is used to model the area at risk of future spread. An example from EFSA Plant Health risk assessment is the analysis of long-distance dispersal events of *Dryocosmus kuriphilus* (EFSA Panel on Plant Health (PLH), 2010b). The third scenario is where the current distribution of a spreading pest is well established but there is little data on its spread history. This is the current situation for the bacterial tree pathogen *Xylella fastidiosa*, which is the subject of current EFSA risk assessment (EFSA PLH Panel (EFSA Panel on Plant Health), 2015). Finally, the fourth scenario is for cases where there is good data on the spread of a pest from which future spread should be predicted. EFSA's previous modelling of *Dryocosmus kuriphilus* spread falls under this scenario (EFSA Panel on Plant Health (PLH), 2010b).

Table 19: Four risk assessment scenarios where EFSA may consider using spread or dispersal modelling. The case studies are designed around these scenarios. In the suggested modelling options we distinguish between the general categories of modelling that are from bottom-up (process-based equations parameterised empirically) or top down (spread data driven) perspectives.

Risk assessment modelling scenario	Scenario description	Modelling options
1	A single outbreak (or small number of outbreaks) of a pest is detected. Modelling should be used to estimate the potential range of dispersal from the outbreak location.	Bottom-up modelling of single dispersal events, based on knowledge of the dispersal mechanism (e.g. Cluster B or C).
2	Following an initial detection, a pest is documented dispersing to new locations. The dispersal range is to be characterised by using this information in a model.	Top-down modelling of single dispersal events as a phenomenological dispersal kernel (e.g. Cluster A).
3	A new pest is detected in the risk assessment area. Surveys quickly determine its current distribution but no information is available on its spread history, including the location or time of entry. Modelling should be used to estimate the potential rate at which the pest may spread.	A. Estimate the rate of spread from a bottom-up approach, using parameter estimates from the literature (e.g. Cluster C or D). B. Calibrate a generic top-down spread model to the current distribution pattern. It will be necessary to assume that entry occurred in the centre of the distribution, and use expert opinion on a plausible range of possible entry times (e.g. Cluster E, F, G, or H).
4	Risk assessment is required for a pest that has been recorded spreading in the risk assessment area over a number of years. By using this information in a model, the future pest spread should be predicted.	Fit a generic top-down model to the observed pattern of spread (e.g. Cluster E, F, G, or H). The model can be tailored to known aspects of the pest's spread dynamics (e.g. habitat preference, climatic tolerance or dispersal mechanism).

Each of these scenarios was matched to the status of some specific pest organisms, providing the basis for the case studies. The chosen pest species are either subject of current EFSA Plant Health risk assessment (*Xylella fastidiosa*), pests that may be subject of future mandates for EFSA (*Erwinia amylovora*) or other important pests for which we have sufficient parameters or data for modelling (*Cameraria ohridella*, *Conyza canadensis*, *Phakopsora pachyrhizi*) (Table 20). Some of the risk assessment scenarios had more than one case study, to reflect the diversity of modelling options available. Furthermore some of the pest species apply to more than one risk assessment modelling scenario.

The result is seven case studies (summarised in Table 20) that meet the following criteria:

1. They feature a range of pest taxonomic and functional groups. We specified case studies for insects, fungi, bacteria and plants. Together these account for 92% of models in the model inventory where a specific group is mentioned (Table 10).

2. They feature a range of dispersal mechanisms, including wind, humans, active movement and insect vectoring. We also include generic dispersal kernel models suitable for most dispersal mechanisms.

3. For most of the case studies, we used sensitivity analyses to determine how the pest spread or dispersal is affected by biological characteristics of the pest or external factors such as the configuration of the landscape.

We included sensitivity analysis because it is useful for gaining understanding of the uncertainty in the model estimates of spread. It can also identify key features of the pest that promote spread, as in sensitivity analysis for the effect of long distance-dispersal on modelled spread of *Dryocosmus kuriphilus* (EFSA Panel on Plant Health (PLH), 2010b). Finally, sensitivity analysis can be helpful for suggesting effective risk reduction options. For example, the model of *D. kuriphilus* was useful for demarcating buffer zones around pest occurrences for surveillance of further spread (EFSA Panel on Plant Health (PLH), 2010b). Also, management effectiveness was investigated by modifying parameters of the *Pomacea* (non-spread) population dynamics model (EFSA PLH Panel (EFSA Panel on Plant Health), 2014).

Table 20: Overview of the modelling case studies covering the risk assessment modelling scenarios in Table 18. The choice of pest species reflects their applicability for the scenario, rather than necessarily their actual dynamics (see footnotes for explanations). For each pest we used the Decision Support Scheme to search the inventory for useful models and then practically applied the models.

Case study	Risk assessment scenario	Pest type	Dispersal mechanism	Cluster selected by DSS	Model(s) selected for application using the DSS	Sensitivity analysis	Data needed
1	1	Fungal crop pathogen (*Phakopsora pachyrhizi*) (1) (2)	Wind	B	Pan et al. (2006)	None	None (parameterisation from the literature).
2	2	Bacterial crop pathogen (*Erwinia amylovora*) (3)	Several mechanisms (generic kernel)	A	Soubeyrand et al. (2009)	Type of dispersal kernel	Outbreak locations over time provided by the Italian Phytosanitary Service.
3	3A	Bacterial crop pathogen (*Xylella fastidiosa*)	Insect vector	C	Kinezaki et al. (2010)	Demographic and dispersal parameters.	None (parameterisation from the literature).
4	3A	Invasive weed (*Conyza canadensis*) (2)	Wind	D	Bullock et al. (2012), Dauer et al. (2006), Dauer et al. (2007)	Demographic parameters.	None (parameterisation from the literature).
5	3B	Bacterial crop pathogen (*Xylella fastidiosa*)	Insect vector	H	Sisterson and Stenger (2013)	Management efficiency (roguing)	Data on current distribution of *Xylella fastidiosa* and its host plants (olive trees *Olea europeae*) in Puglia, Italy.
6	4	Bacterial crop pathogen (*Erwinia amylovora*)	Several mechanisms (generic kernel)	F	Richter et al. (2012) and Cook et al. (2007)	Type of dispersal kernel and annual variation in spread	Outbreak locations over time provided by the Italian Phytosanitary Service.
7	4	Insect herbivore (*Cameraria ohridella*(2)).	Active flight and human (vehicle)	F	Gilbert et al. (2004)	Type of dispersal model	*Cameraria ohridella* spread data from the UK

(1): We modelled dispersal from a hypothetical outbreak in Europe.
(2): Pest species chosen as it had sufficient information in the literature to parameterise the model.
(3): We used the first few years of data on *Erwinia amylovora* spread to mimic risk assessment Scenario 2.

Each case study is fully documented in a separate report accompanying this main report. The case study reports document the background to each case study, the selection of models from the inventory for application using the Decision Support Scheme (DSS), the methods and results of applying the models and (where relevant) computer code for the algorithms developed during the case studies. Briefly, the case studies consisted of the following:

1. Mechanistic modelling of the wind dispersal process for spores released from a hypothetical outbreak of the fungal pathogen *Phakopsora pachyrhizi*[13]. The bottom-up HYSPLIT-WEB atmospheric model was parameterised from known traits of the spores, such as their release height and terminal velocity, and characteristics of the outbreak, such as its location and timing. The model represents the release, advection and deposition of spores. In so doing, it predicts the region in which viable spores are deposited following dispersal from the hypothetical outbreak at a European scale. Model outputs suggested that dispersal patterns were strongly dependent on meteorological conditions during the disease outbreak and indicated a major potential for long-distance spore dispersal.

2. A major dispersal event of the bacterial pathogen *Erwinia amylovora* in the Emilia-Romagna region of Italy was modelled using a generic anisotropic (i.e. directional) dispersal kernel[14]. *E. amylovora* spreads via a range of dispersal mechanisms. This model does not give clear insight into any particular mechanism, but instead attempts to model their aggregated effects. The model was fitted to dispersal data inferred from the locations of new outbreaks, relative to earlier ones which were presumed to be their sources. The fitted model suggested highly directional spread, suggestive of important roles for directed dispersal mechanisms such as wind and humans. The fitted model can be overlain onto existing outbreak locations to model the region at risk of further dispersal.

3. A reaction-diffusion model was applied to estimate the spread rate of the insect-vectored bacterium *Xylella fastidiosa* among olive trees in Apulia, Italy[15]. The model is a bottom-up approach relying on estimates of the bacterial population growth rate and insect-vector diffusion rate obtained from the literature. However, the limited available evidence for parameterisation demonstrated major differences in its epidemiology in the risk assessment area compared to other regions in which it has spread. Therefore, we considered it was not possible to accurately predict the spread rate in this instance, because it would be highly uncertain and potentially misleading. This highlights the important need to understand the pest biology and data availability when selecting a model using the DSS.

4. Use of the generic Integro-difference equation for modelling spread of the invasive weed plant *Conyza canadensis* by wind dispersal[16]. This bottom-up model predicts the rate of spread of the pest based on demographic and dispersal traits that are commonly available in the literature. From literature values of these traits, we parameterised an annual matrix projection model for the population dynamics, and derived the mechanistic WALD wind-dispersal kernel to represent seed dispersal. From the final model, we estimated the wavespeed on invasion, which is a measure of the potential rate at which *C. canadensis* spreads through wind dispersal. Sensitivity analysis of the parameterised model suggested that rapid spread of the weed is most dependent on high adult

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[13] The report for Case Study 1 can be downloaded at http://www.efsa.europa.eu/en/supporting/doc/795eax1.zip
[14] The report for Case Study 2 can be downloaded at http://www.efsa.europa.eu/en/supporting/doc/795eax1.zip
[15] The report for Case Study 3 can be downloaded at http://www.efsa.europa.eu/en/supporting/doc/795eax1.zip
[16] The report for Case Study 4 can be downloaded at http://www.efsa.europa.eu/en/supporting/doc/795eax1.zip

survival and fecundity. Therefore these demographic stages could be the most effective for targeting control efforts.

5. A stochastic simulation model was developed for the spread of the insect-vectored bacterium *Xylella fastidiosa* among olive trees in Apulia, Italy[17]. Although the DSS selected an existing generic model, we had to make substantial modifications to apply in this study. For example, we developed a computationally-efficient approximation to local population growth, and implemented 'stratified' dispersal with deterministic local diffusion and stochastic long-distance jumps. However, most of the information for parameterisation came from behaviour of the disease and its vectors outside the risk assessment area, and expert opinion suggested that the disease behaved differently in Italy. With reasonable estimates of parameter values for Italy, the model qualitatively reproduced similar distribution patterns to those observed in the affected region. This highlights the dependence of this model, and other bottom-up approaches, on good data on the disease dynamics. We used the model to implemented a risk reduction scenario (roguing – removal and replacement of infected crops), which showed that roguing has little impact on local diffusive spread, but has a significant impact on disease incidence. However, this reduces the probability of the long-distance jumps and therefore slows down spread at a landscape scale.

6. A simulation model for spread of the bacterial pathogen *Erwinia amylovora*[18]. A very simple and generic, top-down model was fitted to data on the pathogen spread over seven years in the Emilia-Romagna region of Italy. An important advantage of this model is its ability to represent a heterogeneous landscape, which we defined using land cover maps for the study region. The model characterised the dispersal range of the pathogen, as well as quantifying the suitability of different land cover types for outbreaks. Furthermore, the model also indicated significant variability in spread rates between years, which may be related to meteorological conditions being favourable or unfavourable for the pathogen. Stochastic simulations of the model allowed us to predict the region at risk of future spread.

7. A top-down simulation model was used to represent human-dispersed spread of an invasive pest insect *Cameraria ohridella* in the UK[19]. We investigated how well two alternative models for human dispersal fitted the spread pattern documented in the UK over 10 years. Both models were able to explain a large proportion of the observed spread, demonstrating the important role of human traffic in causing long-distance dispersal of the insect. However, the data indicated a recent slowing of the northwards invasion, which did not appear to be explained by the model, despite there being lower human population densities in the north. This suggests that the insect may have reached a climatic limit to invasion, potentially because low temperatures may reduce the number of generations per year. More information on the pest's life history responses to temperature are needed to include this in the model, highlighting a research priority for improving understanding and modelling of its spread.

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[17] The report for Case Study 5 can be downloaded at http://www.efsa.europa.eu/en/supporting/doc/795eax1.zip

[18] The report for Case Study 6 can be downloaded at http://www.efsa.europa.eu/en/supporting/doc/795eax1.zip

[19] The report for Case Study 7 can be downloaded at http://www.efsa.europa.eu/en/supporting/doc/795eax1.zip

DISCUSSION

16. Extensive literature search on quantitative models of spatial and temporal spread and dispersal of plant pests

The extensive literature review provided a comprehensive overview of scientific research on quantitative models of the spread and dispersal of plant pests. The review highlighted the wide diversity of modelling strategies, applications and analysis techniques that are used. Nevertheless, through a data-driven unsupervised cluster analysis we were able to find significant commonalities among the reviewed models, resulting in eight distinct strategies:

- **Cluster A: Single-event pest dispersal**, generally dispersal kernel or disease gradient models for a single pest spreading over a fixed time period.

- **Cluster B: Large-scale simulation of pest dispersal events**, generally wind dispersal of the pest simulated through Lagrangian atmospheric dispersion, advection-diffusion, or wind trajectory models.

- **Cluster C: Pest spread or dispersal in continuous space and time**, generally reaction-diffusion and diffusion models without explicit modelling of the host plant.

- **Cluster D: Continuous-space pest spread in discrete time**, generally integro-difference models for pest spread through a homogeneous landscape with no explicit host plant representation.

- **Cluster E: Iterative colonisation of hosts at small scales**, generally simulation of spatial susceptible-infected epidemic models and network contact spread models.

- **Cluster F: Simulation of specific pest spread at large scales**, generally cellular automata or metapopulation models for pests without an explicit host plant model.

- **Cluster G: Simulation of specific pest and host dynamics**, generally cellular automata or individual-based models incorporating a large amount of of biological detail on the focal pest and host.

- **Cluster H: Generic pest and host dynamics**, generally cellular automata or individual-based models for generic organisms.

The eight Clusters were statistically differentiated by the ways in which they represented space and time. A further main differentiation was how pests and host plants were modelled, especially with regard to whether pest and host plant dynamics and/or dispersal were explicitly represented. There were also significant differences in the taxonomic and functional groups of pests that were modelled by each cluster, representing differences in the biology of the pest organisms. For example, micro-organisms were more often represented in models for spread over a single growing season than plants, probably because most plants have longer generation times. There were also pronounced differences in the way the models were parameterised and analysed, in ways that are potentially relevant for pest spread risk assessment. For example, the two strategies with the highest representation of models for risk reduction options measures were Cluster G and Cluster F. Therefore if a modelling goal for risk assessment is to make recommendations on the best way to manage a pest's spread, then these clusters may likely contain relevant models for application.

Examination of these models also revealed some common deficits in the typical modelling practice:

- Few models considered interactions among multiple pest or host plant species, or the impacts of natural enemies on the pests. Spatial and temporal structuring of these biotic interactions may be extremely important in determining the rate at which pests can spread (EFSA Panel on Plant Health, 2010b).

- Few models coupled ecological and evolutionary dynamics during spread, despite recognition that dispersal and pest virulence and host preferences undergo strong selection during range expansions (Sapoukhina et al., 2009; Wingen et al., 2013).

- Few models represented spread driven by multiple pest entry or introduction events. Pests strongly associated with human activities and trade are likely to be repeatedly introduced into new areas through time, allowing rapid spread at large spatial scales beyond that of their own 'natural' dispersal abilities (EFSA Panel on Plant Health, 2010a; Bullock, 2012).

- Although models for a range of dispersal mechanisms were found, very few considered spread in water, though this may be a mechanism for long distance spread of many invasive plants and other pests (EFSA Panel on Plant Health, 2013).

- Some taxonomic and functional groups were very under-represented in the results of the literature review including viruses, bacteria, nematodes, mites and protists as well as disease vectors (though many insect pests may not have been mentioned as such) and macro-parasites of plants.

- Relatively few models considered ways in which scenarios of abiotic change may affect pest spread, despite a clear interest in understanding how future ongoing climate change will promote spread of new pests (Moorcroft et al., 2006; Walters et al., 2006; Bullock et al., 2012).

For use in Plant Health risk assessment, where rapid deployment of simple models for spread is a requirement, the most serious deficiencies are the paucity of models coupling entry and spread processes, models for micro-organisms and models for scenarios of environmental change.

17. Electronic inventory of models of spread and dispersal of plant pests

The results of the extensive literature search, including data on model formulation and use and the outputs of the cluster analysis, were captured in an Electronic Model Inventory. This provides a convenient and secure interface for viewing and searching the models located in the review. Some of the key functionalities of the Electronic Model Inventory are the ability to search for records and to access and export the underlying data on their bibliography, formulation and usage. Also, when linked with the EndNote library it is possible to open the PDF document of the paper from within the inventory. This should allow EFSA to identify and review quickly existing models for pests that are the subject of new risk assessments. It should therefore provide a useful tool for rapidly determining whether models already exist for pests that are the subject of future Plant Health risk assessments. However, to remain useful, consideration should be given into procedures for maintaining and updating the inventory over the long term.

17.1. Updating the inventory with newly published models

The inventory represents our survey of the scientific literature published by April 2013. There is no active updating scheme in place and therefore as time passes and new models are published the information contained within the inventory will become increasingly outdated. It would therefore be desirable to establish a system for updating the inventory so that it remains up to date.

The simplest system would be to add records of newer literature on an *ad hoc* basis. In other words, as EFSA staff or other collaborating researchers come across new modelling literature that pass the screening criteria in section 2.4, they create a new record in the database and populate the fields. An advantage of this is that it does not require significant resourcing, provided that there is a willingness among inventory users to add new records to the database. However, a disadvantage is that the literature review was produced via an extensive search protocol, based on systematic reviewing and mapping (Bates et al., 2007; Randall and James, 2012). By contrast, *ad hoc* updating would be likely to produce a less complete, consistent or 'systematic' sample of the literature and therefore it may introduce more subjectivity or bias into the inventory. It would therefore be sensible to add a new data field to the inventory to clearly flag the *ad hoc* additions.

There would also need to be a system in place to allow multiple users to access and add records to the central inventory database. One solution would be to store the inventory on a secure web portal where during the time that a user opens it to add records it is locked or available in read-only form to other users. Unless the EFSA extranet has this functionality then there would be some cost in establishing this interface.

A second option is to commit to periodically repeating the extensive literature review, following the same protocols we established here for surveying the literature, selecting relevant studies and characterising their formulation and use (see sections 2.3 and 2.4). An appropriate time period may be every three to five years and the repeat review would only consider literature published since the current searches were performed, i.e. from April 2013 onwards. As such the new review would likely be a smaller exercise than the one we performed, although as can be seen from Figure 4 the rate of model publication has increased over time. We designed and documented the screening protocols of the literature search so that they could be independently followed by different reviewers on our project team. As such it should be possible for existing team or a new team of reviewers to follow them closely and produce a new set of results that are comparable to the existing inventory.

17.2. Assigning new models to clusters

After periodic repeating of the literature review, there are two options for categorising the new modelling strategies of the new results. The first is to assign the new results to one of the existing model clusters. This could potentially be done manually by a careful consideration of the model properties with respect to each cluster's defining characteristics. A potentially less subjective approach would be to use the existing clustering model (section 2.7.3) for the assignment. Currently, the clustering model is saved as an R object[20], which has a prediction capability for cluster assignment of new models based on their scorings for the data fields in Table 5 (see help file for R function Mclust::predict.Mclust()). This would give each new model a probability of assignment to each of the eight model clusters identified and analysed in this report.

The advantages of this approach are speed and simplicity. However a potential disadvantage is that the existing clustering may not adequately represent radically new modelling strategies that might be developed in the future. We would expect this problem to be increasingly evident over longer time periods, because of new modelling opportunities afforded by advances in ecological theory, data availability and computational power. Such a problem might be identified by assessing the quality of clustering for the new results using the existing model with the quality of clustering of the original data. A comparison of summary statistics such as the Dunn index (Dunn, 1974) and silhouette width

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[20] The clustering model R object can be downloaded at http://www.efsa.europa.eu/en/supporting/doc/795eax1.zip

(Rousseeuw, 1987) should indicate the adequacy of the existing scheme to categorise newly discovered models.

If this analysis suggests the current clustering is no longer adequate then a second option would be to repeat the cluster analysis on the whole updated inventory. This would provide the best description of the updated range of models. However, a disadvantage of this is that it would then require re-interpretation of the new clustering output, in terms of differences in the ways the models within each cluster are formulated and applied (see section 4) and evaluation of their suitability for risk assessment tasks (see section 12). Furthermore, the Decision Support Scheme (section 13) based on the current clustering would also require substantial revision.

18. Assessment of the models of spread and dispersal of plant pests for their use in pest risk assessment

18.1. Evaluation of model fitness

The fitness scoring and discussion of model pros and cons suggested that there was no clear winner among the modelling strategies identified in the cluster analysis. Instead, each of the strategies had a combination of strengths and weaknesses meaning there is no one-size-fits all solution for using spread and dispersal models within Plant Health risk assessments. However, there were two clusters that had narrower utility for EFSA Plant Health risk assessment tasks than the other clusters. Clusters A (Single-event pest dispersal) and E (Iterative colonisation of hosts at small scales) obtained a far lower number of High fitness scores than the other clusters. The main reason for this was their simplicity and restriction to small spatial scales and a single growing season. We highlighted that these clusters may be useful for identifying the range of local dispersal from current infestations over a short period. However, we considered that they have limited suitability for application in other tasks of risk assessment.

A general issue that emerged in the comparison of the remaining clusters was a distinction between bottom-up and top-down modelling approaches. Bottom-up models are more strongly focused on writing equations or computer algorithms for the mechanistic processes that define how the species reproduces, dies and/or disperses. To predict spread or dispersal, parameters of these equations are estimated from specific experimental data, published values or expert knowledge. Alternatively, arbitrary values may be used for establishing general or theoretical principles from the modelling. The clusters most closely aligned to the bottom-up approach are B (Large-scale simulation of dispersal events), C (Pest spread or dispersal in continuous space and time), D (Continuous-space pest spread in discrete time) and H (Generic pest and host dynamics). An advantage of bottom-up approaches is that they can be used to analyse the biological processes and interactions that cause the pest to spread or to produce testable hypotheses and theory.

By contrast, top-down models are more driven by spread data and are generally parameterised by fitting to spread patterns using an appropriate statistical method. The equations used in top-down models may be more phenomenological than the strongly-mechanistic equations of bottom-up models. For example, top-down models may use a habitat suitability index to drive the spread dynamics (e.g. Smolik et al., 2010), without a mechanistic understanding of how the habitat characteristics are really affecting the demography or population dynamics of the pest species. Because of this reliance on spread data, the predictive outcome of the model is tightly coupled to the quality and quantity of spread data, which for emerging invasive pest organisms may be sparse. The clusters most strongly aligned to the top-down approach are A (Single event pest dispersal), E (Iterative colonisation of hosts at small scales) and F (Simulation of specific pest spread at large scales).

In general, bottom-up models are more reliant on biological data but less reliant on distribution or spread data than top-down models. This can be seen from the fitness scorings for data-reliance in Table 13. As a result, bottom-up approaches may be better suited to predicting future spread of species where data on recent spread are not available. This is often expected to be the case for pests that have only recently entered the risk assessment area. The corollary is that bottom-up modelling relies on knowledge of the key biological model parameters in the risk assessment area. This may also be lacking for recent arrivals, especially if they exhibit different behaviour or population dynamics in the risk assessment area than other regions in which they have been studied. By contrast, top-down approaches are more useful when data on how the pest has spread are available and where it can be reasonably assumed that the pest will continue to behave similarly in the future. This probably means the pest must be already established and has been documented as actively spreading over several years.

In terms of using the models for scenario experiments, the mechanistic basis of bottom-up approaches generally makes them better suited to biological scenarios. For example, one can compare control measures that target particular life history stages (e.g. Shea et al., 2010) or investigate the dynamic effects of biological control agents (e.g. Fagan et al., 2002). The top-down models are probably better for comparing different spatial control scenarios, such as identifying where is best to target eradication measures (Richter et al., 2012). Because the top-down approaches are more strongly driven by spread data and often use gridded climate or land use data as inputs, they are also probably the most suited to predicting spread under realistic climate or land use change scenarios (e.g. Richardson et al., 2010). However, the more bottom-up approaches may be better for making mechanistic predictions of how ecological or evolutionary spread dynamics respond to climate change (e.g. Bullock et al., 2012).

It is important to note that the distinction between top-down and bottom-up is by no means absolute, and all clusters probably contain some element of both. For example, within the predominantly bottom-up models in Cluster C there are some examples of using complex statistical methods to fit the reaction-diffusion model to spread patterns (e.g. Roques et al., 2011). Likewise, some models in the predominantly top-down Cluster F are formulated from a strongly bottom-up perspective but then fitted to data (e.g. Lele et al., 1998). In other cases, biological knowledge about key model processes or parameter values is used to constrain top-down fitting of the model to spread data (e.g. Pitt et al., 2009). This emphasises the point that data-availability is a key determinant of whether model development proceeds from a more top-down or bottom-up direction. Ideally good biological and spread data would both be available, which facilitates the more intermediate approaches benefitting from both biological mechanism and a calibrated or validated ability to emulate realistic spread pattern.

Our analysis highlighted that some risk assessment tasks were generally poorly covered by all the model clusters. Explicit modelling of the pest entry process was very rarely performed in the reviewed literature, meaning that modelling the effectiveness of phytosanitary measures was not well addressed by any of the clusters (Table 13). Where the models incorporated environmental heterogeneity, this was generally as a static landscape input. Therefore temporal forcing and fluctuating environments were largely ignored, though these may be very relevant for the rate of species spread (Neubert et al., 2000) under climate change scenarios. Human-mediated dispersal mechanisms were also rarely explicitly modelled, and even when this was done it was mainly through the use of generic dispersal kernels rather than mechanistic models for non-random human behaviour. Finally, most models represented a single dispersal mechanism (or aggregated multiple mechanisms into a single kernel) and so cannot be used for identifying the dispersal mechanism most important for pest spread. However, across the reviewed literature there are individual, atypical models that have incorporated these factors.

18.2. Decision Support Scheme

The fitness evaluation was used to develop a Decision Support Scheme (DSS) that allows risk assessors to select the most appropriate models to apply in risk assessment for a specific pest. The DSS consists of a number of steps beginning with a preliminary review of data and existing models, which we expect would happen as part of the standard EFSA risk assessment initiation process (EFSA Panel on Plant Health, 2010a). The main stages in the DSS are then to: (1) search the Electronic Model Inventory for any existing spread models for the focal pest; (2) select the most suitable and feasible model clusters, given the risk assessment goals of the modelling and data constraints; (3) examine models with desirable properties from the selected clusters; and (4) apply a similar search across other clusters in case insufficient results are found in the previous steps. The result is a shortlist of models that should be well suited for application in the current risk assessment.

We do not view the DSS as generally being a rigid prescription for picking a single model for direct application. This may be possible in some cases where the underlying assumptions are valid for the focal pest and appropriate data exist, such as in our application of the HYSPLIT model in Case Study 1[21]. However, generally we would not expect this to be the case. Rather, we expect the DSS to provide guidance on choosing appropriate modelling strategies and example models from which to develop bespoke pest spread models that would provide useful information for the current risk assessment. Therefore, the DSS recognised the range of risk assessment questions that the modelling could contribute to and the focal pest-host system in order to rank model clusters in terms of their suitability. The DSS also considers constraints on modelling in terms of missing data or modelling expertise to rank model clusters in terms of their feasibility. Another property of the DSS is that it recognises the heterogeneity within each of the modelling clusters by specifying a procedure for identifying potentially useful models assigned to other clusters. The aim is that by using the DSS a group of useful models will be identified and the assessor can either identify a directly applicable model for re-use or draw on the whole group to develop a similar model for the risk assessment.

A key part of the DSS is that the reviewer is required to assign weightings to the relevance of the fitness criteria to the specific goals of modelling for the current risk assessment. The weightings should be chosen to reflect where modelling should contribute to the risk assessment questions and any known constraints on the modelling. As such we expect that the pre-DSS initiation phase will be feed directly into the DSS by defining the key elements of the pest’s biology to model and available data sources. The weighting will inevitably introduce subjectivity to the process and require careful choice of weights. In particular, success of the DSS will likely depend on the weighting of the criteria concerning modelling goals and applications (Table 17). If the weights on model uses are too liberal, i.e. if the assessor is over-optimistic about how much can be achieved through modelling, then it is likely that none of these clusters will be especially well suited to encompass all the highly-weighted modelling tasks. In our view, it is advisable to use the weightings to specify more restricted aims and consequently select a type of model that is highly suitable for these aims. This echoes our previous discussion about there being no one-size-fits-all modelling strategy.

We consider the DSS to be a flexible system for both guiding towards the appropriate model formulation and for determining where modelling can usefully contribute to risk assessment. However, as described above successful application is likely to require a good understanding of the pests’ biology and available data sources and a clear definition of the goals of modelling for risk assessment.

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[21] The report for Case Study 1 can be downloaded at http://www.efsa.europa.eu/en/supporting/doc/795eax1.zip

19. Case studies of model selection and application

Across seven case studies, representing a diversity of plant pest organisms, risk assessment scenarios and dispersal mechanisms, we showed how the Decision Support Scheme (DSS) can be used to select models from the Electronic Model Inventory for practical application during risk assessment. In most of the case studies we made substantial modifications to the published models to adapt them to the data sources and biology of the focal pest. Full details are given in the separate reports for each case study, which accompany this main report. This emphasises that although the literature documented in the Electronic Model Inventory provides a valuable source of information, it may not provide ready-made or off-the-shelf solutions. Rather, it may be necessary to customise the existing models to suit the particular risk assessment.

Even when a fairly well-known modelling method can be used, such as reaction-diffusion or integrodifference equations, it will still generally require coding of the model equations rather than use of modelling software. Indeed, six of the seven case studies were implemented by re-coding the equations of the published models, while only one (Case Study 1[22]) used existing software. This facilitates modification of the published models to suit the current risk assessment needs, but also requires computer programming and mathematical skills. Therefore, this suggests that EFSA will need to draw on modelling experts to make greater use of quantitative models during Plant Health risk assessments.

Although the DSS successfully located models for our application, there may be occasions where the DSS indicates that none of the Clusters can be applied because modelling constraints are too severe. We expect the main constraint preventing model application would be lack of data for parameterisation or model-fitting. However, this is still a useful outcome for risk assessment as it will quickly indicate that quantitative modelling is not feasible, and so the risk assessor should use the existing qualitative protocols for the exercise.

CONCLUSIONS

Risk assessment forms an important element in the armoury against the long-term threat of invasive organisms that damage economically valuable plants and plant products (Keller et al., 2007; Kehlenbeck et al., 2012). The potential benefits of quantitative modelling of spread and dispersal for pest risk assessment are clear, both in terms of dynamically predicting the region at risk of pest colonisation and in gaining greater understanding of the processes driving spread (Kehlenbeck et al., 2012; Truscott and Ferguson, 2012). Therefore it would be desirable for EFSA to make greater use of spread and dispersal modelling in EU Plant Health risk assessment.

However, in order for spread and dispersal modelling to be used more frequently, risk assessors require an overview of current modelling approaches and a system for identifying the appropriate models to apply in their current assessment. In this report we have made progress towards those goals. The extensive literature review delivered the searchable Electronic Model Inventory of models, while the cluster analysis identified eight common strategies for modelling pest spread and dispersal. After considering the strengths and weaknesses of the modelling strategies we developed the Decision Support Scheme to allow risk assessors to locate models for application for the particular risk assessment tasks and constraints they face. The decision process was tested by application of the DSS across seven risk assessment modelling case studies, successfully demonstrating the utility of the approach.

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[22] The report for Case Study 1 can be downloaded at http://www.efsa.europa.eu/en/supporting/doc/795eax1.zip

We therefore conclude that the tools and systems developed in this project should make it feasible for EFSA to include quantitative spread and dispersal modelling in a greater proportion of Plant Health risk assessments than has previously been the case. By making use of the Electronic Model Inventory and Decision Support Scheme we expect that suitable models can be found for direct application or adaptation in many risk assessments. It was beyond the scope of this project to assess whether this might provide more accurate or precise risk estimates than the qualitative procedures currently employed by EFSA (EFSA Panel on Plant Health (PLH), 2010a). However, spread and dispersal models can provide answers to many considerations of risk assessment. For example, models can estimate the rate and extent of pest spread, the role of environmental conditions and host plants in mediating spread, the biological traits of the pest that promote spread and the effectiveness of alternative phytosanitary and other risk reduction measures. Therefore, incorporating the systems developed in this report and expertise in spread and dispersal modelling into risk assessment teams is likely to at least offer new ways to address the questions that need answering for effective risk assessment.

RECOMMENDATIONS

Our overall recommendation is that EFSA should use the systems developed in this report to make greater use of pest spread and dispersal models in Plant Health risk assessments. The identification and characterisation of the model clusters, Electronic Model Inventory and Decision Support Scheme should make it possible for EFSA risk assessors to focus on modelling approaches that are well-suited to their current risk assessment scenario.

The main specific recommendations arising from this project are as follows:

- We recommend that EFSA should not view the clusters as “off-the-shelf” solutions for direct application in risk assessment. Our clustering represents the best partition of the spectrum of extensively reviewed models, using statistical criteria based on their structure and formulation. Nevertheless there is a high diversity of model types within each cluster. Before application of a model, EFSA should get an overview of the whole cluster, which the latter steps of the Decision Support Scheme are designed to achieve. It may often be the case that a combination and adaptation of more than one model in the cluster will give the optimal solution.

- We recommend that it will often be necessary for EFSA to modify an existing model rather than directly apply it in risk assessment. This was reflected in our experience performing the seven case studies. In most cases the published models required self-coding and modification to their equations or simulation procedures to be applied to the focal pest. Reasons for this include known differences in the biology of the focal pest and the one modelled previously and different data available or relevant to the modelling. This emphasises a requirement for expertise in modelling among the risk assessors to ensure flexible development of models tailored to the specific risk assessment. EFSA should ensure that the working groups tasked with performing risk assessments have access to modelling expertise. Possible options for EFSA to achieve this include having modellers as members of the working group, providing internal modelling support from EFSA staff, or procurement of the modelling task to external modelling experts.

- We recommend that EFSA should not use available generic models simply because they are ready to use as software packages. For example, in one case study we were able to apply HYSPLIT-WEB, an ‘off-the-shelf’ model for atmospheric particle dispersion (Draxler et al., 1999) which we used for wind dispersal of fungal spores (see Case Study 1[23]). Although our team does not consist of atmospheric modellers, we were able to use its simple web interface to parameterise and run simulations and then obtain model outputs for interpretation. However, even though we were able to run the model, our lack of expertise in atmospheric modelling meant it was difficult for us to interpret the realism or validity of the outputs. This underlines our previous recommendation that modelling expertise is highly recommended to prevent inappropriate model use or interpretation.

- Our recommendations for successful application of the Decision Support Scheme (DSS) by EFSA are as follows:

  - We recommend that the DSS should be used as a system to guide a risk assessor in the direction of useful models rather than a rigid prescription for picking a model. Several elements of the DSS are unavoidably subjective judgements; not least the selection of weights for suitability and feasibility (see Section 13.2.2) and the choice of filters applied to the selected cluster (see Section 13.2.3). Both of these steps require the assessor to consider what they want to achieve with the model, the important biological processes and data to include in the model, and the assessor's own expertise for implementing different models. We recommend EFSA ensure that these considerations are discussed with the whole working group and fully documented in resulting opinions. In practice this may mean that an assessor goes through multiple iterations of the DSS, refining their choices to produce a satisfactory outcome. Again, we recommend that this process should be fully documented to ensure transparency of the modelling.

  - We recommend that EFSA should ensure dialogue and collaboration between modellers and pest species' experts for the best possible use of the DSS. We consider that modelling expertise is highly desirable for successful use of the DSS by EFSA, as well as being essential for the subsequent application of the models. We generally expect an experienced modeller to have a level of intuition about the kinds of tasks suited to modelling based on the pest's biology and available sources of data, which will guide their selection of modelling goals and weightings in the DSS. Likewise, the prior review stage of the DSS will strongly benefit from input by pest experts as well as modellers. In this prior review the pest's biology, previous models and data availability are researched and the risk assessment goals for modelling are decided, setting the scene for model selection. The importance of the prior review was demonstrated in our attempt to use a reaction-diffusion equation for *Xylella fastidiosa* spread (Case Study 3[24]). After we had begun the case study, new information on the epidemiology of this emerging disease was released indicating very different behaviour in the risk assessment area than in North America, where it has been well-studied. Therefore using model parameter values derived from North America was not appropriate and, if reported earlier, would have been picked up in the initial review stage. All these considerations lead to our recommendation that EFSA ensure close collaboration between the modellers and pest species' experts during the whole exercise. Inclusion of the modellers on the working group carrying out the risk assessment may be the best option for EFSA to achieve the necessary dialogue.

  - We recommend that the EFSA working group should clearly define a small number of complementary modelling goals for getting the best results from the DSS. This is because our evaluation of model fitness indicated that no one cluster was well suited to all possible

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[23] The report for Case Study 1 can be downloaded at http://www.efsa.europa.eu/en/supporting/doc/795eax1.zip

[24] The report for Case Study 3 can be downloaded at http://www.efsa.europa.eu/en/supporting/doc/795eax1.zip

  elements of risk assessment. As such the DSS will be most effective when the goals of the modelling used to score the suitability of each cluster (see Section 13.2.2) are clearly stated and relatively small in number.

  - We recommend that in any future development of the DSS, EFSA should elaborate on the model feasibility criteria to refine the assessment of the clusters. The current procedure features four feasibility weightings to evaluate possible constraints on modelling (see Section 13.2.2). During our practical application for the case studies we found that this relatively small number meant that the scoring and therefore ranking of cluster feasibility was less precise than was the case for model suitability. One option for this would be to provide more detailed breakdown of the data constraints that may affect the modelling.

- We recommend that EFSA establish a procedure for regular updating of the literature search and the Electronic Model Inventory that stores details of the models. As discussed above (Section 17) we consider that the best option is to repeat the extensive literature search every three to five years and append the new results to the inventory, including the scoring. The next step would be to assign the new models to the existing clusters using the clustering model developed here, and to then assess whether the current clustering model is adequate for the new models. If this is so, then the new models can be assigned to the existing clusters and feature in ongoing use of the Decision Support Scheme. If not, then it would be necessary to update the cluster analysis, interpret the new clusters and their pros and cons for risk assessments, and revise the Decision Support Scheme accordingly.

- We recommend the use of quantitative spread and dispersal models for potential benefits to EFSA risk assessment in addition to providing direct answers to many of the questions addressed by Plant Health risk assessment (see Table 14). For example, models can generate hypotheses about how a pest spreads. This was seen in Case Study 5[25] where rare long-distance dispersal events were required for the model to produce the observed pattern of *Xylella fastidiosa* spread. Models can also guide data requirements, as for example when sensitivity analyses determine the most important parameters on which to obtain reliable information. Furthermore, models can be used for experimenting with risk reduction options in a way that is impossible in the real world.

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[25] The report for Case Study 5 can be downloaded at http://www.efsa.europa.eu/en/supporting/doc/795eax1.zip

REFERENCES

Aylor DE, Schmale DG, III, Shields EJ, Newcomb M and Nappo CJ, 2011. Tracking the potato late blight pathogen in the atmosphere using unmanned aerial vehicles and Lagrangian modeling. Agricultural and Forest Meteorology, 151, 251-260.

Bates S, Clapton J and Coren E, 2007. Systematic maps to support the evidence base in social care. Evidence & Policy: A Journal of Research, Debate and Practice, 3, 539-551.

Beaumont MA, 2010. Approximate Bayesian computation in evolution and ecology. Annual review of ecology, evolution, and systematics, 41, 379-406.

Bhatia PS, 2012. A tutorial for blockcluster R package Version 2.

Blackmer JL, Hagler JR, Simmons GS and Cañas LA, 2004. Comparative Dispersal of Homalodisca coagulata and Homalodisca liturata (Homoptera: Cicadellidae). Environmental Entomology, 33, 88-99.

Blackmer JL, Hagler JR, Simmons GS and Henneberry TJ, 2006. Dispersal of Homalodisca vitripennis (Homoptera : Cicacellidae) from a point release site in citrus. Environmental Entomology, 35, 1617-1625.

Blenis PV, Chang KF and Hiratsuka Y, 1993. Spore Dispersal Gradients and Disease Gradients of Western Gall Rust. Canadian Journal of Forest Research-Revue Canadienne De Recherche Forestiere, 23, 2481-2486.

Bolker BM and Pacala SW, 1999. Spatial moment equations for plant competition: Understanding spatial strategies and the advantages of short dispersal. American Naturalist, 153, 575-602.

Brewster CC and Allen JC, 1997. Spatiotemporal Model for Studying Insect Dynamics in Large-Scale Cropping Systems. Environmental Entomology, 26, 473-482.

Brown DH and Hastings A, 2003. Resistance may be futile: dispersal scales and selection for disease resistance in competing plants. Journal of Theoretical Biology, 222, 373-388.

Bullock J (Natural Environment Research Council, UK), 2012. Assessing and controlling the spread and the effects of common ragweed in Europe.

Bullock JM, Pywell RF and Coulson-Phillips SJ, 2008. Managing plant population spread: prediction and analysis using a simple model. Ecological Applications, 18, 945-953.

Bullock JM, White SM, Prudhomme C, Tansey C, Perea R and Hooftman DAP, 2012. Modelling spread of British wind-dispersed plants under future wind speeds in a changing climate. Journal of Ecology, 100, 104-115.

Calonnec A, Cartolaro P, Naulin JM, Bailey D and Langlais M, 2008. A host-pathogen simulation model: powdery mildew of grapevine. Plant Pathology, 57, 493-508.

Caplat P, Nathan R and Buckley YM, 2012. Seed terminal velocity, wind turbulence, and demography drive the spread of an invasive tree in an analytical model. Ecology, 93, 368-377.

Carrasco LR, Harwood TD, Toepfer S, MacLeod A, Levay N, Kiss J, Baker RHA, Mumford JD and Knight JD, 2010a. Dispersal kernels of the invasive alien western corn rootworm and the effectiveness of buffer zones in eradication programmes in Europe. Annals of Applied Biology, 156, 63-77.

Carrasco LR, Mumford JD, MacLeod A, Harwood T, Grabenweger G, Leach AW, Knight JD and Baker RHA, 2010b. Unveiling human-assisted dispersal mechanisms in invasive alien insects: Integration of spatial stochastic simulation and phenology models. Ecological Modelling, 221, 2068-2075.

CEBC (Centre for Evidence-Based Conservation), 2010. Guidelines for Systematic Review in Environmental Management. Version 4.0.

Chaianunporn T and Hovestadt T, 2012. Evolution of dispersal in metacommunities of interacting species. Journal of Evolutionary Biology, 25, 2511-2525.

Cook A, Marion G, Butler A and Gibson G, 2007. Bayesian Inference for the Spatio-Temporal Invasion of Alien Species. Bulletin of Mathematical Biology, 69, 2005-2025.

Cousens R, Dytham C and Law R, 2008. Dispersal in plants: A population perspective. Editor. Oxford University Press, Oxford, UK,

Dauer JT, Mortensen DA and Humston R, 2006. Controlled experiments to predict horseweed (Conyza canadensis) dispersal distances. Weed Science, 54, 484-489.

Dauer JT, Mortensen DA and Vangessel MJ, 2007. Temporal and spatial dynamics of long-distance Conyza canadensis seed dispersal. Journal of Applied Ecology, 44, 105-114.

Draxler RR, Stunder B, Rolph G and Taylor A 1999. HYSPLIT4 user's guide. NOAA Technical Memorandum ERL ARL. 230, 35.

Dunn JC, 1974. Well-separated clusters and optimal fuzzy partitions. Journal of cybernetics, 4, 95-104.

EFSA, 2009. Evaluation of pest risk assessments and risk management options prepared to justify requests for phytosanitary measures under Council Directive 2000/29/EC [1] - Guidance of the Panel on Plant Health The EFSA Journal, 1194, 1-18.

EFSA, 2010. Application of systematic review methodology to food and feed safety assessments to support decision making. EFSA Journal, 8, 90.

EFSA Panel on Plant Health, 2010a. Guidance on a harmonised framework for pest risk assessment and the identification and evaluation of pest risk management options by EFSA. EFSA Journal, 8, 1495.

EFSA Panel on Plant Health, 2010b. Risk assessment of the oriental chestnut gall wasp, *Dryocosmus kuriphilus* for the EU territory and identification and evaluation of risk management options. EFSA Journal, 8, 1619.

EFSA Panel on Plant Health, 2013. Scientific Opinion on the risks to plant health posed by *Bemisia tabaci* species complex and viruses it transmits for the EU territory. EFSA Journal, 11, 3162.

EFSA Panel on Plant Health (PLH), 2010a. Guidance on a harmonised framework for pest risk assessment and the identification and evaluation of pest risk management options by EFSA. EFSA Journal, 8, 1495.

EFSA Panel on Plant Health (PLH), 2010b. Risk assessment of the oriental chestnut gall wasp, Dryocosmus kuriphilus for the EU territory and identification and evaluation of risk management options EFSA Journal, 8, 1619.

EFSA Panel on Plant Health (PLH), 2011. Pest risk assessment of Monilinia fructicola for the EU territory and identification and evaluation of risk management options. EFSA Journal, 9, 2119.

EFSA Panel on Plant Health (PLH), 2013. Scientific Opinion on the risks to plant health posed by *Bemisia tabaci* species complex and viruses it transmits for the EU territory. EFSA Journal, 11, 3162.

EFSA PLH Panel (EFSA Panel on Plant Health), 2014. Scientific Opinion on the environmental risk assessment of the apple snail for the EU. EFSA Journal, 12, 3641.

EFSA PLH Panel (EFSA Panel on Plant Health), 2015. Scientific Opinion on the risks to plant health posed by Xylella fastidiosa in the EU territory, with the identification and evaluation of risk reduction options. EFSA Journal, 13, 262.

Ellner SP and Schreiber SJ, 2012. Temporally variable dispersal and demography can accelerate the spread of invading species. Theoretical Population Biology, 82, 283-298.

Epanchin-Niell RS, Haight RG, Berec L, Kean JM and Liebhold AM, 2012. Optimal surveillance and eradication of invasive species in heterogeneous landscapes. Ecology Letters, 15, 803-812.

EPPO, 2013. PQR - EPPO database on quarantine pests (available online). http://www.eppo.int.

Eppstein MJ and Molofsky J, 2007. Invasiveness in plant communities with feedbacks. Ecology Letters, 10, 253-263.

Fagan WF, Lewis MA, Neubert MG and van den Driessche P, 2002. Invasion theory and biological control. Ecology Letters, 5, 148-157.

Fennell M, Murphy JE, Armstrong C, Gallagher T and Osborne B, 2012. Plant Spread Simulator: A model for simulating large-scale directed dispersal processes across heterogeneous environments. Ecological Modelling, 230, 1-10.

Ferrandino FJ and Elmer WH, 1996. Septoria leaf spot lesion density on trap plants exposed at varying distances from infected tomatoes. Plant Disease, 80, 1059-1062.

Ferrari MJ, Bjørnstad ON, Partain JL and Antonovics J, 2006. A gravity model for the spread of a pollinator-borne plant pathogen. American Naturalist, 168, 294-303.

Filipe JAN, Maule MM and Gilligan CA, 2004a. On 'Analytical models for the patchy spread of plant disease'. Bulletin of Mathematical Biology, 66, 1027-1037.

Filipe JAN, Otten W, Gibson GJ and Gilligan CA, 2004b. Inferring the dynamics of a spatial epidemic from time-series data. Bulletin of Mathematical Biology, 66, 373-391.

Fraley C and Raftery AE, 2002. Model-based clustering, discriminant analysis, and density estimation. Journal of the American Statistical Association, 97, 611-631.

Fraley C, Raftery AE, Murphy TB and Scrucca L (Technical report), 2012. MCLUST version 4 for R: normal mixture modeling for model-based clustering, classification, and density estimation.

Furuno A, Chino M, Otuka A, Watanabe T, Matsumura M and Suzuki Y, 2005. Development of a numerical simulation model for long-range migration of rice planthoppers. Agricultural and Forest Meteorology, 133, 197-209.

Garnier A, Pivard S and Lecomte J, 2008. Measuring and modelling anthropogenic secondary seed dispersal along roadverges for feral oilseed rape. Basic and Applied Ecology, 9, 533-541.

Gharekhani G, 2009. Modeling population dynamics and dispersion of codling moth Cydia pomonella L.(Lepidoptera, Tortricidae). Doctoral thesis. Faculty of Agricultural Sciences at the University of Hohenheim, Stuttgart, Germany,

Gilbert M, Grégoire JC, Freise JF and Heitland W, 2004. Long-distance dispersal and human population density allow the prediction of invasive patterns in the horse chestnut leafminer *Cameraria ohridella*. Journal of Animal Ecology, 73, 459-468.

Gilligan CA, Truscott JE and Stacey AJ, 2007. Impact of scale on the effectiveness of disease control strategies for epidemics with cryptic infection in a dynamical landscape: an example for a crop disease. Journal of the Royal Society Interface, 4, 925-934.

Gottwald TR, Gibson GJ, Garnsey SM and Irey M, 1999. Examination of the effect of aphid vector population composition on the spatial dynamics of citrus tristeza virus spread by stochastic modeling. Phytopathology, 89, 603-608.

Govaert G and Nadif M, 2003. Clustering with block mixture models. Pattern Recognition, 36, 463-473.

Harrison S, Hastings A and Strong DR, 2005. Spatial and temporal dynamics of insect outbreaks in a complex multitrophic system: tussock moths, ghost moths, and their natural enemies on bush lupines. Annales Zoologici Fennici, 42, 409-419.

Harwood TD, Xu X, Pautasso M, Jeger MJ and Shaw MW, 2009. Epidemiological risk assessment using linked network and grid based modelling: *Phytophthora ramorum* and *Phytophthora kernoviae* in the UK. Ecological Modelling, 220, 3353-3361.

Hester S and Cacho O, 2012. Optimization of Search Strategies in Managing Biological Invasions: A Simulation Approach. Human and Ecological Risk Assessment, 18, 181-199.

Hopkinson RF and Soroka JJ, 2010. Air trajectory model applied to an in-depth diagnosis of potential diamondback moth infestations on the Canadian Prairies. Agricultural and Forest Meteorology, 150, 1-11.

Hulme PE, 2009. Trade, transport and trouble: managing invasive species pathways in an era of globalization. Journal of Applied Ecology, 46, 10-18.

IPPC, 2010. International Standards for Phytosanitary Measures No. 5. Glossary of Phytosanitary Terms. Secretariat of the International Plant Protection Convention,

Isard SA, Russo JM and Ariatti A, 2007. The Integrated Aerobiology Modeling System applied to the spread of soybean rust into the Ohio River valley during September 2006. Aerobiologia, 23, 271-282.

Iverson LR, Prasad A, Bossenbroek J, Sydnor D and Schwartz MW, 2010. Modeling Potential Movements of the Emerald Ash Borer: the Model Framework. U S Forest Service Pacific Northwest Research Station General Technical Report PNW-GTR, 581-597.

Johnson AR and Turner SJ, 2010. Relevance of Spatial and Temporal Scales to Ecological Risk Assessment. In: Environmental Risk Assessment and Management from a Landscape Perspective. John Wiley & Sons, Inc., 55-74.

Kapustka LA, 2010. Ecological Risk Assessment toward a Landscape Perspective. In: Environmental Risk Assessment and Management from a Landscape Perspective. John Wiley & Sons, Inc., 11-31.

Kareiva PM, 1983. Local movement in herbivorous insects: applying a passive diffusion model to mark-recapture field experiments. Oecologia, 57, 322-327.

Katul G, Porporato A, Nathan R, Siqueira M, Soons M, Poggi D, Horn H and Levin S, 2005. Mechanistic analytical models for long-distance seed dispersal by wind. The American Naturalist, 166, 368-381.

Kehlenbeck H, Robinet C, van der Werf W, Kriticos D, Reynaud P and Baker R, 2012. Modelling and mapping spread in pest risk analysis: a generic approach. EPPO Bulletin, 42, 74-80.

Keller RP, Lodge DM and Finnoff DC, 2007. Risk assessment for invasive species produces net bioeconomic benefits. Proceedings of the National Academy of Sciences, 104, 203-207.

Kinezaki N, Kawasaki K and Shigesada N, 2010. The effect of the spatial configuration of habitat fragmentation on invasive spread. Theoretical Population Biology, 78, 298-308.

Korniss G and Caraco T, 2005. Spatial dynamics of invasion: the geometry of introduced species. Journal of Theoretical Biology, 233, 137-150.

Kot M, Lewis MA and Van Den Driessche P, 1996. Dispersal data and the spread of invading organisms. Ecology, 77, 2027-2042.

Laranjeira FF, Barbosa CJ, Santos-Filho HP, Gonçalves TF and Nickel O, 2006. Progress, spread and natural transmission of Bahia bark scaling of citrus in Brazil. Annals of Applied Biology, 148, 187-195.

Lele S, Taper ML and Gage S, 1998. Statistical analysis of population dynamics in space and time using estimating functions. Ecology, 79, 1489-1502.

Leskinen M, Markkula I, Koistinen J, Pylkkö P, Ooperi S, Siljamo P, Ojanen H, Raiskio S and Tiilikkala K, 2011. Pest insect immigration warning by an atmospheric dispersion model, weather radars and traps. Journal of Applied Entomology, 135, 55-67.

Liebhold AM, Work TT, McCullough DG and Cavey JF, 2006. Airline baggage as a pathway for alien insect species invading the United States. American Entomologist, 52, 48-54.

Lô-Pelzer E, Bousset L, Jeuffroy MH, Salam MU, Pinochet X, Boillot M and Aubertot JN, 2010. SIPPOM-WOSR: A Simulator for Integrated Pathogen POpulation Management of phoma stem canker on Winter OilSeed Rape. I. Description of the model. Field Crops Research, 118, 73-81.

Mahdjoub T and Menu F, 2008. Prolonged diapause: A trait increasing invasion speed? Journal of Theoretical Biology, 251, 317-330.

Marion G, Gibson G and Renshaw E, 2003. Estimating likelihoods for spatio-temporal models using importance sampling. Statistics and Computing, 13, 111-119.

Meentemeyer RK, Cunniffe NJ, Cook AR, Filipe JAN, Hunter RD, Rizzo DM and Gilligan CA, 2011. Epidemiological modeling of invasion in heterogeneous landscapes: spread of sudden oak death in California (1990–2030). Ecosphere, 2, art17.

Mercader RJ, Siegert NW, Liebhold AM and McCullough DG, 2011. Simulating the effectiveness of three potential management options to slow the spread of emerald ash borer (Agrilus planipennis) populations in localized outlier sites. Canadian Journal of Forest Research-Revue Canadienne De Recherche Forestiere, 41, 254-264.

Meyerson LA and Mooney HA, 2007. Invasive alien species in an era of globalization. Frontiers in Ecology and the Environment, 5, 199-208.

Moorcroft PR, Pacala SW and Lewis MA, 2006. Potential role of natural enemies during tree range expansions following climate change. Journal of Theoretical Biology, 241, 601-616.

Morton D, Rowland C, Wood C, Meek L, Marston C, Smith G, Wadsworth R and Simpson I, 2011. Final Report for LCM2007-the new UK land cover map. Countryside Survey Technical Report No 11/07.

Muirhead JR, Leung B, van Overdijk C, Kelly DW, Nandakumar K, Marchant KR and MacIsaac HJ, 2006. Modelling local and long-distance dispersal of invasive emerald ash borer Agrilus planipennis (Coleoptera) in North America. Diversity and Distributions, 12, 71-79.

Neubert MG, Kot M and Lewis MA, 2000. Invasion speeds in fluctuating environments. Proceedings of the Royal Society B: Biological Sciences, 267, 1603-1610.

Niggemann M, Jetzkowitz J, Brunzel S, Wichmann MC and Bialozyt R, 2009. Distribution patterns of plants explained by human movement behaviour. Ecological Modelling, 220, 1339-1346.

Ntahimpera N, Ellis MA, Wilson LL and Madden LV, 1998. Effects of a cover crop on splash dispersal of Colletotrichum acutatum conidia. Phytopathology, 88, 536-543.

Oerke EC and Dehne HW, 2004. Safeguarding production—losses in major crops and the role of crop protection. Crop Protection, 23, 275-285.

Pan Z, Yang XB, Pivonia S, Xue L, Pasken R and Roads J, 2006. Long-term prediction of soybean rust entry into the continental United States. Plant Disease, 90, 840-846.

Park AW, Gubbins S and Gilligan CA, 2001. Invasion and persistence of plant parasites in a spatially structured host population. Oikos, 94, 162-174.

Parry H, Sadler R and Kriticos D, 2013. Practical guidelines for modelling post-entry spread in invasion ecology. NeoBiota, 18, 41-66.

Paulitz TC, Dutilleul P, Yamasaki SH, Fernando WGD and Seaman WL, 1999. A generalized two-dimensional Gaussian model of disease foci of head blight of wheat caused by Gibberella zeae. Phytopathology, 89, 74-83.

Pergl J, Müllerová J, Perglová I, Herben T and Pyšek P, 2011. The role of long-distance seed dispersal in the local population dynamics of an invasive plant species. Diversity and Distributions, 17, 725-738.

Peterson AT, Scachetti-Pereira R and Hargrove WW, 2004. Potential geographic distribution of Anoplophora glabripennis (Coleoptera : Cerambycidae) in North America. American Midland Naturalist, 151, 170-178.

Pethybridge SJ and Madden LV, 2003. Analysis of spatiotemporal dynamics of virus spread in an Australian hop garden by stochastic modeling. Plant Disease, 87, 56-62.

Pimentel D, 2002. Introduction: non-native species in the world. Biological invasions: economic and environmental costs of alien plant, animal, and microbe species, 3-8.

Pitt JPW, Kriticos DJ and Dodd MB, 2011. Temporal limits to simulating the future spread pattern of invasive species: Buddleja davidii in Europe and New Zealand. Ecological Modelling, 222, 1880-1887.

Pitt JPW, Worner SP and Suarez AV, 2009. Predicting Argentine ant spread over the heterogeneous landscape using a spatially explicit stochastic model. Ecological Applications, 19, 1176-1186.

Pocock MJ and Evans DM, 2014. The success of the horse-chestnut leaf-miner, Cameraria ohridella, in the UK revealed with hypothesis-led citizen science. Plos One, 9, e86226.

Randall N and James K, 2012. The effectiveness of integrated farm management, organic farming and agri-environment schemes for conserving biodiversity in temperate Europe - A systematic map. Environmental Evidence, 1, 4.

Richardson DM, Iponga DM, Roura-Pascual N, Krug RM, Milton SJ, Hughes GO and Thuiller W, 2010. Accommodating scenarios of climate change and management in modelling the distribution of the invasive tree Schinus molle in South Africa. Ecography, 33, 1049-1061.

Richter R, Dullinger S, Essl F, Leitner M and Vogl G, 2012. How to account for habitat suitability in weed management programmes? Biological Invasions, 15, 657-669.

Roques L, Soubeyrand S and Rousselet J, 2011. A statistical-reaction-diffusion approach for analyzing expansion processes. Journal of Theoretical Biology, 274, 43-51.

Rossi V, Salinari F, Bernazzani R, Giosuè S and Mazzoni E, 2009. Models for pest’s epidemiology: review, documentation and evaluation for Pest Risk Analysis (Mopest). Editor.

Rothlisberger JD and Lodge DM, 2011. Limitations of Gravity Models in Predicting the Spread of Eurasian Watermilfoil. Conservation Biology, 25, 64-72.

Rousseeuw PJ, 1987. Silhouettes: a graphical aid to the interpretation and validation of cluster analysis. Journal of computational and applied mathematics, 20, 53-65.

Sapoukhina N, Durel CE and Le Cam B, 2009. Spatial deployment of gene-for-gene resistance governs evolution and spread of pathogen populations. Theoretical Ecology, 2, 229-238.

Shea K, Jongejans E, Skarpaas O, Kelly D and Sheppard AW, 2010. Optimal management strategies to control local population growth or population spread may not be the same. Ecological Applications, 20, 1148-1161.

Sisterson MS, 2008. Effects of insect-vector preference for healthy or infected plants on pathogen spread: insights from a model. Journal of Economic Entomology, 101, 1-8.

Sisterson MS and Stenger DC, 2013. Roguing with Replacement in Perennial Crops: Conditions for Successful Disease Management. Phytopathology, 103, 117-128.

Skarpaas O, Silverman EJ, Jongejans E and Shea K, 2011. Are the best dispersers the best colonizers? Seed mass, dispersal and establishment in Carduus thistles. Evolutionary Ecology, 25, 155-169.

Skellam J, 1951. Random dispersal in theoretical populations. Biometrika, 196-218.

Skelsey P, Rossing WAH, Kessel GJT and van der Werf W, 2010. Invasion of Phytophthora infestans at the Landscape Level: How Do Spatial Scale and Weather Modulate the Consequences of Spatial Heterogeneity in Host Resistance? Phytopathology, 100, 1146-1161.

Smolik MG, Dullinger S, Essl F, Kleinbauer I, Leitner M, Peterseil J, Stadler LM and Vogl G, 2010. Integrating species distribution models and interacting particle systems to predict the spread of an invasive alien plant. Journal of Biogeography, 37, 411-422.

Soubeyrand S, Enjalbert J, Kretzschmar A and Sache I, 2009. Building anisotropic sampling schemes for the estimation of anisotropic dispersal. Annals of Applied Biology, 154, 399-411.

Stanaway MA, Reeves R and Mengersen KL, 2011. Hierarchical Bayesian modelling of plant pest invasions with human-mediated dispersal. Ecological Modelling, 222, 3531-3540.

Stephenson CM, Kohn DD, Park KJ, Atkinson R, Edwards C and Travis JM, 2007. Testing mechanistic models of seed dispersal for the invasive Rhododendron ponticum (L.). Perspectives in Plant Ecology Evolution and Systematics, 9, 15-28.

Travis JMJ, Harris CM, Park KJ and Bullock JM, 2011. Improving prediction and management of range expansions by combining analytical and individual-based modelling approaches. Methods in Ecology and Evolution, 2, 477-488.

Truscott J and Ferguson NM, 2012. Evaluating the adequacy of gravity models as a description of human mobility for epidemic modelling. PLoS computational biology, 8, e1002699.

Tyson RC, Wilson JB and Lane WD, 2011. Beyond diffusion: Modelling local and long-distance dispersal for organisms exhibiting intensive and extensive search modes. Theoretical Population Biology, 79, 70-81.

Waage JK, Woodhall JW, Bishop SJ, Smith JJ, Jones DR and Spence NJ, 2008. Patterns of plant pest introductions in Europe and Africa. Agricultural Systems, 99, 1-5.

Wadsworth RA, Collingham YC, Willis SG, Huntley B and Hulme PE, 2000. Simulating the spread and management of alien riparian weeds: are they out of control? Journal of Applied Ecology, 37, 28-38.

Walters RJ, Hassall M, Telfer MG, Hewitt GM and Palutikof JP, 2006. Modelling dispersal of a temperate insect in a changing climate. Proceedings of the Royal Society B-Biological Sciences, 273, 2017-2023.

Walther G-R, Roques A, Hulme PE, Sykes MT, Pyšek P, Kühn I, Zobel M, Bacher S, Botta-Dukát Z, Bugmann H, Czúcz B, Dauber J, Hickler T, Jarošík V, Kenis M, Klotz S, Minchin D, Moora M, Nentwig W, Ott J, Panov VE, Reineking B, Robinet C, Semenchenko V, Solarz W, Thuiller W, Vilà M, Vohland K and Settele J, 2009. Alien species in a warmer world: risks and opportunities. Trends in Ecology & Evolution, 24, 686-693.

Wingen LU, Shaw MW and Brown JKM, 2013. Long-distance dispersal and its influence on adaptation to host resistance in a heterogeneous landscape. Plant Pathology, 62, 9-20.

Yemshanov D, Koch FH, Barry Lyons D, Ducey M and Koehler K, 2012. A dominance-based approach to map risks of ecological invasions in the presence of severe uncertainty. Diversity and Distributions, 18, 33-46.

Zhen J, Quan-Xing L and Haque M, 2007. A cellular automata model with probability infection and spatial dispersion. Chinese Physics, 16, 1267.

Zipf GK, 1946. The P1 P2/D hypothesis: On the intercity movement of persons. American sociological review, 677-686.

APPENDICES

Appendix A. Rejected search terms

Table 21: Potential search terms considered and tested but not used in the final search string.

Category	Rejected synonyms	Reason
Pest	prokaryot*, eukaryot*	Too generic to be useful for locating pest organisms.
	compet*	Captures papers with very generic terms such as ‘competition’ and ‘compete’ so we preferred ‘competitor’ as a more specific term to identify weed pests.
Host plant	leaf, leaves, stem, bud, flower, floral, fruit, seed, root	Plant organs were not included as we are not interested in spread within a plant, but rather spread between plants – so it is not sufficient to just name a plant organ.
Spread	invas*, invad*	Covers ‘invasive’ and ‘invader’, which may be used as an adjective pertaining to the organism. We preferred ‘invasion’, which is the spreading process or event to be modelled.
	infest*, outbreak	These terms are more relevant to single-location models or events, rather than spread or dispersal in space.
	Transport, range, distribution	Generic terms used in many contexts other than for species’ spread.
Modelling	equation, mathematic*, dynamic*, forecast*, predict*	These potential terms relating to modelling were considered too generic.

Appendix B. List of search terms for specific plant pest organisms

abutilon
acacia
acalla
acanthocinus
acer
acidovorax
acleris
acrobasis
acroptilon
acrotoxa
acryptorhynchus
aculops
aecidium
aeolesthes
agrilus
agromyces
agromyza
ailanthus
akebia
aleurocanthus
aleurocantus
aleurodes
aleurodicus
aleyrodes
allantophoma
allewia
allium
alternanthera
alternanthera mosaic virus
alternaria
alucita
amaranthus
amauromyza
ambrosia
ambulia
amelanchier
american plum line pattern ilarvirus
american plum line pattern virus
amorpha
ampelomyces
anaphothrips
anastrepha
anatherum
andean potato latent tymovirus
andean potato latent virus
andean potato mottle comovirus
andean potato mottle virus
andropogon
angiosorus
anguillulina
anguina
anisogramma
anomala
anoplophora
anthomyia
anthonomochaeta
anthonomus
anychus
aonidella
aonidiella
aphelenchoides
aphelenchus
aphis
apioporthe
apiosporina
aplanobacter
aplpv
aplv
apmov
aponogeton
aposphaeria
apple flat apple virus
apple proliferation mycoplasm
apple proliferation phytoplasma
apple witches broom phytoplasma
apricot chlorotic leafroll mycoplasm
aproceros
arabis mosaic virus
araujia
arceuthobium
archips
argyroploce
aromia
aronia x prunifolia
arracacha virus
arrachaca virus
arrhenodes
arsenophonus
arthraxon
aschistonyx
asclepias
ascochyta
asparagus
aspidiotus
asteroaphelenchoides
asteromella
atropellis
aulacaspis
austrodacus
azolla
baccharis
bacillus
bactericera cockerelli
bacterium amylovorum
bacterium flaccumfaciens
bacterium michiganense
bacterium solanacearum
bacterium stewartii
bactrocera
bakerophoma
bean golden mosaic begomovirus

bean golden mosaic bigeminivirus
bean golden mosaic geminivirus
bean golden mosaic virus
bean golden yellow mosaic begomovirus
bean golden yellow mosaic virus
bean yellow mosaic virus
beet curly top virus
beet leaf curl rhabdovirus
beet leaf curl virus
beet necrotic yellow vein benyvirus
beet necrotic yellow vein furovirus
beet necrotic yellow vein virus
beet rhizomania virus
beet ringpsot virus
bemisia
berberis
beverwykella
bgmv
bgymv
bidens
black raspberry latent virus
blackberry himalaya mosaic virus
blcv
blitopertha
blmov
blueberry leaf mottle nepovirus
blueberry leaf mottle virus
blueberry scorch carlavirus
blueberry scorch virus
bnyvv
boeremia
bombyx
bostrichus
botryosphaeria
brown marmorated stink bug
buddleja
bunias
burkholderia
bursaphelenchus
byssothecium
cabomba
cacoecia
cacoecimorpha
cactodera
cacyreus
cadang-cadang viroid
caeoma
calandra
callantra
calloplophora
cape st paul wilt phytoplasma
caradrina
cardiophorus
cardiospermum
carneocephala
carpobrotus
carposina
castnia
cccvd
cellulomonas
cenangium
cenchrus
cephalcia
cerambyx
ceratitis
ceratocystis
ceratophyllum
cercoseptoria
cercospora
cercosporella
chaetasbolisia
chaetocnema
chaetoconis
chaetodacus
chaetodiplodia
chaetophoma
chaetopyrena
chaetosphaeronema
chalara
cherry leafroll virus
cherry rasp leaf cheravirus
cherry rasp leaf nepovirus
cherry rasp leaf virus
chionaspis
chloethrips
chloridea
choristoneura
chromatomyia
chrysanthemum stem necrosis tospovirus
chrysanthemum stem necrosis virus
chrysanthemum stunt mottle virus
chrysanthemum stunt pospiviroid
chrysanthemum stunt viroid
chrysomela
chrysomyxa
chrysophlyctis
chrysophtharta
ciborinia
cilv
cimv
circulifer
citrange stunt virus
citrus blight agent
citrus exocortis viroid
citrus greening bacterium
citrus leprosis rhabdovirus
citrus leprosis virus
citrus mosaic badnavirus
citrus mosaic virus

citrus tatter leaf capillovirus
citrus tatter leaf virus
citrus tristeza closterovirus
citrus tristeza virus
citrus variegated chlorosis
citrus variegated chlorosis agent
citrus vein enation woody gall
citrus yellow mosaic virus
ciymv
classical stolbur phytoplasma
clavibacter
cmbv
coccionella
cochliobolus
coconut cadang-cadang cocadviroid
coconut cadang-cadang viroid
coconut lethal yellowing phytoplasma
coleophoma
colletotrichum
columnea latent viroid
comstockaspis
coniella
coniothyrium
conotrachelus
coraebus
cordyle
cornus
cortaderia
corynebacterium flaccumfaciens
corynebacterium insidiosum
corynebacterium michiganense
corynebacterium sepedonicum
corythucha
cosmopolites
cotoneaster
cowpea mild mottle virus
crassula
crioceris
crlv
cronartium
cryphalus
cryphonectria
cryptophlebia
cryptorhynchus
cryptosporella
crypturgus
csnv
csvd
ctenarytaina
ctlv
ctv
cucumber vein yellowing ipomovirus
cucumber vein yellowing virus
cucumber yellow stunting crinivirus
cucumber yellow stunting disorder crinivirus
cucurbit chlorotic yellows virus
cucurbit yellow stunting closterovirus
cucurbit yellow stunting disorder closterovirus
cucurbit yellow stunting disorder crinivirus
cucurbit yellow stunting disorder virus
cucurbit yellow stunting virus
cucurbitaria
curculio
curtobacterium citreum
curtobacterium flaccumfaciens
curtobacterium luteum
cuscuta
cydia
cylindrophora
cylindrosporella
cymbdium mosaic virus
cyperus
cyrtogenius
cyrtotrachelus
cysdv
cytospora
dacnirotatus
dactylosphaera
dacus
dacus apoxanthus decolor
daktulosphaira
dasyneura
davidiella
dendroctonus
dendrolimus
deuterophoma
diabrotica
diaphania
diaphorina
diaporthe
diaspidiotus
dibotryon
dickeya
didacus
didymella
digitaria
dinaspis
diocalandra
diphtherophora
diplodia
diplodina
ditylenchus
dolichos
doryphora
dothidea
dothidella

dothiora
dothiorella
dothistroma
draeculacephala
drosophila
dryocoetes
dryocosmus
eccoptogaster
ecphyadophora
egeria
eggplant mosaic tymovirus
eggplant mosaic virus
eichhornia
elater
elatine
eleutheromyces
elide
elm phloem necrosis mycoplasm
elm phloem necrosis phytoplasma
elm yellows phytoplasma
elodea
elsinoe
enaphalodes
enarmonia
endoconidiophora
endocronartium
endothia
endoxyla
entodesmium
epicoccum
epinotia
epitrix
epochra
erechtites
eriochloa
erschoviella
erwinia
eucryptorrhychus
eulalia
euphalerus
euphorbia mosaic virus
euphranta
eurhodope
eutetranychus
eutetranychus lewisi
eutetranychus orientalis
euthrips
exomala
falciformispora
falcisormispora
fallopia
fallopia x bohemica
florida tomato virus
foaiella
fomitiporia
frankliniella
fusarium
gaillardia x grandiflora
gaultheria
gibberella
gilphinia
gilpinia
globodera
gloeosporium
glomerella
gnathotrichus
gnomonia
gnorimoschema
godronia
gonipterus
grapevine
grapevine bois noir phytoplasma
grapevine pierce's disease agent
grapevine yellow vein virus
graphocephala
graphognathus
grapholita
gremmeniella
guignardia
gunnera
gymnosporangium
hadena
hakea
halenchus
halyomorpha
haptocillium
harmologa
helianthus
helianthus x laetiflorus
helicotylenchus
helicoverpa
heliothis
heliothrips
hemerocampa
hemicriconemoides
hemicycliophora
hendersonia
heracleum
herpotrichia
hesperophanes
heterodera
heterognomon
heteronychus
heterospora
hirschmanniella
hishomonus
homalodisca
homolodisca
hosta virus
humulus
hydrangea ringspot virus
hydrilla
hydrocotyle
hygroryza
hylesinus
hylobius
hylurgops
hylurgus
hymenoscyphus

hyperodes
hypothenemus
hypoxylon
impatiens
impatiens necrotic spot tospovirus
impatiens necrotic spot virus
inonotus
insv
ipomoea
ips
iresine viroid
iris yellow spot virus
iva
jussiaea
keiferia
kuehneola
kyllinga
lagarosiphon
laimaphelenchus
lambro
landoltia
laphygma
lasiomma
laspeyresia
lecanicillium
lecanosticta
leifsonia
lemna
lepidosaphes
leprosis
leptinotarsa
leptocybe
leptoglossus
leptographium
leptosphaeria
leptosphaerulina
leptoxyda
lettuce infectious yellows closterovirus
lettuce infectious yellows crinivirus
lettuce infectious yellows virus
leucaspis
leucinodes
liberibacter
liberobacter
limnobium
limnophila
limonius
liriomyza
lissorhoptrus
listronotus
little cherry pathogen
liyv
lobelia
longidorus
lopholeucaspis
loxotaenia
lozotaenia
ludwigia
lupinus
lygus
lymantria
lysichiton
maconellicoccus
macrodiplodia
macrophoma
macrophomina
macrotrophurus
macroventuria
mahonia
maize redness phytoplasma
malacosoma
marchalina
margarodes
massaria
massarina
matricaria
matsucoccus
medeola
medicopsis
megaplatypus
melampsora
melampsoropsis
melanauster
melanomma
melanotus
mellesis
meloidogyne
mesocriconema
metamasius
mexican papita viroid
microbacterium foliorum
microbacterium phyllosphaerae
micrococcus
microsphaeropsis
microstegium
mimulus
minyrus
miscanthus
monarthrum
monascostroma
monilia
monilinia
monochamus
mycosphaerella
myndus
myopites
myriophyllum
myrsiphyllum
myzus
nacobbus
nacobbus serendipiticus bolivianus
nagelus
narcissus mosaic virus
naturally spreading psorosis
naupactus
necium

nemapogon
nematostoma
nemorimyza
neoaliturus
neobagous
neoceratitis
neodolichorhynchus
neoleucinodes
neophaeosphaeria
neophysopus
neosetophoma
neottiosporina
neovossia
nephopterix
nicotiana virus 12
nicotiana virus 13
nigrograna
nothotylenchus
numonia
nycteola
nysius
ocneria
odoiporus
oemona
oerskovia
ogma
oligonychus
ophelimus
ophiognomonia
ophiosphaerella
ophiostoma
opogona
orellia
orgyia
orthotomicus
otthia
oxalis
ozonium
pachyrrhizus
palm cadang-cadang viroid
palm lethal yellowing mycoplasm
palm lethal yellowing phytoplasma
panicum
pantoea
pantomorus
papaver
paraconiothyrium
paralepidosaphes
paraleptosphaeria
paraphaeosphaeria
paraphoma
parasaissetia
paratoxoptera
paratrichodorus
paratrioza
paratylenchus
pardalaspis
parthenium
paspalum
passalora
paururus
paysandisia
pbrsv
pcmv
pdmv
peach american mosaic virus
peach little peach phytoplasma
peach mosaic closterovirus
peach mosaic trichovirus
peach mosaic virus
peach phony agent
peach phony rickettsia
peach red suture phytoplasma
peach rosette mosaic nepovirus
peach rosette mosaic virus
peach rosette mycoplasm
peach rosette phytoplasma
peach virus
peach western x phytoplasma
peach x disease phytoplasma
peach x-disease mycoplasm
peach yellow bud mosaic virus
peach yellow leafroll phytoplasma
peach yellows mycoplasm
peach yellows phytoplasma
pear decline mycoplasm
pear decline phytoplasma
pectobacterium chrysanthemi
pectobacterium parthenii
pemphigus
pennisetum
pepino mosaic potexvirus
pepino mosaic virus
pepmv
pepper chat fruit viroid
pepper mild tigre virus
peridermium
peritymbia
peronea
persicaria
peyronellaea
phaedon
phaeocytostroma
phaeophleospora
phaeoramularia
phaeosphaeria
phaeosphaeriopsis
phalaena
pheletes
phellinus
phenacoccus
phialophora
phoma

phomopsis
phthorimaea
phyllanthus
phyllonorycter
phyllopertha
phyllosticta
phyllostictina
phylloxera
phyloosticta
phymatotrichopsis
phymatotrichum
physalospora
phytobia
phytolacca
phytomonas
phytophthora
phytoplasma asteris
phytoplasma aurantifolia
phytoplasma australiense
phytoplasma brasiliense
phytoplasma cocosnigeriae
phytoplasma cocostanzaniae
phytoplasma fraxini
phytoplasma mali
phytoplasma oryzae
phytoplasma palmi
phytoplasma phoenicium
phytoplasma pini
phytoplasma pruni
phytoplasma prunorum
phytoplasma pyri
phytoplasma rhamni
phytoplasma rubi
phytoplasma solani
phytoplasma trifolii
phytoplasma ulmi
phytoplasma vitis
phytoplasma ziziphi
piaropus
pileolaria
pissodes
pistia
pityogenes
pityophthorus
plagiostoma
plasmopara
platychora
platypus
plenodomus
pleomassaria
pleospora
pleurophoma
plowrightia
plum american line pattern ilarvirus
plum line pattern virus
plum pox potyvirus
plum pox virus
pochonia
podisoma
polistomimetes
polygonum
polygramma
polygraphus
pomacea
pontederia
popilia
popillia
poria
porthetria
potato andean calico virus
potato andean latent tymovirus
potato andean latent virus
potato andean mottle comovirus
potato andean mottle virus
potato aucuba mosaic virus
potato black ringspot nepovirus
potato black ringspot virus
potato brown rot
potato deforming mosaic begomovirus
potato deforming mosaic virus
potato deforming mosaic virus argentina
potato gothic virus
potato leafroll virus
potato purple-top wilt agent
potato ring rot
potato spindle tuber pospiviroid
potato spindle tuber viroid
potato spindle tuber virus
potato stolbur mycoplasm
potato stolbur phytoplasma
potato t capillovirus
potato t trichovirus
potato virus
potato wart disease
potato yellow dwarf nucleorhabdovirus
potato yellow dwarf rhabdovirus
potato yellow dwarf virus
potato yellow vein crinivirus
potato yellow vein virus
potato yellowing alfamovirus
potato yellowing virus
ppv
pratylenchoides
pratylenchus
premnotrypes
preussia
prmv
procecidochares
prodenia
prontaspis
prunus
prunus necrotic ringspot virus

prunus virus
pseudhalenchus
pseudocercospora
pseudodiplodia
pseudomonas
pseudopityophthorus
pseudorobillarda
pstvd
pterandrus
puccinia
pueraria
punctodera
pvt
pycnarmon
pydv
pyrenochaeta
pyrenochaetopsis
pyrenophora
pyv
pyvv
quadraspidiotus
radopholus
ralstonia
ranunculus
raoiella
raspberry leaf curl luteovirus
raspberry leaf curl nepovirus
raspberry leaf curl virus
raspberry ringspot nepovirus
raspberry ringspot virus
rathayibacter
readeriella
reticulitermes
rhacochlaena
rhagoletis
rhizaphis
rhizoecus
rhizosphaera
rhododendron
rhodophaea
rhus
rhynchophorus
ripersiella
rivellia
rlcv
robinia
roestelia
rosa
rotylenchulus
rotylenchus
roussoella
rprsv
rudbeckia
rusticoclytus
sagittaria
saissetia
salvinia
saperda
sarrothripus
satsuma dwarf nepovirus
satsuma dwarf sadwavirus
satsuma dwarf virus
sauertylenchus
scaphoideus
scarabaeus
scirrhia
scirtothrips
sclerotinia
scolecobasidium
scolytus
scrobipalpopsis
scrobipalpula
scrobipalpuloides
scuttelonema
scyphophorus
sdv
selenophoma
semasia
senecio
septoria
sesbania
setomelanomma
setophoma
setosphaeria
sicyos
simplicillium
sirex
sirococcus
slcv
solanum
solidago
sorghum
spanioza
spartina
sphaeraspis
sphaeria
sphaeropsis
spilographa
spiroplasma
spodoptera
sporormiella
squash leaf curl begomovirus
squash leaf curl bigeminivirus
squash leaf curl geminivirus
squash leaf curl virus
stagonospora
stagonosporopsis
steganoptycha
stegophora
stenocarpella
sternochetus
stlcv
stolbur phytoplasma
straussia
strauzia
strawberry crinkle virus
strawberry latent c rhabdovirus
strawberry latent c virus

strawberry latent ringspot virus
strawberry mild yellow edge virus
strawberry vein banding caulimovirus
strawberry vein banding virus
strawberry virus
strawberry witches broom mycoplasm
strobilomya
strobilomyia
strumeta
subanguina
subplenodomus
sugarbeet leaf crinkle virus
sugarbeet virus
sunflower chlorotic mottle virus
svbv
symphoricarpus
synchytrium
systremma
tachypterellus
tanzanian lethal decline phytoplasma
tasvd
tatter leaf virus
tecia
tellima
tephritis
teras
tetradacus
tetranychus
tetropium
thaumastocoris
thaumatotibia
thaumetopoea
thecaphora
thrips
thyridaria
ticv
tillaea
tilletia
tinea
tmov
tobacco ringspot nepovirus
tobacco ringspot virus
tobacco streak ilarvirus
tobacco streak virus
tocv
tomato apical stunt pospiviroid
tomato apical stunt viroid
tomato black ring virus
tomato bunchy top viroid
tomato chlorosis closterovirus
tomato chlorosis crinivirus
tomato chlorosis virus
tomato chlorotic dwarf viroid
tomato chocolate virus
tomato infectious chlorosis closterovirus
tomato infectious chlorosis crinivirus
tomato infectious chlorosis virus
tomato leaf curl bigeminivirus
tomato leaf curl geminivirus
tomato marchitez virus
tomato mottle begomovirus
tomato mottle bigeminivirus
tomato mottle geminivirus
tomato mottle virus
tomato planta macho viroid
tomato ringspot nepovirus
tomato ringspot virus
tomato spotted wilt tospovirus
tomato spotted wilt virus
tomato torrado virus
tomato yellow leaf curl begomovirus
tomato yellow leaf curl bigeminivirus
tomato yellow leaf curl geminivirus
tomato yellow leaf curl sardinia begomovirus
tomato yellow leaf curl sardinia virus
tomato yellow leaf curl virus
tomicus
torsv
tortrix
toxicodendron
toxoptera
toxotrypana
tranzschelia
trechispora
trematophoma
trematosphaeria
trialeurodes
tribolium
trichodorus
trichoferus
tridacus
trioza
trogoderma
trophurus
trsv
trypeta
tsvp
tswv
tulip virus
turanoclytus
tuta
tylcv
tylencholaimus
tylenchorhynchus
tylenchulus
tylenchus

tylolaimophorus
unaspis
uredo
uromyces
vaccinium
venturia
verbesina
verticicladiella
verticillium
viteus
watermelon silver mottle tospovirus
watermelon silver mottle virus
westerdykella
western x disease phytoplasma
winter peach mosaic virus
witches broom
wmsmov
wojnowicia
xanthomonas
xiphinema
xyleborinus
xyleborus
xylella
xyloclytus
xylomyges
xylophilus
xylosandrus
xylotrechus
xyphon
yucatan lethal decline phytoplasma
zaprionus
zeugodacus
zonosema

Appendix C. Web of knowledge search string

(((pest OR disease OR pathogen* OR parasit* OR herbivor* OR weed* OR competitor OR alien OR non*native OR invasive OR insect* OR mite OR acari* OR nematod* OR fung* OR oomyc* OR bacteri* OR phytoplasm* OR *virus* OR *viroid OR coleoptera* OR beetle OR diptera* OR fly OR hemiptera* OR *bug OR cicad* OR aphid* OR *hopper OR hymenoptera* OR sawfly OR *wasp OR lepidoptera* OR moth OR caterpillar OR thysanoptera* OR thrip OR gastropod* OR gasteropod* OR snail OR slug) AND (plant OR crop OR tree OR shrub OR herb OR forb OR grass* OR gramin* OR *berry OR *corn OR allspice OR almond OR angelica OR anise OR apple OR apricot OR arbutus OR arrowroot OR artichoke OR asparagus OR aubergine OR avocado OR azarole OR balm OR bamboo OR banana OR barley OR basil OR bay OR bean OR beet OR beetroot OR bergamot OR bilimbi OR borage OR borecole OR brassica* OR broccoli OR buckthorn OR buckwheat OR bulb OR cabbage OR cactus OR calabrese OR camomile OR cane OR canistel OR caper OR carambola OR caraway OR cardamom OR cardoon OR carob OR carrot OR cashew OR cassava OR cassia OR cauliflower OR celeriac OR celery OR cereal OR cherimoya OR cherry OR chervil OR chestnut OR chickling*vetch OR chickpea OR chicory OR chinotto OR chive OR chokeberry OR cinnamon OR citron OR citrus OR clementine OR clove OR cocoa OR coconut OR coffee OR collard OR coriander OR corn OR cornsalad OR cotton OR courgette OR cowpea OR cress OR cucumber OR cucurbit OR cumin OR curcuma OR currant OR damson OR dasheen OR date OR dewberry OR dill OR durian OR eddoe OR eggplant OR endive OR fennel OR fenugreek OR fig OR filbert OR flageolet OR flax OR fruit OR garlic OR gherkin OR ginger OR ginseng OR glassworth OR gooseberry OR grape OR grapefruit OR greengage OR grumichama OR guanabana OR guava OR hawthorn OR hazelnut OR hemp OR hempseed OR herb* OR hibiscus OR hops OR horseradish OR hyssop OR jackfruit OR jambolan OR jasmine OR juniper OR kaki OR kale OR kapok OR kiwano OR kiwi OR kohlrabi OR kumquat OR laurel OR leek OR legume OR lemon OR lentil OR lettuce OR lime OR linden OR linseed OR liquorice OR lollo*rosso OR loquat OR lovage OR lupin OR lychee OR macadamia OR mace OR maize OR mandarin OR mangetout OR mango OR marjoram OR marrow OR mate OR medlar OR melon OR millet OR mint OR mirabelle OR mizuna OR mountain*ash OR mulberry OR mustard OR nectarine OR nut OR nutmeg OR oat OR oilfruit OR oilseed OR okra OR olive OR onion OR orange OR oregano OR oysterplant OR pak*choi OR palm OR palmfruit OR palmoil OR papaya OR parsley OR parsnip OR passion*fruit OR patisson OR pe-tsai OR pea OR peach OR peanut OR pear OR pecan OR pepino OR pepper OR peppermint OR persimmon OR pine*nut OR pineapple OR pistachio OR plantain OR plum OR pome OR pomegranate OR pomelo OR pomerac OR poppy OR potato OR pulasan OR pulse OR pumpkin OR purslane OR quince OR radicchio OR radish OR rambutan OR rape*seed OR raspberry OR rhubarb OR rice OR rocket OR rooibos OR root OR rose*hip OR rosemary OR rye OR safflower OR saffron OR sage OR salad OR sallowthorn OR salsify OR sapote OR savory OR scarole OR scorzonera OR seed OR sesame OR shaddock OR shallot OR sorghum OR sorrel OR soursop OR soya OR spelt OR spice OR spinach OR sprout OR squash OR strawberry OR sugar OR sunflower OR swede OR sweet*cicely OR sweetsop OR tai*goo*choi OR tamarind OR tangelo OR tangerine OR tannia OR taro OR tarragon OR tea OR teff OR thyme OR tomato OR treeberry OR triticale OR tuber OR turmeric OR turnip OR ugli OR valerian OR vanilla OR vegetable OR vine OR walnut OR water*cress OR watermelon OR wheat OR wineberry OR witloof OR yam)) OR ("abutilon" OR "acacia" OR "acalla" OR "acanthocinus" OR "acer" OR "acidovorax" OR "acleris" OR "acrobasis" OR "acroptilon" OR "acrotoxa" OR "acryptorhynchus" OR "aculops" OR "aecidium" OR "aeolesthes" OR "agrilus" OR "agromyces" OR "agromyza" OR "ailanthus" OR "akebia" OR "aleurocanthus" OR "aleurocantus" OR "aleurodes" OR "aleurodicus" OR "aleyrodes" OR "allantophoma" OR "allewia" OR "allium" OR "alternanthera" OR "alternanthera mosaic virus" OR "alternaria" OR "alucita" OR "amaranthus" OR "amauromyza" OR "ambrosia" OR "ambulia" OR "amelanchier" OR "american plum line pattern ilarvirus" OR "american plum line pattern virus" OR "amorpha" OR "ampelomyces" OR "anaphothrips" OR "anastrepha" OR "anatherum" OR "andean potato latent tymovirus" OR "andean potato latent virus" OR "andean potato mottle comovirus" OR "andean potato mottle virus" OR "andropogon" OR "angiosorus" OR "anguillulina" OR "anguina" OR "anisogramma" OR "anomala" OR "anoplophora" OR "anthomyia" OR "anthonomochaeta" OR "anthonomus" OR "anychus" OR "aonidella" OR "aonidiella" OR "aphelenchoides" OR "aphelenchus" OR "aphis" OR "apioporthe" OR "apiosporina" OR "aplanobacter" OR "aplpv" OR "aplv" OR "apmov" OR "aponogeton" OR "aposphaeria" OR "apple flat apple virus" OR "apple proliferation mycoplasm" OR "apple proliferation phytoplasma" OR "apple witches broom phytoplasma" OR "apricot chlorotic leafroll mycoplasm" OR "aproceros" OR "arabis mosaic virus" OR "araujia" OR "arceuthobium" OR "archips" OR "argyroploce" OR "aromia" OR "aronia x prunifolia" OR "arracacha virus" OR "arrachaca virus" OR "arrhenodes" OR "arsenophonus" OR "arthraxon" OR "aschistonyx" OR "asclepias" OR "ascochyta" OR "asparagus" OR "aspidiotus" OR "asteroaphelenchoides" OR "asteromella" OR "atropellis" OR "aulacaspis" OR "austrodacus" OR "azolla" OR "baccharis" OR "bacillus" OR "bactericera cockerelli" OR "bacterium amylovorum" OR "bacterium flaccumfaciens" OR "bacterium michiganense" OR "bacterium solanacearum" OR "bacterium stewartii" OR "bactrocera" OR "bakerophoma" OR "bean golden mosaic begomovirus" OR "bean golden mosaic bigeminivirus" OR "bean golden mosaic geminivirus" OR "bean golden mosaic virus" OR "bean golden yellow mosaic begomovirus" OR "bean golden yellow mosaic virus" OR "bean yellow mosaic virus" OR "beet curly top virus" OR "beet leaf curl rhabdovirus" OR "beet leaf curl virus" OR "beet necrotic yellow vein benyvirus" OR "beet necrotic yellow vein furovirus" OR "beet necrotic yellow vein virus" OR "beet rhizomania virus" OR "beet ringpsot virus" OR "bemisia" OR "berberis" OR "beverwykella" OR "bgmv" OR "bgymv" OR "bidens" OR "black raspberry latent virus" OR "blackberry himalaya mosaic virus" OR "blcv" OR "blitopertha" OR "blmov" OR "blueberry leaf mottle nepovirus" OR "blueberry leaf mottle virus" OR "blueberry scorch carlavirus" OR "blueberry scorch virus" OR "bnyvv" OR "boeremia" OR "bombyx" OR "bostrichus" OR "botryosphaeria" OR "brown marmorated stink bug" OR "buddleja" OR "bunias" OR "burkholderia" OR "bursaphelenchus" OR "byssothecium" OR "cabomba" OR "cacoecia" OR "cacoecimorpha" OR "cactodera" OR "cacyreus" OR "cadang-cadang viroid" OR "caeoma" OR "calandra" OR "callantra" OR "calloplophora" OR "cape st paul wilt phytoplasma" OR "caradrina" OR "cardiophorus" OR "cardiospermum" OR "carneocephala" OR "carpobrotus" OR "carposina" OR "castnia" OR "cccvd" OR "cellulomonas" OR "cenangium" OR "cenchrus" OR "cephalcia" OR "cerambyx" OR "ceratitis" OR "ceratocystis" OR "ceratophyllum" OR "cercoseptoria" OR "cercospora" OR "cercosporella" OR "chaetasbolisia" OR "chaetocnema" OR "chaetoconis" OR "chaetodacus" OR "chaetodiplodia" OR "chaetophoma" OR "chaetopyrena" OR "chaetosphaeronema" OR "chalara" OR "cherry leafroll virus" OR "cherry rasp leaf cheravirus" OR "cherry rasp leaf nepovirus" OR "cherry rasp leaf virus" OR "chionaspis" OR "chloethrips" OR "chloridea" OR "choristoneura" OR "chromatomyia" OR "chrysanthemum stem necrosis tospovirus" OR "chrysanthemum stem necrosis virus" OR "chrysanthemum stunt mottle virus" OR "chrysanthemum stunt pospiviroid" OR "chrysanthemum stunt viroid" OR "chrysomela" OR "chrysomyxa" OR "chrysophlyctis" OR "chrysophtharta" OR "ciborinia" OR "cilv" OR "cimv" OR "circulifer" OR "citrange stunt virus" OR "citrus blight agent" OR "citrus exocortis viroid" OR "citrus greening bacterium" OR "citrus leprosis rhabdovirus" OR "citrus leprosis virus" OR "citrus mosaic badnavirus" OR "citrus mosaic virus" OR "citrus tatter leaf capillovirus" OR "citrus tatter leaf virus" OR "citrus tristeza closterovirus" OR "citrus tristeza virus" OR "citrus variegated chlorosis" OR "citrus variegated chlorosis agent" OR "citrus vein enation woody gall" OR "citrus yellow mosaic virus" OR "ciymv" OR "classical stolbur phytoplasma" OR "clavibacter" OR "cmbv" OR "coccionella" OR "cochliobolus" OR "coconut cadang-cadang cocadviroid" OR "coconut cadang-cadang viroid" OR "coconut lethal yellowing phytoplasma" OR "coleophoma" OR "colletotrichum" OR "columnea latent viroid" OR "comstockaspis" OR "coniella" OR "coniothyrium" OR "conotrachelus" OR "coraebus" OR "cordyle" OR "cornus" OR "cortaderia" OR "corynebacterium flaccumfaciens" OR "corynebacterium insidiosum" OR "corynebacterium michiganense" OR "corynebacterium sepedonicum" OR "corythucha" OR "cosmopolites" OR "cotoneaster" OR "cowpea mild mottle virus" OR "crassula" OR "crioceris" OR "crlv" OR "cronartium" OR "cryphalus" OR "cryphonectria" OR "cryptophlebia" OR "cryptorhynchus" OR "cryptosporella" OR "crypturgus" OR "csnv" OR "csvd" OR "ctenarytaina" OR "ctlv" OR "ctv" OR "cucumber vein yellowing ipomovirus" OR "cucumber vein yellowing virus" OR "cucumber yellow stunting crinivirus" OR "cucumber yellow stunting disorder crinivirus" OR "cucurbit chlorotic yellows virus" OR "cucurbit yellow stunting closterovirus" OR "cucurbit yellow stunting disorder closterovirus" OR "cucurbit yellow stunting disorder crinivirus" OR "cucurbit yellow stunting disorder virus" OR "cucurbit yellow stunting virus" OR "cucurbitaria" OR "curculio" OR "curtobacterium citreum" OR "curtobacterium flaccumfaciens" OR "curtobacterium luteum" OR "cuscuta" OR "cydia" OR "cylindrophora" OR "cylindrosporella" OR "cymbdium mosaic virus" OR "cyperus" OR "cyrtogenius" OR "cyrtotrachelus" OR "cysdv" OR "cytospora" OR "dacnirotatus" OR "dactylosphaera" OR "dacus" OR "dacus apoxanthus decolor" OR "daktulosphaira" OR "dasyneura" OR "davidiella" OR "dendroctonus" OR "dendrolimus" OR "deuterophoma" OR "diabrotica" OR "diaphania" OR "diaphorina" OR "diaporthe" OR "diaspidiotus" OR "dibotryon" OR "dickeya" OR "didacus" OR "didymella" OR "digitaria" OR "dinaspis" OR "diocalandra" OR "diphtherophora" OR "diplodia" OR "diplodina" OR "ditylenchus" OR "dolichos" OR "doryphora" OR "dothidea" OR "dothidella" OR "dothiora" OR "dothiorella" OR "dothistroma" OR "draeculacephala" OR "drosophila" OR "dryocoetes" OR "dryocosmus" OR "eccoptogaster" OR "ecphyadophora" OR "egeria" OR "eggplant mosaic tymovirus" OR "eggplant mosaic virus" OR "eichhornia" OR "elater" OR "elatine" OR "eleutheromyces" OR "elide" OR "elm phloem necrosis mycoplasm" OR "elm phloem necrosis phytoplasma" OR "elm yellows phytoplasma" OR "elodea" OR "elsinoe" OR "enaphalodes" OR "enarmonia" OR "endoconidiophora" OR "endocronartium" OR "endothia" OR "endoxyla" OR "entodesmium" OR "epicoccum" OR "epinotia" OR "epitrix" OR "epochra" OR "erechtites" OR "eriochloa" OR "erschoviella" OR "erwinia" OR "eucryptorrhychus" OR "eulalia" OR "euphalerus" OR "euphorbia mosaic virus" OR "euphranta" OR "eurhodope" OR "eutetranychus" OR "eutetranychus lewisi" OR "eutetranychus orientalis" OR "euthrips" OR "exomala" OR "falciformispora" OR "falcisormispora" OR "fallopia" OR "fallopia x bohemica" OR "florida tomato virus" OR "foaiella" OR "fomitiporia" OR "frankliniella" OR "fusarium" OR "gaillardia x grandiflora" OR "gaultheria" OR "gibberella" OR "gilphinia" OR "gilpinia" OR "globodera" OR "gloeosporium" OR "glomerella" OR "gnathotrichus" OR "gnomonia" OR "gnorimoschema" OR "godronia" OR "gonipterus" OR "grapevine" OR "grapevine bois noir phytoplasma" OR "grapevine pierce's disease agent" OR "grapevine yellow vein virus" OR "graphocephala" OR "graphognathus" OR "grapholita" OR "gremmeniella" OR "guignardia" OR "gunnera" OR "gymnosporangium" OR "hadena" OR "hakea" OR "halenchus" OR "halyomorpha" OR "haptocillium" OR "harmologa" OR "helianthus" OR "helianthus x laetiflorus" OR "helicotylenchus" OR "helicoverpa" OR "heliothis" OR "heliothrips" OR "hemerocampa" OR "hemicriconemoides" OR "hemicycliophora" OR "hendersonia" OR "heracleum" OR "herpotrichia" OR "hesperophanes" OR "heterodera" OR "heterognomon" OR "heteronychus" OR "heterospora" OR "hirschmanniella" OR "hishomonus" OR "homalodisca" OR "homolodisca" OR "hosta virus" OR "humulus" OR "hydrangea ringspot virus" OR "hydrilla" OR "hydrocotyle" OR "hygroryza" OR "hylesinus" OR "hylobius" OR "hylurgops" OR "hylurgus" OR "hymenoscyphus" OR "hyperodes" OR "hypothenemus" OR "hypoxylon" OR "impatiens" OR "impatiens necrotic spot tospovirus" OR "impatiens necrotic spot virus" OR "inonotus" OR "insv" OR "ipomoea" OR "ips" OR "iresine viroid" OR "iris yellow spot virus" OR "iva" OR "jussiaea" OR "keiferia" OR "kuehneola" OR "kyllinga" OR "lagarosiphon" OR "laimaphelenchus" OR "lambro" OR "landoltia" OR "laphygma" OR "lasiomma" OR "laspeyresia" OR "lecanicillium" OR "lecanosticta" OR "leifsonia" OR "lemna" OR "lepidosaphes" OR "leprosis" OR "leptinotarsa" OR "leptocybe" OR "leptoglossus" OR "leptographium" OR "leptosphaeria" OR "leptosphaerulina" OR "leptoxyda" OR "lettuce infectious yellows closterovirus" OR "lettuce infectious yellows crinivirus" OR "lettuce infectious yellows virus" OR "leucaspis" OR "leucinodes" OR "liberibacter" OR "liberobacter" OR "limnobium" OR "limnophila" OR "limonius" OR "liriomyza" OR "lissorhoptrus" OR "listronotus" OR "little cherry pathogen" OR "liyv" OR "lobelia" OR "longidorus" OR "lopholeucaspis" OR "loxotaenia" OR "lozotaenia" OR "ludwigia" OR "lupinus" OR "lygus" OR "lymantria" OR "lysichiton" OR "maconellicoccus" OR "macrodiplodia" OR "macrophoma" OR "macrophomina" OR "macrotrophurus" OR "macroventuria" OR "mahonia" OR "maize redness phytoplasma" OR "malacosoma" OR "marchalina" OR "margarodes" OR "massaria" OR "massarina" OR "matricaria" OR "matsucoccus" OR "medeola" OR "medicopsis" OR "megaplatypus" OR "melampsora" OR "melampsoropsis" OR "melanauster" OR "melanomma" OR "melanotus" OR "mellesis" OR "meloidogyne" OR "mesocriconema" OR "metamasius" OR "mexican papita viroid" OR "microbacterium foliorum" OR "microbacterium phyllosphaerae" OR "micrococcus" OR "microsphaeropsis" OR "microstegium" OR "mimulus" OR "minyrus" OR "miscanthus" OR "monarthrum" OR "monascostroma" OR "monilia" OR "monilinia" OR "monochamus" OR "mycosphaerella" OR "myndus" OR "myopites" OR "myriophyllum" OR "myrsiphyllum" OR "myzus" OR "nacobbus" OR "nacobbus serendipiticus bolivianus" OR "nagelus" OR "narcissus mosaic virus" OR "naturally spreading psorosis" OR "naupactus" OR "necium" OR "nemapogon" OR "nematostoma" OR "nemorimyza" OR "neoaliturus" OR "neobagous" OR "neoceratitis" OR "neodolichorhynchus" OR "neoleucinodes" OR "neophaeosphaeria" OR "neophysopus" OR "neosetophoma" OR "neottiosporina" OR "neovossia" OR "nephopterix" OR "nicotiana virus 12" OR "nicotiana virus 13" OR "nigrograna" OR "nothotylenchus" OR "numonia" OR "nycteola" OR "nysius" OR "ocneria" OR "odoiporus" OR "oemona" OR "oerskovia" OR "ogma" OR "oligonychus" OR "ophelimus" OR "ophiognomonia" OR "ophiosphaerella" OR "ophiostoma" OR "opogona" OR "orellia" OR "orgyia" OR "orthotomicus" OR "otthia" OR "oxalis" OR "ozonium" OR "pachyrrhizus" OR "palm cadang-cadang viroid" OR "palm lethal yellowing mycoplasm" OR "palm lethal yellowing phytoplasma" OR "panicum" OR "pantoea" OR "pantomorus" OR "papaver" OR "paraconiothyrium" OR "paralepidosaphes" OR "paraleptosphaeria" OR "paraphaeosphaeria" OR "paraphoma" OR "parasaissetia" OR "paratoxoptera" OR "paratrichodorus" OR "paratrioza" OR "paratylenchus" OR "pardalaspis" OR "parthenium" OR "paspalum" OR "passalora" OR "paururus" OR "paysandisia" OR "pbrsv" OR "pcmv" OR "pdmv" OR "peach american mosaic virus" OR "peach little peach phytoplasma" OR "peach mosaic closterovirus" OR "peach mosaic trichovirus" OR "peach mosaic virus" OR "peach phony agent" OR "peach phony rickettsia" OR "peach red suture phytoplasma" OR "peach rosette mosaic nepovirus" OR "peach rosette mosaic virus" OR "peach rosette mycoplasm" OR "peach rosette phytoplasma" OR "peach virus" OR "peach western x phytoplasma" OR "peach x-disease mycoplasm" OR "peach x disease phytoplasma" OR "peach yellow bud mosaic virus" OR "peach yellow leafroll phytoplasma" OR "peach yellows mycoplasm" OR "peach yellows phytoplasma" OR "pear decline mycoplasm" OR "pear decline phytoplasma" OR "pectobacterium chrysanthemi" OR "pectobacterium parthenii" OR "pemphigus" OR "pennisetum" OR "pepino mosaic potexvirus" OR "pepino mosaic virus" OR "pepmv" OR "pepper chat fruit viroid" OR "pepper mild tigre virus" OR "peridermium" OR "peritymbia" OR "peronea" OR "persicaria" OR "peyronellaea" OR "phaedon" OR "phaeocytostroma" OR "phaeophleospora" OR "phaeoramularia" OR "phaeosphaeria" OR "phaeosphaeriopsis" OR "phalaena" OR "pheletes" OR "phellinus" OR "phenacoccus" OR "phialophora" OR "phoma" OR "phomopsis" OR "phthorimaea" OR "phyllanthus" OR "phyllonorycter" OR "phyllopertha" OR "phyllosticta" OR "phyllostictina" OR "phylloxera" OR "phyloosticta" OR "phymatotrichopsis" OR "phymatotrichum" OR "physalospora" OR "phytobia" OR "phytolacca" OR "phytomonas" OR "phytophthora" OR "phytoplasma asteris" OR "phytoplasma aurantifolia" OR "phytoplasma australiense" OR "phytoplasma brasiliense" OR "phytoplasma cocosnigeriae" OR "phytoplasma cocostanzaniae" OR "phytoplasma fraxini" OR "phytoplasma mali" OR "phytoplasma oryzae" OR "phytoplasma palmi" OR "phytoplasma phoenicium" OR "phytoplasma pini" OR "phytoplasma pruni" OR "phytoplasma prunorum" OR "phytoplasma pyri" OR "phytoplasma rhamni" OR "phytoplasma rubi" OR "phytoplasma solani" OR "phytoplasma trifolii" OR "phytoplasma ulmi" OR "phytoplasma vitis" OR "phytoplasma ziziphi" OR "piaropus" OR "pileolaria" OR "pissodes" OR "pistia" OR "pityogenes" OR "pityophthorus" OR "plagiostoma" OR "plasmopara" OR "platychora" OR "platypus" OR "plenodomus" OR "pleomassaria" OR "pleospora" OR "pleurophoma" OR "plowrightia" OR "plum american line pattern ilarvirus" OR "plum line pattern virus" OR "plum pox potyvirus" OR "plum pox virus" OR "pochonia" OR "podisoma" OR "polistomimetes" OR "polygonum" OR "polygramma" OR "polygraphus" OR "pomacea" OR "pontederia" OR "popilia" OR "popillia" OR "poria" OR "porthetria" OR "potato andean calico virus" OR "potato andean latent tymovirus" OR "potato andean latent virus" OR "potato andean mottle comovirus" OR "potato andean mottle virus" OR "potato aucuba mosaic virus" OR "potato black ringspot nepovirus" OR "potato black ringspot virus" OR "potato brown rot" OR "potato deforming mosaic begomovirus" OR "potato deforming mosaic virus" OR "potato deforming mosaic virus argentina" OR "potato gothic virus" OR "potato leafroll virus" OR "potato purple-top wilt agent" OR "potato ring rot" OR "potato spindle tuber pospiviroid" OR "potato spindle tuber viroid" OR "potato spindle tuber virus" OR "potato stolbur mycoplasm" OR "potato stolbur phytoplasma" OR "potato t capillovirus" OR "potato t trichovirus" OR "potato virus" OR "potato wart disease" OR "potato yellow dwarf nucleorhabdovirus" OR "potato yellow dwarf rhabdovirus" OR "potato yellow dwarf virus" OR "potato yellow vein crinivirus" OR "potato yellow vein virus" OR "potato yellowing alfamovirus" OR "potato yellowing virus" OR "ppv" OR "pratylenchoides" OR "pratylenchus" OR "premnotrypes" OR "preussia" OR "prmv" OR "procecidochares" OR "prodenia" OR "prontaspis" OR "prunus" OR "prunus necrotic ringspot virus" OR "prunus virus" OR "pseudhalenchus" OR "pseudocercospora" OR "pseudodiplodia" OR "pseudomonas" OR "pseudopityophthorus" OR "pseudorobillarda" OR "pstvd" OR "pterandrus" OR "puccinia" OR "pueraria" OR "punctodera" OR "pvt" OR "pycnarmon" OR "pydv" OR "pyrenochaeta" OR "pyrenochaetopsis" OR "pyrenophora" OR "pyv" OR "pyvv" OR "quadraspidiotus" OR "radopholus" OR "ralstonia" OR "ranunculus" OR "raoiella" OR "raspberry leaf curl luteovirus" OR "raspberry leaf curl nepovirus" OR "raspberry leaf curl virus" OR "raspberry ringspot nepovirus" OR "raspberry ringspot virus" OR "rathayibacter" OR "readeriella" OR "reticulitermes" OR "rhacochlaena" OR "rhagoletis" OR "rhizaphis" OR "rhizoecus" OR "rhizosphaera" OR "rhododendron" OR "rhodophaea" OR "rhus" OR "rhynchophorus" OR "ripersiella" OR "rivellia" OR "rlcv" OR "robinia" OR "roestelia" OR "rosa" OR "rotylenchulus" OR "rotylenchus" OR "roussoella" OR "rprsv" OR "rudbeckia" OR "rusticoclytus" OR "sagittaria" OR "saissetia" OR "salvinia" OR "saperda" OR "sarrothripus" OR "satsuma dwarf nepovirus" OR "satsuma dwarf sadwavirus" OR "satsuma dwarf virus" OR "sauertylenchus" OR "scaphoideus" OR "scarabaeus" OR "scirrhia" OR "scirtothrips" OR "sclerotinia" OR "scolecobasidium" OR "scolytus" OR "scrobipalpopsis" OR "scrobipalpula" OR "scrobipalpuloides" OR "scuttelonema" OR "scyphophorus" OR "sdv" OR "selenophoma" OR "semasia" OR "senecio" OR "septoria" OR "sesbania" OR "setomelanomma" OR "setophoma" OR "setosphaeria" OR "sicyos" OR "simplicillium" OR "sirex" OR "sirococcus" OR "slcv" OR "solanum" OR "solidago" OR "sorghum" OR "spanioza" OR "spartina" OR "sphaeraspis" OR "sphaeria" OR "sphaeropsis" OR "spilographa" OR "spiroplasma" OR "spodoptera" OR "sporormiella" OR "squash leaf curl begomovirus" OR "squash leaf curl bigeminivirus" OR "squash leaf curl geminivirus" OR "squash leaf curl virus" OR "stagonospora" OR "stagonosporopsis" OR "steganoptycha" OR "stegophora" OR "stenocarpella" OR "sternochetus" OR "stlcv" OR "stolbur phytoplasma" OR "straussia" OR "strauzia" OR "strawberry crinkle virus" OR "strawberry latent c rhabdovirus" OR "strawberry latent c virus" OR "strawberry latent ringspot virus" OR "strawberry mild yellow edge virus" OR "strawberry vein banding caulimovirus" OR "strawberry vein banding virus" OR "strawberry virus" OR "strawberry witches broom mycoplasm" OR "strobilomya" OR "strobilomyia" OR "strumeta" OR "subanguina" OR "subplenodomus" OR "sugarbeet leaf crinkle virus" OR "sugarbeet virus" OR "sunflower chlorotic mottle virus" OR "svbv" OR "symphoricarpus" OR "synchytrium" OR "systremma" OR "tachypterellus" OR "tanzanian lethal decline phytoplasma" OR "tasvd" OR "tatter leaf virus" OR "tecia" OR "tellima" OR "tephritis" OR "teras" OR "tetradacus" OR "tetranychus" OR "tetropium" OR "thaumastocoris" OR "thaumatotibia" OR "thaumetopoea" OR "thecaphora" OR "thrips" OR "thyridaria" OR "ticv" OR "tillaea" OR "tilletia" OR "tinea" OR "tmov" OR "tobacco ringspot nepovirus" OR "tobacco ringspot virus" OR "tobacco streak ilarvirus" OR "tobacco streak virus" OR "tocv" OR "tomato apical stunt pospiviroid" OR "tomato apical stunt viroid" OR "tomato black ring virus" OR "tomato bunchy top viroid" OR "tomato chlorosis closterovirus" OR "tomato chlorosis crinivirus" OR "tomato chlorosis virus" OR "tomato chlorotic dwarf viroid" OR "tomato chocolate virus" OR "tomato infectious chlorosis closterovirus" OR "tomato infectious chlorosis crinivirus" OR "tomato infectious chlorosis virus" OR "tomato leaf curl bigeminivirus" OR "tomato leaf curl geminivirus" OR "tomato marchitez virus" OR "tomato mottle begomovirus" OR "tomato mottle bigeminivirus" OR "tomato mottle geminivirus" OR "tomato mottle virus" OR "tomato planta macho viroid" OR "tomato ringspot nepovirus" OR "tomato ringspot virus" OR "tomato spotted wilt tospovirus" OR "tomato spotted wilt virus" OR "tomato torrado virus" OR "tomato yellow leaf curl begomovirus" OR "tomato yellow leaf curl bigeminivirus" OR "tomato yellow leaf curl geminivirus" OR "tomato yellow leaf curl sardinia begomovirus" OR "tomato yellow leaf curl sardinia virus" OR "tomato yellow leaf curl virus" OR "tomicus" OR "torsv" OR "tortrix" OR "toxicodendron" OR "toxoptera" OR "toxotrypana" OR "tranzschelia" OR "trechispora" OR "trematophoma" OR "trematosphaeria" OR "trialeurodes" OR "tribolium" OR "trichodorus" OR "trichoferus" OR "tridacus" OR "trioza" OR "trogoderma" OR "trophurus" OR "trsv" OR "trypeta" OR "tsvp" OR "tswv" OR "tulip virus" OR "turanoclytus" OR "tuta" OR "tylcv" OR "tylencholaimus" OR "tylenchorhynchus" OR "tylenchulus" OR "tylenchus" OR "tylolaimophorus" OR "unaspis" OR "uredo" OR "uromyces" OR "vaccinium" OR "venturia" OR "verbesina" OR "verticicladiella" OR "verticillium" OR "viteus" OR "watermelon silver mottle tospovirus" OR "watermelon silver mottle virus" OR "westerdykella" OR "western x disease phytoplasma" OR "winter peach mosaic virus" OR "witches broom" OR "wmsmov" OR "wojnowicia" OR "xanthomonas" OR "xiphinema" OR "xyleborinus" OR "xyleborus" OR "xylella" OR "xyloclytus" OR "xylomyges" OR "xylophilus" OR "xylosandrus" OR "xylotrechus" OR "xyphon" OR "yucatan lethal decline phytoplasma" OR "zaprionus" OR "zeugodacus" OR "zonosema")) AND (spread* OR dispers* OR invasion OR colonis* OR movement* OR diffus*) AND (model* OR simulat*) NOT (medic* OR clinic* OR veterinar*)

Appendix D. Scopus search strings

Generic pest and host search:

TITLE-ABS-KEY((pest OR disease OR pathogen* OR parasit* OR herbivor* OR weed* OR competitor OR alien OR non*native OR invasive OR insect* OR mite OR acari* OR nematod* OR fung* OR oomyc* OR bacteri* OR phytoplasm* OR *virus* OR *viroid OR coleoptera* OR beetle OR diptera* OR fly OR hemiptera* OR *bug OR cicad* OR aphid* OR *hopper OR hymenoptera* OR sawfly OR *wasp OR lepidoptera* OR moth OR caterpillar OR thysanoptera* OR thrip OR gastropod* OR gasteropod* OR snail OR slug) AND (plant OR crop OR tree OR shrub OR herb OR forb OR grass* OR gramin* OR *berry OR *corn OR allspice OR almond OR angelica OR anise OR apple OR apricot OR arbutus OR arrowroot OR artichoke OR asparagus OR aubergine OR avocado OR azarole OR balm OR bamboo OR banana OR barley OR basil OR bay OR bean OR beet OR beetroot OR bergamot OR bilimbi OR borage OR borecole OR brassica* OR broccoli OR buckthorn OR buckwheat OR bulb OR cabbage OR cactus OR calabrese OR camomile OR cane OR canistel OR caper OR carambola OR caraway OR cardamom OR cardoon OR carob OR carrot OR cashew OR cassava OR cassia OR cauliflower OR celeriac OR celery OR cereal OR cherimoya OR cherry OR chervil OR chestnut OR chickling*vetch OR chickpea OR chicory OR chinotto OR chive OR chokeberry OR cinnamon OR citron OR citrus OR clementine OR clove OR cocoa OR coconut OR coffee OR collard OR coriander OR corn OR cornsalad OR cotton OR courgette OR cowpea OR cress OR cucumber OR cucurbit OR cumin OR curcuma OR currant OR damson OR dasheen OR date OR dewberry OR dill OR durian OR eddoe OR eggplant OR endive OR fennel OR fenugreek OR fig OR filbert OR flageolet OR flax OR fruit OR garlic OR gherkin OR ginger OR ginseng OR glassworth OR gooseberry OR grape OR grapefruit OR greengage OR grumichama OR guanabana OR guava OR hawthorn OR hazelnut OR hemp OR hempseed OR herb* OR hibiscus OR hops OR horseradish OR hyssop OR jackfruit OR jambolan OR jasmine OR juniper OR kaki OR kale OR kapok OR kiwano OR kiwi OR kohlrabi OR kumquat OR laurel OR leek OR legume OR lemon OR lentil OR lettuce OR lime OR linden OR linseed OR liquorice OR lollo*rosso OR loquat OR lovage OR lupin OR lychee OR macadamia OR mace OR maize OR mandarin OR mangetout OR mango OR marjoram OR marrow OR mate OR medlar OR melon OR millet OR mint OR mirabelle OR mizuna OR mountain*ash OR mulberry OR mustard OR nectarine OR nut OR nutmeg OR oat OR oilfruit OR oilseed OR okra OR olive OR onion OR orange OR oregano OR oysterplant OR pak*choi OR palm OR palmfruit OR palmoil OR papaya OR parsley OR parsnip OR passion*fruit OR patisson OR pe-tsai OR pea OR peach OR peanut OR pear OR pecan OR pepino OR pepper OR peppermint OR persimmon OR pine*nut OR pineapple OR pistachio OR plantain OR plum OR pome OR pomegranate OR pomelo OR pomerac OR poppy OR potato OR pulasan OR pulse OR pumpkin OR purslane OR quince OR radicchio OR radish OR rambutan OR rape*seed OR raspberry OR rhubarb OR rice OR rocket OR rooibos OR root OR rose*hip OR rosemary OR rye OR safflower OR saffron OR sage OR salad OR sallowthorn OR salsify OR sapote OR savory OR scarole OR scorzonera OR seed OR sesame OR shaddock OR shallot OR sorghum OR sorrel OR soursop OR soya OR spelt OR spice OR spinach OR sprout OR squash OR strawberry OR sugar OR sunflower OR swede OR sweet*cicely OR sweetsop OR tai*goo*choi OR tamarind OR tangelo OR tangerine OR tannia OR taro OR tarragon OR tea OR teff OR thyme OR tomato OR treeberry OR triticale OR tuber OR turmeric OR turnip OR ugli OR valerian OR vanilla OR vegetable OR vine OR walnut OR water*cress OR watermelon OR wheat OR wineberry OR witloof OR yam) AND (spread* OR dispers* OR invasion OR colonis* OR movement* OR diffus*) AND (model* OR simulat*) AND NOT (medic* OR clinic* OR veterinar*)) AND SUBJAREA(AGRI OR ENVI OR IMMU OR MATH OR COMP AND NOT (ARTS OR BIOC OR BUSI OR CENG OR CHEM OR DECI OR EART OR ECON OR ENER OR MATE OR MEDI OR NEUR OR NURS OR PSYC OR SOCI OR VETE OR DENT OR HEAL)) AND DOCTYPE(ar OR le) AND LANGUAGE(english)

Specific pest searches:

TITLE-ABS-KEY(("abutilon" OR "acacia" OR "acalla" OR "acanthocinus" OR "acer" OR "acidovorax" OR "acleris" OR "acrobasis" OR "acroptilon" OR "acrotoxa" OR "acryptorhynchus" OR "aculops" OR "aecidium" OR "aeolesthes" OR "agrilus" OR "agromyces" OR "agromyza" OR "ailanthus" OR "akebia" OR "aleurocanthus" OR "aleurocantus" OR "aleurodes" OR "aleurodicus" OR "aleyrodes" OR "allantophoma" OR "allewia" OR "allium" OR "alternanthera" OR "alternanthera mosaic virus" OR "alternaria" OR "alucita" OR "amaranthus" OR "amauromyza" OR "ambrosia" OR "ambulia" OR "amelanchier" OR "american plum line pattern ilarvirus" OR "american plum line pattern virus" OR "amorpha" OR "ampelomyces" OR "anaphothrips" OR "anastrepha" OR "anatherum" OR "andean potato latent tymovirus" OR "andean potato latent virus" OR "andean potato mottle comovirus" OR "andean potato mottle virus" OR "andropogon" OR "angiosorus" OR "anguillulina" OR "anguina" OR "anisogramma" OR "anomala" OR "anoplophora" OR "anthomyia" OR "anthonomochaeta" OR "anthonomus" OR "anychus" OR "aonidella" OR "aonidiella" OR "aphelenchoides" OR "aphelenchus" OR "aphis" OR "apioporthe" OR "apiosporina" OR "aplanobacter" OR "aplpv" OR "aplv" OR "apmov" OR "aponogeton" OR "aposphaeria" OR "apple flat apple virus" OR "apple proliferation mycoplasm" OR "apple proliferation phytoplasma" OR "apple witches broom phytoplasma" OR "apricot chlorotic leafroll mycoplasm" OR "aproceros" OR "arabis mosaic virus" OR "araujia" OR "arceuthobium" OR "archips" OR "argyroploce" OR "aromia" OR "aronia x prunifolia" OR "arracacha virus" OR "arrachaca virus" OR "arrhenodes" OR "arsenophonus" OR "arthraxon" OR "aschistonyx" OR "asclepias" OR "ascochyta" OR "asparagus" OR "aspidiotus" OR "asteroaphelenchoides" OR "asteromella" OR "atropellis" OR "aulacaspis" OR "austrodacus" OR "azolla" OR "baccharis" OR "bacillus" OR "bactericera cockerelli" OR "bacterium amylovorum" OR "bacterium flaccumfaciens" OR "bacterium michiganense" OR "bacterium solanacearum" OR "bacterium stewartii" OR "bactrocera" OR "bakerophoma" OR "bean golden mosaic begomovirus" OR "bean golden mosaic bigeminivirus" OR "bean golden mosaic geminivirus" OR "bean golden mosaic virus" OR "bean golden yellow mosaic begomovirus" OR "bean golden yellow mosaic virus" OR "bean yellow mosaic virus" OR "beet curly top virus" OR "beet leaf curl rhabdovirus" OR "beet leaf curl virus" OR "beet necrotic yellow vein benyvirus" OR "beet necrotic yellow vein furovirus" OR "beet necrotic yellow vein virus" OR "beet rhizomania virus" OR "beet ringpsot virus" OR "bemisia" OR "berberis" OR "beverwykella" OR "bgmv" OR "bgymv" OR "bidens" OR "black raspberry latent virus" OR "blackberry himalaya mosaic virus" OR "blcv" OR "blitopertha" OR "blmov" OR "blueberry leaf mottle nepovirus" OR "blueberry leaf mottle virus" OR "blueberry scorch carlavirus" OR "blueberry scorch virus" OR "bnyvv" OR "boeremia" OR "bombyx" OR "bostrichus" OR "botryosphaeria" OR "brown marmorated stink bug" OR "buddleja" OR "bunias" OR "burkholderia" OR "bursaphelenchus" OR "byssothecium" OR "cabomba" OR "cacoecia" OR "cacoecimorpha" OR "cactodera" OR "cacyreus" OR "cadang-cadang viroid" OR "caeoma" OR "calandra" OR "callantra" OR "calloplophora" OR "cape st paul wilt phytoplasma" OR "caradrina" OR "cardiophorus" OR "cardiospermum" OR "carneocephala" OR "carpobrotus" OR "carposina" OR "castnia" OR "cccvd" OR "cellulomonas" OR "cenangium" OR "cenchrus" OR "cephalcia" OR "cerambyx" OR "ceratitis" OR "ceratocystis" OR "ceratophyllum" OR "cercoseptoria" OR "cercospora" OR "cercosporella" OR "chaetasbolisia" OR "chaetocnema" OR "chaetoconis" OR "chaetodacus" OR "chaetodiplodia" OR "chaetophoma" OR "chaetopyrena" OR "chaetosphaeronema" OR "chalara" OR "cherry leafroll virus" OR "cherry rasp leaf cheravirus" OR "cherry rasp leaf nepovirus" OR "cherry rasp leaf virus" OR "chionaspis" OR "chloethrips" OR "chloridea" OR "choristoneura" OR "chromatomyia" OR "chrysanthemum stem necrosis tospovirus" OR "chrysanthemum stem necrosis virus" OR "chrysanthemum stunt mottle virus" OR "chrysanthemum stunt pospiviroid" OR "chrysanthemum stunt viroid" OR "chrysomela" OR "chrysomyxa" OR "chrysophlyctis" OR "chrysophtharta") AND (spread* OR dispers* OR invasion OR colonis* OR movement* OR diffus*) AND (model* OR simulat*) AND NOT (medic* OR clinic* OR veterinar*))

AND SUBJAREA(AGRI OR ENVI OR IMMU OR MATH OR COMP AND NOT (ARTS OR BIOC OR BUSI OR CENG OR CHEM OR DECI OR EART OR ECON OR ENER OR MATE OR MEDI OR NEUR OR NURS OR PSYC OR SOCI OR VETE OR DENT OR HEAL)) AND DOCTYPE(ar OR le) AND LANGUAGE(english)

TITLE-ABS-KEY(("ciborinia" OR "cilv" OR "cimv" OR "circulifer" OR "citrange stunt virus" OR "citrus blight agent" OR "citrus exocortis viroid" OR "citrus greening bacterium" OR "citrus leprosis rhabdovirus" OR "citrus leprosis virus" OR "citrus mosaic badnavirus" OR "citrus mosaic virus" OR "citrus tatter leaf capillovirus" OR "citrus tatter leaf virus" OR "citrus tristeza closterovirus" OR "citrus tristeza virus" OR "citrus variegated chlorosis" OR "citrus variegated chlorosis agent" OR "citrus vein enation woody gall" OR "citrus yellow mosaic virus" OR "ciymv" OR "classical stolbur phytoplasma" OR "clavibacter" OR "cmbv" OR "coccionella" OR "cochliobolus" OR "coconut cadang-cadang cocadviroid" OR "coconut cadang-cadang viroid" OR "coconut lethal yellowing phytoplasma" OR "coleophoma" OR "colletotrichum" OR "columnea latent viroid" OR "comstockaspis" OR "coniella" OR "coniothyrium" OR "conotrachelus" OR "coraebus" OR "cordyle" OR "cornus" OR "cortaderia" OR "corynebacterium flaccumfaciens" OR "corynebacterium insidiosum" OR "corynebacterium michiganense" OR "corynebacterium sepedonicum" OR "corythucha" OR "cosmopolites" OR "cotoneaster" OR "cowpea mild mottle virus" OR "crassula" OR "crioceris" OR "crlv" OR "cronartium" OR "cryphalus" OR "cryphonectria" OR "cryptophlebia" OR "cryptorhynchus" OR "cryptosporella" OR "crypturgus" OR "csnv" OR "csvd" OR "ctenarytaina" OR "ctlv" OR "ctv" OR "cucumber vein yellowing ipomovirus" OR "cucumber vein yellowing virus" OR "cucumber yellow stunting crinivirus" OR "cucumber yellow stunting disorder crinivirus" OR "cucurbit chlorotic yellows virus" OR "cucurbit yellow stunting closterovirus" OR "cucurbit yellow stunting disorder closterovirus" OR "cucurbit yellow stunting disorder crinivirus" OR "cucurbit yellow stunting disorder virus" OR "cucurbit yellow stunting virus" OR "cucurbitaria" OR "curculio" OR "curtobacterium citreum" OR "curtobacterium flaccumfaciens" OR "curtobacterium luteum" OR "cuscuta" OR "cydia" OR "cylindrophora" OR "cylindrosporella" OR "cymbdium mosaic virus" OR "cyperus" OR "cyrtogenius" OR "cyrtotrachelus" OR "cysdv" OR "cytospora" OR "dacnirotatus" OR "dactylosphaera" OR "dacus" OR "dacus apoxanthus decolor" OR "daktulosphaira" OR "dasyneura" OR "davidiella" OR "dendroctonus" OR "dendrolimus" OR "deuterophoma" OR "diabrotica" OR "diaphania" OR "diaphorina" OR "diaporthe" OR "diaspidiotus" OR "dibotryon" OR "dickeya" OR "didacus" OR "didymella" OR "digitaria" OR "dinaspis" OR "diocalandra" OR "diphtherophora" OR "diplodia" OR "diplodina" OR "ditylenchus" OR "dolichos" OR "doryphora" OR "dothidea" OR "dothidella" OR "dothiora" OR "dothiorella" OR "dothistroma" OR "draeculacephala" OR "drosophila" OR "dryocoetes" OR "dryocosmus" OR "eccoptogaster" OR "ecphyadophora" OR "egeria" OR "eggplant mosaic tymovirus" OR "eggplant mosaic virus" OR "eichhornia" OR "elater" OR "elatine" OR "eleutheromyces" OR "elide" OR "elm phloem necrosis mycoplasm" OR "elm phloem necrosis phytoplasma" OR "elm yellows phytoplasma" OR "elodea" OR "elsinoe" OR "enaphalodes" OR "enarmonia" OR "endoconidiophora" OR "endocronartium" OR "endothia" OR "endoxyla" OR "entodesmium" OR "epicoccum" OR "epinotia" OR "epitrix" OR "epochra" OR "erechtites" OR "eriochloa" OR "erschoviella" OR "erwinia" OR "eucryptorrhychus" OR "eulalia" OR "euphalerus" OR "euphorbia mosaic virus" OR "euphranta" OR "eurhodope" OR "eutetranychus" OR "eutetranychus lewisi" OR "eutetranychus orientalis" OR "euthrips" OR "exomala" OR "falciformispora" OR "falcisormispora" OR "fallopia" OR "fallopia x bohemica" OR "florida tomato virus" OR "foaiella" OR "fomitiporia" OR "frankliniella" OR "fusarium" OR "gaillardia x grandiflora" OR "gaultheria" OR "gibberella" OR "gilphinia" OR "gilpinia" OR "globodera" OR "gloeosporium" OR "glomerella" OR "gnathotrichus" OR "gnomonia" OR "gnorimoschema" OR "godronia" OR "gonipterus" OR "grapevine" OR "grapevine bois noir phytoplasma" OR "grapevine pierce's disease agent" OR "grapevine yellow vein virus" OR "graphocephala" OR "graphognathus" OR "grapholita" OR "gremmeniella" OR "guignardia" OR "gunnera" OR "gymnosporangium" OR "hadena" OR "hakea" OR "halenchus" OR "halyomorpha" OR "haptocillium" OR "harmologa" OR "helianthus" OR "helianthus x laetiflorus" OR "helicotylenchus" OR "helicoverpa") AND (spread* OR dispers* OR invasion OR colonis* OR movement* OR diffus*) AND (model* OR simulat*) AND NOT (medic* OR clinic* OR veterinar*)) AND SUBJAREA(AGRI OR ENVI OR IMMU OR MATH OR COMP AND NOT (ARTS OR BIOC OR BUSI OR CENG OR CHEM OR DECI OR EART OR ECON OR ENER OR MATE OR MEDI OR NEUR OR NURS OR PSYC OR SOCI OR VETE OR DENT OR HEAL)) AND DOCTYPE(ar OR le) AND LANGUAGE(english)

TITLE-ABS-KEY(("heliothis" OR "heliothrips" OR "hemerocampa" OR "hemicriconemoides" OR "hemicycliophora" OR "hendersonia" OR "heracleum" OR "herpotrichia" OR "hesperophanes" OR "heterodera" OR "heterognomon" OR "heteronychus" OR "heterospora" OR "hirschmanniella" OR "hishomonus" OR "homalodisca" OR "homolodisca" OR "hosta virus" OR "humulus" OR "hydrangea ringspot virus" OR "hydrilla" OR "hydrocotyle" OR "hygroryza" OR "hylesinus" OR "hylobius" OR "hylurgops" OR "hylurgus" OR "hymenoscyphus" OR "hyperodes" OR "hypothenemus" OR "hypoxylon" OR "impatiens" OR "impatiens necrotic spot tospovirus" OR "impatiens necrotic spot virus" OR "inonotus" OR "insv" OR "ipomoea" OR "ips" OR "iresine viroid" OR "iris yellow spot virus" OR "iva" OR "jussiaea" OR "keiferia" OR "kuehneola" OR "kyllinga" OR "lagarosiphon" OR "laimaphelenchus" OR "lambro" OR "landoltia" OR "laphygma" OR "lasiomma" OR "laspeyresia" OR "lecanicillium" OR "lecanosticta" OR "leifsonia" OR "lemna" OR "lepidosaphes" OR "leprosis" OR "leptinotarsa" OR "leptocybe" OR "leptoglossus" OR "leptographium" OR "leptosphaeria" OR "leptosphaerulina" OR "leptoxyda" OR "lettuce infectious yellows closterovirus" OR "lettuce infectious yellows crinivirus" OR "lettuce infectious yellows virus" OR "leucaspis" OR "leucinodes" OR "liberibacter" OR "liberobacter" OR "limnobium" OR "limnophila" OR "limonius" OR "liriomyza" OR "lissorhoptrus" OR "listronotus" OR "little cherry pathogen" OR "liyv" OR "lobelia" OR "longidorus" OR "lopholeucaspis" OR "loxotaenia" OR "lozotaenia" OR "ludwigia" OR "lupinus" OR "lygus" OR "lymantria" OR "lysichiton" OR "maconellicoccus" OR "macrodiplodia" OR "macrophoma" OR "macrophomina" OR "macrotrophurus" OR "macroventuria" OR "mahonia" OR "maize redness phytoplasma" OR "malacosoma" OR "marchalina" OR "margarodes" OR "massaria" OR "massarina" OR "matricaria" OR "matsucoccus" OR "medeola" OR "medicopsis" OR "megaplatypus" OR "melampsora" OR "melampsoropsis" OR "melanauster" OR "melanomma" OR "melanotus" OR "mellesis" OR "meloidogyne" OR "mesocriconema" OR "metamasius" OR "mexican papita viroid" OR "microbacterium foliorum" OR "microbacterium phyllosphaerae" OR "micrococcus" OR "microsphaeropsis" OR "microstegium" OR "mimulus" OR "minyrus" OR "miscanthus" OR "monarthrum" OR "monascostroma" OR "monilia" OR "monilinia" OR "monochamus" OR "mycosphaerella" OR "myndus" OR "myopites" OR "myriophyllum" OR "myrsiphyllum" OR "myzus" OR "nacobbus" OR "nacobbus serendipiticus bolivianus" OR "nagelus" OR "narcissus mosaic virus" OR "naturally spreading psorosis" OR "naupactus" OR "necium" OR "nemapogon" OR "nematostoma" OR "nemorimyza" OR "neoaliturus" OR "neobagous" OR "neoceratitis" OR "neodolichorhynchus" OR "neoleucinodes" OR "neophaeosphaeria" OR "neophysopus" OR "neosetophoma" OR "neottiosporina" OR "neovossia" OR "nephopterix" OR "nicotiana virus 12" OR "nicotiana virus 13" OR "nigrograna" OR "nothotylenchus" OR "numonia" OR "nycteola" OR "nysius" OR "ocneria" OR "odoiporus" OR "oemona" OR "oerskovia" OR "ogma" OR "oligonychus" OR "ophelimus" OR "ophiognomonia" OR "ophiosphaerella" OR "ophiostoma" OR "opogona" OR "orellia" OR "orgyia" OR "orthotomicus" OR "otthia" OR "oxalis" OR "ozonium" OR "pachyrrhizus" OR "palm cadang-cadang viroid" OR "palm lethal yellowing mycoplasm" OR "palm lethal yellowing phytoplasma" OR "panicum" OR "pantoea" OR "pantomorus" OR "papaver" OR "paraconiothyrium" OR "paralepidosaphes" OR "paraleptosphaeria" OR "paraphaeosphaeria" OR "paraphoma" OR "parasaissetia" OR "paratoxoptera" OR "paratrichodorus" OR "paratrioza" OR "paratylenchus" OR "pardalaspis" OR "parthenium" OR "paspalum" OR "passalora" OR "paurus" OR "paysandisia" OR "pbrsv" OR "pcmv" OR "pdmv") AND (spread* OR dispers* OR invasion OR colonis* OR movement* OR diffus*) AND (model* OR simulat*) AND NOT (medic* OR clinic* OR veterinar*)) AND SUBJAREA(AGRI OR ENVI OR IMMU OR MATH OR COMP AND NOT (ARTS OR BIOC OR BUSI OR CENG OR CHEM OR DECI OR EART OR ECON OR ENER OR MATE OR MEDI OR NEUR OR NURS OR PSYC OR SOCI OR VETE OR DENT OR HEAL)) AND DOCTYPE(ar OR le) AND LANGUAGE(english)

TITLE-ABS-KEY(("peach american mosaic virus" OR "peach little peach phytoplasma" OR "peach mosaic closterovirus" OR "peach mosaic trichovirus" OR "peach mosaic virus" OR "peach phony agent" OR "peach phony rickettsia" OR "peach red suture phytoplasma" OR "peach rosette mosaic nepovirus" OR "peach rosette mosaic virus" OR "peach rosette mycoplasm" OR "peach rosette phytoplasma" OR "peach virus" OR "peach western x phytoplasma" OR "peach x-disease mycoplasm" OR "peach x disease phytoplasma" OR "peach yellow bud mosaic virus" OR "peach yellow leafroll phytoplasma" OR "peach yellows mycoplasm" OR "peach yellows phytoplasma" OR "pear decline mycoplasm" OR "pear decline phytoplasma" OR "pectobacterium chrysanthemi" OR "pectobacterium parthenii" OR "pemphigus" OR "pennisetum" OR "pepino mosaic potexvirus" OR "pepino mosaic virus" OR "pepmv" OR "pepper chat fruit viroid" OR "pepper mild tigre virus" OR "peridermium" OR "peritymbia" OR "peronea" OR "persicaria" OR "peyronellaea" OR "phaedon" OR "phaeocytostroma" OR "phaeophleospora" OR "phaeoramularia" OR "phaeosphaeria" OR "phaeosphaeriopsis" OR "phalaena" OR "pheletes" OR "phellinus" OR "phenacoccus" OR "phialophora" OR "phoma" OR "phomopsis" OR "phthorimaea" OR "phyllanthus" OR "phyllonorycter" OR "phyllopertha" OR "phyllosticta" OR "phyllostictina" OR "phylloxera" OR "phyloosticta" OR "phymatotrichopsis" OR "phymatotrichum" OR "physalospora" OR "phytobia" OR "phytolacca" OR "phytomonas" OR "phytophthora" OR "phytoplasma asteris" OR "phytoplasma aurantifolia" OR "phytoplasma australiense" OR "phytoplasma brasiliense" OR "phytoplasma cocosnigeriae" OR "phytoplasma cocostanzaniae" OR "phytoplasma fraxini" OR "phytoplasma mali" OR "phytoplasma oryzae" OR "phytoplasma palmi" OR "phytoplasma phoenicium" OR "phytoplasma pini" OR "phytoplasma pruni" OR "phytoplasma prunorum" OR "phytoplasma pyri" OR "phytoplasma rhamni" OR "phytoplasma rubi" OR "phytoplasma solani" OR "phytoplasma trifolii" OR "phytoplasma ulmi" OR "phytoplasma vitis" OR "phytoplasma ziziphi" OR "piaropus" OR "pileolaria" OR "pissodes" OR "pistia" OR "pityogenes" OR "pityophthorus" OR "plagiostoma" OR "plasmopara" OR "platychora" OR "platypus" OR "plenodomus" OR "pleomassaria" OR "pleospora" OR "pleurophoma" OR "plowrightia" OR "plum american line pattern ilarvirus" OR "plum line pattern virus" OR "plum pox potyvirus" OR "plum pox virus" OR "pochonia" OR "podisoma" OR "polistomimetes" OR "polygonum" OR "polygramma" OR "polygraphus" OR "pomacea" OR "pontederia" OR "popilia" OR "popillia" OR "poria" OR "porthetria" OR "potato andean calico virus" OR "potato andean latent tymovirus" OR "potato andean latent virus" OR "potato andean mottle comovirus" OR "potato andean mottle virus" OR "potato aucuba mosaic virus" OR "potato black ringspot nepovirus" OR "potato black ringspot virus" OR "potato brown rot" OR "potato deforming mosaic begomovirus" OR "potato deforming mosaic virus" OR "potato deforming mosaic virus argentina" OR "potato gothic virus" OR "potato leafroll virus" OR "potato purple-top wilt agent" OR "potato ring rot" OR "potato spindle tuber pospiviroid" OR "potato spindle tuber viroid" OR "potato spindle tuber virus" OR "potato stolbur mycoplasm" OR "potato stolbur phytoplasma" OR "potato t capillovirus" OR "potato t trichovirus" OR "potato virus" OR "potato wart disease" OR "potato yellow dwarf nucleorhabdovirus" OR "potato yellow dwarf rhabdovirus" OR "potato yellow dwarf virus" OR "potato yellow vein crinivirus" OR "potato yellow vein virus" OR "potato yellowing alfamovirus" OR "potato yellowing virus" OR "ppv" OR "pratylenchoides" OR "pratylenchus" OR "premnotrypes" OR "preussia" OR "prmv" OR "procecidochares" OR "prodenia" OR "prontaspis" OR "prunus" OR "prunus necrotic ringspot virus" OR "prunus virus" OR "pseudhalenchus" OR "pseudocercospora" OR "pseudodiplodia" OR "pseudomonas" OR "pseudopityophthorus" OR "pseudorobillarda" OR "pstvd" OR "pterandrus" OR "puccinia" OR "pueraria" OR "punctodera" OR "pvt" OR "pycnarmon" OR "pydv" OR "pyrenochaeta" OR "pyrenochaetopsis" OR "pyrenophora" OR "pyv" OR "pyvv" OR "quadraspidiotus" OR "radopholus" OR "ralstonia" OR "ranunculus" OR "raoiella" OR "raspberry leaf curl luteovirus" OR "raspberry leaf curl nepovirus" OR "raspberry leaf curl virus" OR "raspberry ringspot nepovirus" OR "raspberry ringspot virus" OR "rathayibacter" OR "readeriella" OR "reticulitermes" OR "rhacochlaena" OR "rhagoletis" OR "rhizaphis" OR "rhizoecus" OR "rhizosphaera" OR "rhododendron" OR "rhodophaea" OR "rhus" OR "rhynchophorus" OR "ripersiella" OR "rivellia" OR "rlcv" OR "robinia" OR "roestelia" OR "rosa" OR "rotylenchulus") AND (spread* OR dispers* OR invasion OR colonis* OR movement* OR diffus*) AND (model* OR simulat*) AND NOT (medic* OR clinic* OR veterinar*)) AND SUBJAREA(AGRI OR ENVI OR IMMU OR MATH OR COMP AND NOT (ARTS OR BIOC OR BUSI OR CENG OR CHEM OR DECI OR EART OR ECON OR ENER OR MATE OR MEDI OR NEUR OR NURS OR PSYC OR SOCI OR VETE OR DENT OR HEAL)) AND DOCTYPE(ar OR le) AND LANGUAGE(english)

TITLE-ABS-KEY(("rotylenchus" OR "roussoella" OR "rprsv" OR "rudbeckia" OR "rusticoclytus" OR "sagittaria" OR "saissetia" OR "salvinia" OR "saperda" OR "sarrothripus" OR "satsuma dwarf nepovirus" OR "satsuma dwarf sadwavirus" OR "satsuma dwarf virus" OR "sauertylenchus" OR "scaphoideus" OR "scarabaeus" OR "scirrhia" OR "scirtothrips" OR "sclerotinia" OR "scolecobasidium" OR "scolytus" OR "scrobipalpopsis" OR "scrobipalpula" OR "scrobipalpuloides" OR "scuttelonema" OR "scyphophorus" OR "sdv" OR "selenophoma" OR "semasia" OR "senecio" OR "septoria" OR "sesbania" OR "setomelanomma" OR "setophoma" OR "setosphaeria" OR "sicyos" OR "simplicillium" OR "sirex" OR "sirococcus" OR "slcv" OR "solanum" OR "solidago" OR "sorghum" OR "spanioza" OR "spartina" OR "sphaeraspis" OR "sphaeria" OR "sphaeropsis" OR "spilographa" OR "spiroplasma" OR "spodoptera" OR "sporormiella" OR "squash leaf curl begomovirus" OR "squash leaf curl bigeminivirus" OR "squash leaf curl geminivirus" OR "squash leaf curl virus" OR "stagonospora" OR "stagonosporopsis" OR "steganoptycha" OR "stegophora" OR "stenocarpella" OR "sternochetus" OR "stlcv" OR "stolbur phytoplasma" OR "straussia" OR "strauzia" OR "strawberry crinkle virus" OR "strawberry latent c rhabdovirus" OR "strawberry latent c virus" OR "strawberry latent ringspot virus" OR "strawberry mild yellow edge virus" OR "strawberry vein banding caulimovirus" OR "strawberry vein banding virus" OR "strawberry virus" OR "strawberry witches broom mycoplasm" OR "strobilomya" OR "strobilomyia" OR "strumeta" OR "subanguina" OR "subplenodomus" OR "sugarbeet leaf crinkle virus" OR "sugarbeet virus" OR "sunflower chlorotic mottle virus" OR "svbv" OR "symphoricarpus" OR "synchytrium" OR "systremma" OR "tachypterellus" OR "tanzanian lethal decline phytoplasma" OR "tasvd" OR "tatter leaf virus" OR "tecia" OR "tellima" OR "tephritis" OR "teras" OR "tetradacus" OR "tetranychus" OR "tetropium" OR "thaumastocoris" OR "thaumatotibia" OR "thaumetopoea" OR "thecaphora" OR "thrips" OR "thyridaria" OR "ticv" OR "tillaea" OR "tilletia" OR "tinea" OR "tmov" OR "tobacco ringspot nepovirus" OR "tobacco ringspot virus" OR "tobacco streak ilarvirus" OR "tobacco streak virus" OR "tocv" OR "tomato apical stunt pospiviroid" OR "tomato apical stunt viroid" OR "tomato black ring virus" OR "tomato bunchy top viroid" OR "tomato chlorosis closterovirus" OR "tomato chlorosis crinivirus" OR "tomato chlorosis virus" OR "tomato chlorotic dwarf viroid" OR "tomato chocolate virus" OR "tomato infectious chlorosis closterovirus" OR "tomato infectious chlorosis crinivirus" OR "tomato infectious chlorosis virus" OR "tomato leaf curl bigeminivirus" OR "tomato leaf curl geminivirus" OR "tomato marchitez virus" OR "tomato mottle begomovirus" OR "tomato mottle bigeminivirus" OR "tomato mottle geminivirus" OR "tomato mottle virus" OR "tomato planta macho viroid" OR "tomato ringspot nepovirus" OR "tomato ringspot virus" OR "tomato spotted wilt tospovirus" OR "tomato spotted wilt virus" OR "tomato torrado virus" OR "tomato yellow leaf curl begomovirus" OR "tomato yellow leaf curl bigeminivirus" OR "tomato yellow leaf curl geminivirus" OR "tomato yellow leaf curl sardinia begomovirus" OR "tomato yellow leaf curl sardinia virus" OR "tomato yellow leaf curl virus" OR "tomicus" OR "torsv" OR "tortrix" OR "toxicodendron" OR "toxoptera" OR "toxotrypana" OR "tranzschelia" OR "trechispora" OR "trematophoma" OR "trematosphaeria" OR "trialeurodes" OR "tribolium" OR "trichodorus" OR "trichoferus" OR "tridacus" OR "trioza" OR "trogoderma" OR "trophurus" OR "trsv" OR "trypeta" OR "tsvp" OR "tswv" OR "tulip virus" OR "turanoclytus" OR "tuta" OR "tylcv" OR "tylencholaimus" OR "tylenchorhynchus" OR "tylenchulus" OR "tylenchus" OR "tylolaimophorus" OR "unaspis" OR "uredo" OR "uromyces" OR "vaccinium" OR "venturia" OR "verbesina" OR "verticicladiella" OR "verticillium" OR "viteus" OR "watermelon silver mottle tospovirus" OR "watermelon silver mottle virus" OR "westerdykella" OR "western x disease phytoplasma" OR "winter peach mosaic virus" OR "witches broom" OR "wmsmov" OR "wojnowicia" OR "xanthomonas" OR "xiphinema" OR "xyleborinus" OR "xyleborus" OR "xylella" OR "xyloclytus" OR "xylomyges" OR "xylophilus" OR "xylosandrus" OR "xylotrechus" OR "xyphon" OR "yucatan lethal decline phytoplasma" OR "zaprionus" OR "zeugodacus" OR "zonosema") AND (spread* OR dispers* OR invasion OR colonis* OR movement* OR diffus*) AND (model* OR simulat*) AND NOT (medic* OR clinic* OR veterinar*)) AND SUBJAREA(AGRI OR ENVI OR IMMU OR MATH OR COMP AND NOT (ARTS OR BIOC OR BUSI OR CENG OR CHEM OR DECI OR EART OR ECON OR ENER OR MATE OR MEDI OR NEUR OR NURS OR PSYC OR SOCI OR VETE OR DENT OR HEAL)) AND DOCTYPE(ar OR le) AND LANGUAGE(english)

Appendix E. Google Scholar search strings

"abutilon theophrasti" spread dispersal model

"acacia dealbata" spread dispersal model

"acanthocinus spectabilis" spread dispersal model

"acer negundo" spread dispersal model

"acidovorax citrulli" OR "pseudomonas avenae" OR "acidovorax avenae" spread dispersal model

"acleris" spread dispersal model

"acleris bergmanniana" spread dispersal model

"acleris gloverana" OR "peronea gloverana" spread dispersal model

"acleris rhombana" spread dispersal model

"acleris semipurpurana" spread dispersal model

"acleris variana" OR "acalla variana" OR "peronea variana" OR "peronea angusana" OR "teras variana" spread dispersal model

"acleris variegana" spread dispersal model

"acrobasis pirivorella" spread dispersal model

"acroptilon repens" spread dispersal model

"aculops fuchsiae" spread dispersal model

"aeolesthes sarta" spread dispersal model

"agrilus anxius" spread dispersal model

"agrilus planipennis" OR "agrilus plannipenis" OR "agrilus feretrius" OR "agrilus marcopoli" spread dispersal model

"agrilus solieri" spread dispersal model

"agrilus vestitus" spread dispersal model

"agromyces cerinus" spread dispersal model

"agromyces ramosus" spread dispersal model

"ailanthus altissima" spread dispersal model

"akebia quinata" spread dispersal model

"aleurocanthus cinnamomi" spread dispersal model

"aleurocanthus spiniferus" OR "aleurocanthus rosae" OR "aleurodes citricola" OR "aleurodes spinifera" OR "aleurocanthus citricola" OR "aleurocanthus citricolus" spread dispersal model

"aleurocanthus woglumi" OR "aleurocanthus punjabensis" OR "aleurodes woglumi" OR "aleurocanthus husaini" spread dispersal model

"aleurocantus" spread dispersal model

"aleurodicus dispersus" spread dispersal model

"aleyrodes proletella" spread dispersal model

"allantophoma endogenospora" spread dispersal model

"allewia eureka" spread dispersal model

"allium paradoxum" spread dispersal model

"alternanthera mosaic virus" spread dispersal model

"alternanthera philoxeroides" spread dispersal model

"alternaria alternata" spread dispersal model

"alternaria mali" spread dispersal model

"alternaria maritima" spread dispersal model

"amaranthus albus" spread dispersal model

"amaranthus blitoides" spread dispersal model

"amaranthus blitum" spread dispersal model

"amaranthus caudatus" spread dispersal model

"amaranthus deflexus" spread dispersal model

"amaranthus graecizans" spread dispersal model

"amaranthus hybridus" spread dispersal model

"amaranthus palmeri" spread dispersal model

"amaranthus retroflexus" spread dispersal model

"amaranthus standleyanus" spread dispersal model

"amauromyza maculosa" spread dispersal model

"ambrosia artemisiifolia" spread dispersal model

"ambrosia psilostachya" spread dispersal model

"ambrosia trifida" spread dispersal model

"amelanchier lamarckii" spread dispersal model

"amelanchier spicata" spread dispersal model

"american plum line pattern virus" OR "plum american line pattern ilarvirus" OR "aplpv"

OR "plum line pattern virus" OR "american plum line pattern ilarvirus" spread dispersal model

"amorpha fruticosa" spread dispersal model

"ampelomyces quisqualis" spread dispersal model

"anastrepha fraterculus" OR "acrotoxa fraterculus" OR "trypeta unicolor" OR "tephritis mellea" OR "anastrepha braziliensis" OR "dacus fraterculus" OR "anastrepha soluta" OR "anthomyia frutalis" OR "anastrepha peruviana" OR "trypeta fraterculus" spread dispersal model

"anastrepha ludens" OR "acrotoxa ludens" OR "trypeta ludens" spread dispersal model

"anastrepha obliqua" OR "acrotoxa obliqua" OR "trypeta obliqua" OR "anastrepha trinidadensis" OR "tephritis obliqua" OR "anastrepha mombinpraeoptans" OR "anastrepha fraterculus" OR "anastrepha fraterculus" OR "anastrepha fraterculus" OR "anastrepha fraterculus" spread dispersal model

"anastrepha serpentina" spread dispersal model

"anastrepha striata" spread dispersal model

"anastrepha suspensa" OR "acrotoxa suspensa" OR "anastrepha longimacula" OR "trypeta suspensa" OR "anastrepha unipuncta" spread dispersal model

"andean potato latent virus" OR "aplv" OR "potato andean latent virus" OR "andean potato latent tymovirus" OR "eggplant mosaic tymovirus" OR "potato andean latent tymovirus" OR "eggplant mosaic virus" spread dispersal model

"andean potato mottle virus" OR "andean potato mottle comovirus" OR "potato andean mottle virus" OR "apmov" OR "potato andean mottle comovirus" spread dispersal model

"andropogon virginicus" OR "anatherum virginicum" OR "andropogon dissitiflorus" spread dispersal model

"anguina tritici" spread dispersal model

"anisogramma anomala" OR "apioporthe anomala" OR "cryptosporella anomala" spread dispersal model

"anomala orientalis" spread dispersal model

"anoplophora chinensis" OR "cerambyx punctator" OR "melanauster chinensis" OR "cerambyx farinosus" OR "anoplophora chinensis" OR "anoplophora chinensis" OR "cerambyx chinensis" OR "anoplophora malasiaca" OR "anoplophora macularia" OR "calloplophora macularia" OR "melanauster chinensis" OR "melanauster macularius" spread dispersal model

"anoplophora glabripennis" spread dispersal model

"anoplophora malasiaca" spread dispersal model

"anthonomus bisignifer" OR "minyrus albopilosus" OR "anthonomus bisignatus" OR "anthonomus signatus" OR "minyrus japonicus" OR "minyrus japonicus" spread dispersal model

"anthonomus eugenii" OR "anthonomochaeta eugenii" OR "anthonomus aeneotinctus" spread dispersal model

"anthonomus grandis" OR "anthonomus grandis" spread dispersal model

"anthonomus piri" spread dispersal model

"anthonomus quadrigibbus" spread dispersal model

"anthonomus signatus" OR "anthonomus bisignatus" OR "anthonomus scutellatus" OR "anthonomus pallidus" spread dispersal model

"anthonomus spilotus" spread dispersal model

"aonidella citrina" spread dispersal model

"aonidiella aurantii" spread dispersal model

"aonidiella citrina" spread dispersal model

"aphelenchoides besseyi" OR "asteroaphelenchoides besseyi" OR "aphelenchoides oryzae" spread dispersal model

"aphelenchoides bicaudatus" spread dispersal model

"aphelenchoides blastophthorus" spread dispersal model

"aphelenchoides composticola" spread dispersal model

"aphelenchoides fragariae" spread dispersal model "aphelenchoides ritzemabosi" spread dispersal model

"aphelenchoides saprophilus" spread dispersal model

"aphelenchoides subtenuis" spread dispersal model

"aphelenchus avenae" spread dispersal model

"apiosporina morbosa" OR "sphaeria morbosa" OR "cucurbitaria morbosa" OR "otthia morbosa" OR "plowrightia morbosa" OR "dibotryon morbosum" OR "botryosphaeria morbosa" spread dispersal model

"aponogeton distachyos" spread dispersal model

"aposphaeria corallinolutea" spread dispersal model

"aposphaeria populina" spread dispersal model

"apple proliferation mycoplasm" spread dispersal model

"apricot chlorotic leafroll mycoplasm" spread dispersal model

"aproceros leucopoda" spread dispersal model

"arabis mosaic virus" spread dispersal model

"araujia sericifera" spread dispersal model

"arceuthobium" spread dispersal model

"arceuthobium abietinum" spread dispersal model

"arceuthobium americanum" spread dispersal model

"arceuthobium campylopodum" spread dispersal model

"arceuthobium douglasii" spread dispersal model

"arceuthobium laricis" spread dispersal model

"arceuthobium minutissimum" spread dispersal model

"arceuthobium occidentale" spread dispersal model

"arceuthobium pusillum" spread dispersal model

"arceuthobium tsugense" spread dispersal model

"arceuthobium vaginatum" spread dispersal model

"aromia bungii" OR "cerambyx bungii" spread dispersal model

"aronia x prunifolia" spread dispersal model

"arracacha virus" spread dispersal model

"arrachaca virus" spread dispersal model

"arrhenodes minutus" spread dispersal model

"arsenophonus phytopathogenicus" spread dispersal model

"arthraxon hispidus" spread dispersal model

"aschistonyx eppoi" spread dispersal model

"asclepias syriaca" spread dispersal model

"ascochyta" spread dispersal model

"ascochyta hordei" spread dispersal model

"asparagus asparagoides" OR "myrsiphyllum asparagoides" OR "medeola asparagoides" OR "elide asparagoides" spread dispersal model

"atropellis" spread dispersal model

"atropellis pinicola" OR "godronia zelleri" spread dispersal model

"atropellis piniphila" OR "cenangium piniphilum" OR "atropellis arizonica" spread dispersal model

"aulacaspis rosae" spread dispersal model

"aulacaspis tubercularis" spread dispersal model

"aulacaspis yasumatsui" spread dispersal model

"azolla filiculoides" spread dispersal model

"baccharis halimifolia" spread dispersal model

"bactericera cockerelli" OR "trioza cockerelli" OR "paratrioza cockerelli" spread dispersal model

"bactrocera carambolae" OR "bactrocera" spread dispersal model

"bactrocera caryeae" OR "dacus caryeae" spread dispersal model

"bactrocera correcta" spread dispersal model

"bactrocera cucumis" OR "austrodacus cucumis" OR "dacus cucumis" OR "dacus tryoni" OR "dacus tryoni" spread dispersal model

"bactrocera cucurbitae" OR "chaetodacus cucurbitae" OR "zeugodacus cucurbitae" OR "strumeta cucurbitae" OR "dacus cucurbitae" spread dispersal model

"bactrocera dorsalis" OR "chaetodacus ferrugineus" OR "dacus dorsalis" OR "chaetodacus dorsalis" OR "strumeta dorsalis" OR "chaetodacus ferrugineus" OR "dacus ferrugineus" spread dispersal model

"bactrocera invadens" spread dispersal model

"bactrocera kandiensis" OR "bactrocera" spread dispersal model

"bactrocera latifrons" spread dispersal model

"bactrocera minax" OR "polistomimetes minax" OR "mellesis citri" OR "tetradacus citri" OR "dacus citri" OR "bactrocera citri" OR "callantra minax" spread dispersal model

"bactrocera occipitalis" OR "dacus occipitalis" OR "chaetodacus ferrugineus" OR "chaetodacus ferrugineus" spread dispersal model

"bactrocera oleae" spread dispersal model

"bactrocera papayae" OR "bactrocera" spread dispersal model

"bactrocera philippinensis" OR "bactrocera" spread dispersal model

"bactrocera pyrifoliae" spread dispersal model

"bactrocera tau" spread dispersal model

"bactrocera tryoni" OR "tephritis tryoni" OR "dacus tryoni" OR "strumeta tryoni" OR "chaetodacus tryoni" OR "dacus ferrugineus" spread dispersal model

"bactrocera tsuneonis" OR "dacus tsuneonis" OR "dacus cheni" OR "tetradacus tsuneonis" spread dispersal model

"bactrocera zonata" OR "dasyneura zonata" OR "strumeta zonatus" OR "dacus persicus" OR "rivellia persicae" OR "dacus zonatus" OR "bactrocera maculigera" OR "strumeta zonata" spread dispersal model

"bean golden mosaic virus" OR "bgmv" OR "bean golden mosaic bigeminivirus" OR "bean golden mosaic geminivirus" OR "bean golden mosaic begomovirus" spread dispersal model

"bean golden yellow mosaic virus" OR "bgymv" OR "bean golden yellow mosaic begomovirus" spread dispersal model

"bean yellow mosaic virus" spread dispersal model

"beet curly top virus" spread dispersal model

"beet leaf curl virus" OR "sugarbeet virus" OR "blcv" OR "sugarbeet leaf crinkle virus" OR "beet leaf curl rhabdovirus" spread dispersal model

"beet necrotic yellow vein virus" OR "beet necrotic yellow vein furovirus" OR "bnyvv" OR "beet necrotic yellow vein benyvirus" OR "beet rhizomania virus" spread dispersal model

"beet ringpsot virus" spread dispersal model

"bemisia afer" spread dispersal model

"bemisia argentifolii" OR "bemisia tabaci" spread dispersal model

"bemisia tabaci" OR "bemisia lonicerae" OR "bemisia hibisci" OR "bemisia goldingi" OR "bemisia emiliae" OR "bemisia rhodesiaensis" OR "bemisia nigeriensis" OR "bemisia achyranthes" OR "bemisia longispina" OR "bemisia bahiana" OR "bemisia gossypiperda" OR "bemisia minuscula" OR "bemisia minima" OR "bemisia manihotis" OR "bemisia vayssieri" OR "aleurodes tabaci" OR "bemisia inconspicua" spread dispersal model

"berberis aquifolium" spread dispersal model

"beverwykella pulmonaria" spread dispersal model

"bidens bipinnata" spread dispersal model

"bidens frondosa" spread dispersal model

"bidens pilosa" spread dispersal model

"black raspberry latent virus" spread dispersal model

"blitopertha orientalis" OR "anomala orientalis" OR "phyllopertha orientalis" OR "exomala orientalis" spread dispersal model

"blueberry leaf mottle virus" OR "blmov" OR "blueberry leaf mottle nepovirus" spread dispersal model

"blueberry scorch virus" OR "blueberry scorch carlavirus" spread dispersal model

"boeremia crinicola" spread dispersal model

"boeremia diversispora" spread dispersal model

"boeremia exigua" spread dispersal model "boeremia foveata" spread dispersal model

"boeremia hedericola" spread dispersal model

"boeremia lycopersici" spread dispersal model

"boeremia noackiana" spread dispersal model

"boeremia sambuci-nigrae" spread dispersal model

"boeremia strasseri" spread dispersal model

"boeremia telephii" spread dispersal model

"botryosphaeria laricina" OR "macrophoma laricina" OR "physalospora laricina" OR "phyllosticta laricis" OR "guignardia laricina" spread dispersal model

"buddleja davidii" spread dispersal model

"bunias orientalis" spread dispersal model

"burkholderia caryophylli" OR "phytomonas caryophylli" OR "pseudomonas caryophylli" spread dispersal model

"bursaphelenchus chengi" spread dispersal model

"bursaphelenchus cocophilus" spread dispersal model

"bursaphelenchus conicaudatus" spread dispersal model

"bursaphelenchus doui" spread dispersal model

"bursaphelenchus eremus" spread dispersal model

"bursaphelenchus fraudulentus" spread dispersal model

"bursaphelenchus mucronatus" spread dispersal model

"bursaphelenchus paraluxuriosae" spread dispersal model

"bursaphelenchus pinophilus" spread dispersal model

"bursaphelenchus thailandae" spread dispersal model

"bursaphelenchus xylophilus" OR "aphelenchoides xylophilus" OR "bursaphelenchus lignicola" OR "bursaphelenchus lignicolus" spread dispersal model

"byssothecium circinans" spread dispersal model

"cabomba aquatica" spread dispersal model

"cabomba caroliniana" spread dispersal model

"cabomba furcata" spread dispersal model

"cacoecimorpha pronubana" OR "cacoecimorpha insolatana" OR "cacoecia pronubana" OR "tortrix pronubana" OR "cacoecimorpha hermineana" OR "cacoecimorpha ambustana" spread dispersal model

"cactodera cacti" spread dispersal model

"cacyreus marshalli" spread dispersal model

"cadang-cadang viroid" spread dispersal model

"cape st paul wilt phytoplasma" OR "phytoplasma cocosnigeriae" spread dispersal model

"cardiospermum grandiflorum" spread dispersal model

"carneocephala fulgida" spread dispersal model

"carpobrotus acinaciformis" spread dispersal model

"carpobrotus edulis" spread dispersal model

"carposina niponensis" spread dispersal model

"carposina sasakii" OR "carposina niponensis" spread dispersal model

"cellulomonas biazotea" spread dispersal model

"cellulomonas fimi" spread dispersal model

"cenchrus incertus" spread dispersal model

"cenchrus pauciflorus" spread dispersal model

"cephalcia lariciphila" spread dispersal model

"ceratitis capitata" OR "ceratitis citriperda" OR "tephritis capitata" OR "pardalaspis asparagi" OR "ceratitis hispanica" spread dispersal model

"ceratitis catoirii" spread dispersal model

"ceratitis cosyra" OR "pterandrus cosyra" OR "pardalaspis cosyra" OR "pardalaspis parinarii" OR "trypeta cosyra" spread dispersal model

"ceratitis quinaria" spread dispersal model

"ceratitis rosa" OR "pterandrus rosa" spread dispersal model

"ceratocystis adiposa" spread dispersal model

"ceratocystis bhutanensis" spread dispersal model

"ceratocystis caryae" spread dispersal model "ceratocystis coerulescens" spread dispersal model

"ceratocystis fagacearum" OR "endoconidiophora fagacearum" OR "chalara quercina" spread dispersal model

"ceratocystis fimbriata" spread dispersal model

"ceratocystis fujiensis" spread dispersal model

"ceratocystis laricicola" spread dispersal model

"ceratocystis major" spread dispersal model

"ceratocystis moniliformis" spread dispersal model

"ceratocystis moniliformopsis" spread dispersal model

"ceratocystis neglecta" spread dispersal model

"ceratocystis omanensis" spread dispersal model

"ceratocystis paradoxa" spread dispersal model

"ceratocystis pinicola" spread dispersal model

"ceratocystis pirilliformis" spread dispersal model

"ceratocystis platani" OR "endoconidiophora fimbriata" OR "ceratocystis fimbriata" OR "ceratocystis fimbriata" spread dispersal model

"ceratocystis polonica" spread dispersal model

"ceratocystis polychroma" spread dispersal model

"ceratocystis populicola" spread dispersal model

"ceratocystis radicicola" spread dispersal model

"ceratocystis resinifera" spread dispersal model

"ceratocystis rufipennis" spread dispersal model

"ceratocystis savannae" spread dispersal model

"ceratocystis smalleyi" spread dispersal model

"ceratocystis subannulata" spread dispersal model

"ceratocystis tribiliformis" spread dispersal model

"ceratocystis tsitsikammensis" spread dispersal model

"ceratocystis variospora" spread dispersal model

"ceratocystis virescens" spread dispersal model

"ceratophyllum demersum" spread dispersal model

"cercoseptoria pini-densiflorae" spread dispersal model

"cercospora angolensis" spread dispersal model

"cercosporella virgaureae" spread dispersal model

"chaetasbolisia erysiphoides" spread dispersal model

"chaetocnema confusa" spread dispersal model

"chaetocnema tibialis" spread dispersal model

"chaetoconis polygoni" spread dispersal model

"chaetodiplodia" spread dispersal model

"chaetophoma" spread dispersal model

"chaetopyrena penicillata" spread dispersal model

"chaetosphaeronema coonsii" spread dispersal model

"chaetosphaeronema hispidulum" spread dispersal model

"cherry leafroll virus" spread dispersal model

"cherry rasp leaf virus" OR "crlv" OR "apple flat apple virus" OR "cherry rasp leaf cheravirus" OR "cherry rasp leaf nepovirus" spread dispersal model

"choristoneura" spread dispersal model

"choristoneura conflictana" OR "archips conflictana" OR "cacoecia conflictana" OR "heterognomon conflictana" OR "tortrix conflictana" spread dispersal model

"choristoneura fumiferana" OR "tortrix nigridia" OR "tortrix fumiferana" OR "choristoneura lambertiana" OR "archips fumiferana" OR "cacoecia fumiferana" OR "harmologa fumiferana" OR "archips retiniana" OR "choristoneura retiniana" OR "lozotaenia retiniana" OR "cacoecia retiniana" spread dispersal model

"choristoneura occidentalis" OR "archips occidentalis" OR "cacoecia occidentalis" spread dispersal model

"choristoneura pinus" spread dispersal model

"choristoneura rosaceana" OR "archips rosaceana" OR "cacoecia rosaceana" OR "loxotaenia rosaceana" OR "tortrix rosaceana" OR "teras vicariana" OR "tortrix gossypiana" spread dispersal model

"chromatomyia horticola" spread dispersal model

"chrysanthemum stem necrosis virus" OR "csnv" OR "chrysanthemum stem necrosis tospovirus" spread dispersal model

"chrysanthemum stunt viroid" OR "chrysanthemum stunt mottle virus" OR "csvd" OR "chrysanthemum stunt pospiviroid" spread dispersal model

"chrysomyxa arctostaphyli" OR "melampsoropsis arctostaphyli" OR "peridermium coloradense" spread dispersal model

"chrysophtharta bimaculata" spread dispersal model

"ciborinia camelliae" OR "sclerotinia camelliae" OR "sclerotinia camelliae" spread dispersal model

"circulifer haematoceps" spread dispersal model

"circulifer tenellus" spread dispersal model

"citrus blight agent" spread dispersal model

"citrus exocortis viroid" spread dispersal model

"citrus greening bacterium" spread dispersal model

"citrus leprosis virus" OR "cilv" OR "citrus leprosis rhabdovirus" spread dispersal model

"citrus mosaic virus" spread dispersal model

"citrus tatter leaf virus" OR "ctlv" OR "citrange stunt virus" OR "citrus tatter leaf capillovirus" spread dispersal model

"citrus tristeza virus" OR "ctv" OR "citrus tristeza closterovirus" spread dispersal model

"citrus variegated chlorosis" spread dispersal model

"citrus vein enation woody gall" spread dispersal model

"citrus yellow mosaic virus" OR "cmbv" OR "citrus mosaic badnavirus" OR "ciymv" OR "cimv" OR "citrus mosaic virus" spread dispersal model

"clavibacter" spread dispersal model

"clavibacter michiganensis" OR "corynebacterium michiganense" OR "bacterium michiganense" OR "pseudomonas michiganensis" OR "clavibacter michiganensis" spread dispersal model

"cochliobolus heterostrophus" spread dispersal model

"cochliobolus sativus" spread dispersal model

"coconut cadang-cadang viroid" OR "cccvd" OR "palm cadang-cadang viroid" OR "coconut cadang-cadang cocadviroid" spread dispersal model

"coconut lethal yellowing phytoplasma" OR "palm lethal yellowing phytoplasma" OR "phytoplasma palmi" spread dispersal model

"coleophoma crateriformis" spread dispersal model

"coleophoma maculans" spread dispersal model

"coleophoma oleae" spread dispersal model

"colletotrichum acerbum" spread dispersal model

"colletotrichum acutatum" spread dispersal model

"colletotrichum aenigma" spread dispersal model

"colletotrichum aeschynomenes" spread dispersal model

"colletotrichum alatae" spread dispersal model

"colletotrichum alienum" spread dispersal model

"colletotrichum annellatum" spread dispersal model

"colletotrichum anthrisci" spread dispersal model

"colletotrichum aotearoa" spread dispersal model

"colletotrichum asianum" spread dispersal model

"colletotrichum australe" spread dispersal model

"colletotrichum beeveri" spread dispersal model

"colletotrichum boninense" spread dispersal model "colletotrichum brasiliense" spread dispersal model

"colletotrichum brassicicola" spread dispersal model

"colletotrichum brisbanense" spread dispersal model

"colletotrichum carthami" spread dispersal model

"colletotrichum chlorophyti" spread dispersal model

"colletotrichum chrysanthemi" spread dispersal model

"colletotrichum circinans" spread dispersal model

"colletotrichum clidemiae" spread dispersal model

"colletotrichum cliviae" spread dispersal model

"colletotrichum coccodes" spread dispersal model

"colletotrichum colombiense" spread dispersal model

"colletotrichum constrictum" spread dispersal model

"colletotrichum cordylinicola" spread dispersal model

"colletotrichum cosmi" spread dispersal model

"colletotrichum costaricense" spread dispersal model

"colletotrichum curcumae" spread dispersal model

"colletotrichum cuscutae" spread dispersal model

"colletotrichum cymbidiicola" spread dispersal model

"colletotrichum dacrycarpi" spread dispersal model

"colletotrichum dematium" spread dispersal model

"colletotrichum dracaenophilum" spread dispersal model

"colletotrichum echinochloae" spread dispersal model

"colletotrichum eleusines" spread dispersal model

"colletotrichum eremochloae" spread dispersal model

"colletotrichum falcatum" spread dispersal model

"colletotrichum fioriniae" spread dispersal model

"colletotrichum fructi" spread dispersal model

"colletotrichum fructicola" spread dispersal model

"colletotrichum gloeosporioides" spread dispersal model

"colletotrichum godetiae" spread dispersal model

"colletotrichum graminicola" spread dispersal model

"colletotrichum guajavae" spread dispersal model

"colletotrichum hanaui" spread dispersal model

"colletotrichum hemerocallidis" spread dispersal model

"colletotrichum hippeastri" spread dispersal model

"colletotrichum horii" spread dispersal model

"colletotrichum indonesiense" spread dispersal model

"colletotrichum jacksonii" spread dispersal model

"colletotrichum jasminigenum" spread dispersal model

"colletotrichum johnstonii" spread dispersal model

"colletotrichum kahawae" spread dispersal model

"colletotrichum karstii" spread dispersal model

"colletotrichum kinghornii" spread dispersal model

"colletotrichum laticiphilum" spread dispersal model

"colletotrichum lilii" spread dispersal model

"colletotrichum limetticola" spread dispersal model

"colletotrichum lineola" spread dispersal model "colletotrichum liriopes" spread dispersal model

"colletotrichum lupini" spread dispersal model

"colletotrichum melonis" spread dispersal model

"colletotrichum miscanthi" spread dispersal model

"colletotrichum musae" spread dispersal model

"colletotrichum navitas" spread dispersal model

"colletotrichum nicholsonii" spread dispersal model

"colletotrichum novae-zelandiae" spread dispersal model

"colletotrichum nupharicola" spread dispersal model

"colletotrichum nymphaeae" spread dispersal model

"colletotrichum oncidii" spread dispersal model

"colletotrichum orchidophilum" spread dispersal model

"colletotrichum parsonsiae" spread dispersal model

"colletotrichum paspali" spread dispersal model

"colletotrichum paxtonii" spread dispersal model

"colletotrichum petchii" spread dispersal model

"colletotrichum phormii" spread dispersal model

"colletotrichum phyllanthi" spread dispersal model

"colletotrichum pseudoacutatum" spread dispersal model

"colletotrichum psidii" spread dispersal model

"colletotrichum pyricola" spread dispersal model

"colletotrichum queenslandicum" spread dispersal model

"colletotrichum rhombiforme" spread dispersal model

"colletotrichum rusci" spread dispersal model

"colletotrichum salicis" spread dispersal model

"colletotrichum salsolae" spread dispersal model

"colletotrichum scovillei" spread dispersal model

"colletotrichum siamense" spread dispersal model

"colletotrichum simmondsii" spread dispersal model

"colletotrichum sloanei" spread dispersal model

"colletotrichum spaethianum" spread dispersal model

"colletotrichum spinaciae" spread dispersal model

"colletotrichum sublineola" spread dispersal model

"colletotrichum tamarilloi" spread dispersal model

"colletotrichum theobromicola" spread dispersal model

"colletotrichum ti" spread dispersal model

"colletotrichum tofieldiae" spread dispersal model

"colletotrichum torulosum" spread dispersal model

"colletotrichum trichellum" spread dispersal model

"colletotrichum tropicale" spread dispersal model

"colletotrichum truncatum" spread dispersal model

"colletotrichum verruculosum" spread dispersal model

"colletotrichum walleri" spread dispersal model

"colletotrichum xanthorrhoeae" spread dispersal model

"colletotrichum yunnanense" spread dispersal model

"columnea latent viroid" spread dispersal model

"coniella fragariae" spread dispersal model

"coniothyrium carteri" spread dispersal model

"coniothyrium cerealis" spread dispersal model "coniothyrium concentricum" spread dispersal model

"coniothyrium dolichi" spread dispersal model

"coniothyrium glycines" spread dispersal model

"coniothyrium multiporum" spread dispersal model

"coniothyrium palmarum" spread dispersal model

"coniothyrium telephii" spread dispersal model

"conotrachelus nenuphar" spread dispersal model

"coraebus rubi" spread dispersal model

"cornus sericea" spread dispersal model

"cortaderia jubata" spread dispersal model

"cortaderia selloana" spread dispersal model

"corythucha ciliata" spread dispersal model

"cosmopolites sordidus" spread dispersal model

"cotoneaster horizontalis" spread dispersal model

"cowpea mild mottle virus" spread dispersal model

"crassula helmsii" OR "tillaea recurva" spread dispersal model

"crassula tillaea" spread dispersal model

"cronartium" spread dispersal model

"cronartium coleosporioides" OR "peridermium stalactiforme" spread dispersal model

"cronartium comandrae" OR "peridermium pyriforme" OR "cronartium pyriforme" spread dispersal model

"cronartium comptoniae" OR "peridermium comptoniae" spread dispersal model

"cronartium fusiforme" OR "peridermium fusiforme" OR "cronartium quercuum" OR "cronartium quercuum" spread dispersal model

"cronartium himalayense" OR "peridermium himalayense" spread dispersal model

"cronartium kamtschaticum" OR "peridermium kurilense" spread dispersal model

"cronartium quercuum" OR "cronartium asclepiadaceum" OR "peridermium giganteum" OR "peridermium cerebrum" OR "cronartium cerebrum" OR "peridermium mexicanum" spread dispersal model

"cryphonectria parasitica" OR "endothia parasitica" OR "cytospora parasitica" spread dispersal model

"ctenarytaina eucalypti" spread dispersal model

"ctenarytaina spatulata" spread dispersal model

"cucumber vein yellowing virus" OR "cucumber vein yellowing ipomovirus" spread dispersal model

"cucurbit chlorotic yellows virus" spread dispersal model

"cucurbit yellow stunting disorder virus" OR "cucurbit yellow stunting closterovirus" OR "cucurbit yellow stunting virus" OR "cucumber yellow stunting crinivirus" OR "cucurbit yellow stunting disorder closterovirus" OR "cysdv" OR "cucurbit yellow stunting disorder crinivirus" OR "cucumber yellow stunting disorder crinivirus" spread dispersal model

"cucurbitaria berberidis" spread dispersal model

"curtobacterium citreum" spread dispersal model

"curtobacterium flaccumfaciens" OR "bacterium flaccumfaciens" OR "pseudomonas flaccumfaciens" OR "corynebacterium flaccumfaciens" OR "corynebacterium flaccumfaciens" spread dispersal model

"curtobacterium luteum" spread dispersal model

"cuscuta campestris" spread dispersal model

"cydia amplana" spread dispersal model

"cydia fagiglandana" spread dispersal model

"cydia inopinata" OR "laspeyresia prunifoliae" OR "grapholita cerasana" OR "grapholita inopinata" spread dispersal model

"cydia packardi" OR "laspeyresia packardi" OR "enarmonia packardi" OR "grapholita packardi" OR "steganoptycha pyricolana" OR "enarmonia pyricolana" OR "laspeyresia pyricolana" spread dispersal model

"cydia pomonella" spread dispersal model "cydia prunivora" OR "laspeyresia prunivora" OR "semasia prunivora" OR "enarmonia prunivora" OR "grapholita prunivora" OR "epinotia prunivora" spread dispersal model

"cydia splendana" spread dispersal model

"cydia triangulella" spread dispersal model

"cymbdium mosaic virus" spread dispersal model

"cyperus eragrostis" spread dispersal model

"cyperus esculentus" spread dispersal model

"cyperus rotundus" spread dispersal model

"cyrtogenius luteus" spread dispersal model

"cyrtotrachelus buqueti" spread dispersal model

"dacus bivittatus" spread dispersal model

"dacus ciliatus" OR "tridacus malleyi" OR "dacus insistens" OR "dacus brevistylus" OR "leptoxyda ciliata" OR "didacus ciliatus" OR "dacus sigmoides" OR "didacus brevistylus" OR "dacus apoxanthus decolor" OR "dacus apoxanthus" spread dispersal model

"dacus curcurbitae" spread dispersal model

"dacus demmerezi" spread dispersal model

"dacus dorsalis" spread dispersal model

"dacus etiennellus" spread dispersal model

"dacus tryoni" spread dispersal model

"dacus tsuneonis" spread dispersal model

"dacus vertebratus" spread dispersal model

"dacus zonatus" spread dispersal model

"daktulosphaira vitifoliae" spread dispersal model

"davidiella populorum" OR "septoria musiva" OR "mycosphaerella populorum" spread dispersal model

"dendroctonus adjunctus" OR "dendroctonus convexifrons" spread dispersal model

"dendroctonus approximatus" spread dispersal model

"dendroctonus brevicomis" OR "dendroctonus barberi" spread dispersal model

"dendroctonus frontalis" OR "dendroctonus arizonicus" spread dispersal model

"dendroctonus jeffreyi" spread dispersal model

"dendroctonus micans" spread dispersal model

"dendroctonus ponderosae" OR "dendroctonus monticolae" spread dispersal model

"dendroctonus pseudotsugae" spread dispersal model

"dendroctonus rufipennis" OR "dendroctonus obesus" OR "dendroctonus similis" OR "hylurgus rufipennis" OR "dendroctonus borealis" OR "dendroctonus engelmanni" OR "dendroctonus piceaperda" spread dispersal model

"dendroctonus terebrans" spread dispersal model

"dendroctonus valens" spread dispersal model

"dendrolimus sibiricus" OR "dendrolimus laricis" OR "dendrolimus superans" spread dispersal model

"dendrolimus superans" OR "dendrolimus superans" spread dispersal model

"deuterophoma tracheiphila" spread dispersal model

"diabrotica balteata" spread dispersal model

"diabrotica barberi" OR "diabrotica longicornis" spread dispersal model

"diabrotica longicornis" spread dispersal model

"diabrotica speciosa" spread dispersal model

"diabrotica undecimpunctata" OR "diabrotica sexpunctata" OR "diabrotica duodecimpunctata" OR "crioceris sexpunctata" OR "diabrotica undecimpunctata" spread dispersal model

"diabrotica virgifera" OR "diabrotica virgifera" spread dispersal model

"diaphania perspectabilis" spread dispersal model

"diaphorina citri" OR "euphalerus citri" spread dispersal model

"diaporthe vaccinii" OR "phomopsis vaccinii" spread dispersal model

"diaspidiotus ostreaeformis" spread dispersal model

"diaspidiotus perniciosus" spread dispersal model

"dickeya dianthicola" OR "pectobacterium parthenii" OR "erwinia chrysanthemi" OR "pectobacterium chrysanthemi" spread dispersal model

"didymella adianticola" spread dispersal model

"didymella applanata" spread dispersal model

"didymella bryoniae" spread dispersal model

"didymella cannabis" spread dispersal model

"didymella catariae" spread dispersal model

"didymella clematidis" spread dispersal model

"didymella exigua" spread dispersal model

"didymella fabae" spread dispersal model

"didymella ligulicola" spread dispersal model

"didymella macropodii" spread dispersal model

"didymella pisi" spread dispersal model

"didymella rabiei" spread dispersal model

"didymella urticicola" spread dispersal model

"didymella vitalbina" spread dispersal model

"digitaria horizontalis" spread dispersal model

"digitaria nuda" spread dispersal model

"diocalandra frumenti" spread dispersal model

"diphtherophora communis" spread dispersal model

"diplodia pinae" spread dispersal model

"diplodina coloradensis" spread dispersal model

"ditylenchus adasi" spread dispersal model

"ditylenchus destructor" spread dispersal model

"ditylenchus dipsaci" OR "ditylenchus phloxidis" OR "ditylenchus fragariae" OR "anguillulina dipsaci" OR "tylenchus devastator" OR "tylenchus dipsaci" spread dispersal model

"ditylenchus myceliophagus" spread dispersal model

"dothidea insculpta" spread dispersal model

"dothiora cannabinae" spread dispersal model

"dothiorella ulmi" spread dispersal model

"dothistroma pini" spread dispersal model

"dothistroma septosporum" spread dispersal model

"draeculacephala minerva" spread dispersal model

"drosophila suzukii" spread dispersal model

"dryocoetes confusus" OR "dryocoetes abietis" OR "dendroctonus abietis" spread dispersal model

"dryocosmus kuriphilus" spread dispersal model

"ecphyadophora tenuissima" spread dispersal model

"egeria densa" spread dispersal model

"egeria naias" spread dispersal model

"eichhornia azurea" spread dispersal model

"eichhornia crassipes" OR "eichhornia speciosa" OR "piaropus crassipes" spread dispersal model

"elatine hexandra" spread dispersal model

"elatine hydropiper" spread dispersal model

"elatine triandra" spread dispersal model

"eleutheromyces subulatus" spread dispersal model

"elm phloem necrosis mycoplasm" spread dispersal model

"elodea callitrichoides" spread dispersal model

"elodea canadensis" spread dispersal model

"elodea nuttallii" spread dispersal model

"elsinoe" spread dispersal model

"enaphalodes rufulus" spread dispersal model

"enarmonia packardi" spread dispersal model

"enarmonia prunivora" spread dispersal model

"endocronartium" spread dispersal model

"endocronartium harknessii" OR "cronartium harknessii" OR "peridermium cerebroides" OR "peridermium harknessii" spread dispersal model

"endoxyla cinereus" spread dispersal model

"entodesmium rude" spread dispersal model

"epicoccum nigrum" spread dispersal model

"epicoccum pimprinum" spread dispersal model

"epicoccum sorghi" spread dispersal model

"epitrix" spread dispersal model

"epitrix cucumeris" spread dispersal model

"epitrix fasciata" spread dispersal model

"epitrix hirtipennis" spread dispersal model "epitrix similaris" spread dispersal model

"epitrix subcrinita" OR "epitrix subcarinata" spread dispersal model

"epitrix tuberis" spread dispersal model

"epochra canadensis" spread dispersal model

"erechtites hieraciifolius" spread dispersal model

"eriochloa villosa" spread dispersal model

"erschoviella musculana" OR "nycteola musculana" OR "sarrothripus musculana" spread dispersal model

"erwinia amylovora" OR "micrococcus amylovorus" OR "bacillus amylovorus" OR "bacterium amylovorum" OR "erwinia amylovora" OR "erwinia amylovora" spread dispersal model

"erwinia chrysanthemi" spread dispersal model

"erwinia rhapontici" spread dispersal model

"erwinia stewartii" spread dispersal model

"eucryptorrhychus chinensis" spread dispersal model

"euphorbia mosaic virus" spread dispersal model

"euphranta canadensis" OR "trypeta lunifera" OR "trypeta canadensis" OR "epochra canadensis" spread dispersal model

"euphranta japonica" OR "rhacochlaena japonica" spread dispersal model

"eutetranychus lewisi" spread dispersal model

"eutetranychus orientalis" spread dispersal model

"eutetranychus orientalis" OR "eutetranychus monodi" OR "eutetranychus anneckei" OR "anychus ricini" OR "anychus orientalis" OR "eutetranychus sudanicus" spread dispersal model

"exomala orientalis" spread dispersal model

"falciformispora lignatilis" spread dispersal model

"falcisormispora lignatilis" spread dispersal model

"fallopia baldschuanica" spread dispersal model

"fallopia japonica" spread dispersal model

"fallopia sachalinensis" spread dispersal model

"fallopia x bohemica" spread dispersal model

"florida tomato virus" spread dispersal model

"frankliniella insularis" spread dispersal model

"frankliniella occidentalis" OR "frankliniella trehernei" OR "frankliniella moultoni" OR "frankliniella californica" OR "frankliniella helianthi" spread dispersal model

"frankliniella tenuicornis" spread dispersal model

"fusarium foetens" spread dispersal model

"fusarium oxysporum" OR "fusarium albedinis" OR "cylindrophora albedinis" spread dispersal model

"gaillardia x grandiflora" spread dispersal model

"gaultheria shallon" spread dispersal model

"gibberella circinata" OR "fusarium circinatum" OR "fusarium lateritium" OR "fusarium subglutinans" spread dispersal model

"gilphinia hercyniae" spread dispersal model

"gilpinia hercyniae" spread dispersal model

"gilpinia polytoma" spread dispersal model

"globodera" spread dispersal model

"globodera achilleae" spread dispersal model

"globodera artemisiae" spread dispersal model

"globodera millefolii" spread dispersal model

"globodera pallida" OR "heterodera pallida" spread dispersal model

"globodera rostochiensis" OR "heterodera rostochiensis" OR "heterodera schachtii" spread dispersal model

"globodera tabacum" spread dispersal model

"glomerella cingulata" spread dispersal model

"glomerella gossypii" OR "gloeosporium rufomaculans" OR "glomerella rufomaculans" OR "colletotrichum gossypii" spread dispersal model

"gnathotrichus sulcatus" OR "cryphalus sulcatus" OR "gnathotrichus aciculatus" spread dispersal model

"godronia urceolus" spread dispersal model

"gonipterus gibberus" OR "dacnirotatus bruchi" spread dispersal model "gonipterus scutellatus" spread dispersal model

"grapevine flavescence" OR "phytoplasma vitis" spread dispersal model

"graphocephala atropunctata" spread dispersal model

"graphocephala fennahi" spread dispersal model

"grapholita funebrana" spread dispersal model

"grapholita inopinata" spread dispersal model

"grapholita janthinana" spread dispersal model

"grapholita molesta" spread dispersal model

"grapholita packardi" spread dispersal model

"grapholita prunivora" spread dispersal model

"gremmeniella abietina" spread dispersal model

"guignardia citricarpa" OR "phoma citricarpa" OR "phyllosticta citricarpa" OR "phyllostictina citricarpa" spread dispersal model

"guignardia laricina" spread dispersal model

"guignardia piricola" spread dispersal model

"gunnera tinctoria" spread dispersal model

"gymnosporangium" spread dispersal model

"gymnosporangium asiaticum" OR "roestelia koreaensis" OR "gymnosporangium japonicum" OR "gymnosporangium haraeanum" OR "gymnosporangium spiniferum" OR "gymnosporangium chinense" OR "gymnosporangium koreaense" spread dispersal model

"gymnosporangium clavipes" OR "caeoma germinale" OR "roestelia aurantiaca" OR "gymnosporangium germinale" OR "podisoma gymnosporangium-clavipes" spread dispersal model

"gymnosporangium globosum" OR "gymnosporangium fuscum" spread dispersal model

"gymnosporangium juniperi-virginianae" OR "gymnosporangium macropus" OR "aecidium pyrolatum" OR "gymnosporangium virginianum" OR "roestelia pyrata" spread dispersal model

"gymnosporangium yamadae" spread dispersal model

"hakea sericea" spread dispersal model

"halenchus fucicola" spread dispersal model

"halyomorpha halys" OR "brown marmorated stink bug" spread dispersal model

"haptocillium balanoides" spread dispersal model

"haptocillium campanulatum" spread dispersal model

"haptocillium glocklingiae" spread dispersal model

"haptocillium sinense" spread dispersal model

"haptocillium sphaerosporum" spread dispersal model

"haptocillium zeosporum" spread dispersal model

"helianthus californicus" spread dispersal model

"helianthus ciliaris" spread dispersal model

"helianthus tuberosus" spread dispersal model

"helianthus x laetiflorus" spread dispersal model

"helicotylenchus canadensis" spread dispersal model

"helicotylenchus crenacauda" spread dispersal model

"helicotylenchus digitiformis" spread dispersal model

"helicotylenchus digonicus" spread dispersal model

"helicotylenchus dihystera" spread dispersal model

"helicotylenchus egyptiensis" spread dispersal model

"helicotylenchus exallus" spread dispersal model

"helicotylenchus indicus" spread dispersal model

"helicotylenchus lobus" spread dispersal model

"helicotylenchus microcephalus" spread dispersal model

"helicotylenchus minzi" spread dispersal model

"helicotylenchus phalerus" spread dispersal model

"helicotylenchus pseudodigonicus" spread dispersal model "helicotylenchus pseudorobustus" spread dispersal model

"helicotylenchus vulgaris" spread dispersal model

"helicoverpa armigera" OR "heliothis obsoleta" OR "chloridea armigera" OR "chloridea obsoleta" OR "heliothis armigera" spread dispersal model

"helicoverpa zea" OR "heliothis umbrosa" OR "bombyx obsoleta" OR "heliothis zea" OR "phalaena zea" spread dispersal model

"heliothis armigera" spread dispersal model

"heliothis zea" spread dispersal model

"hemicriconemoides pseudobrachyurus" spread dispersal model

"hemicycliophora thienemanni" spread dispersal model

"heracleum mantegazzianum" spread dispersal model

"heracleum persicum" OR "heracleum laciniatum" spread dispersal model

"heracleum sosnowskyi" spread dispersal model

"herpotrichia juniperi" spread dispersal model

"hesperophanes campestris" OR "trichoferus campestris" OR "trichoferus turkestanicus" OR "trichoferus flavopubescens" OR "trichoferus rusticus" spread dispersal model

"heterodera arenaria" spread dispersal model

"heterodera avenae" spread dispersal model

"heterodera betae" spread dispersal model

"heterodera bifenestra" spread dispersal model

"heterodera carotae" spread dispersal model

"heterodera cruciferae" spread dispersal model

"heterodera daverti" spread dispersal model

"heterodera fici" spread dispersal model

"heterodera filipjevi" spread dispersal model

"heterodera galeopsidis" spread dispersal model

"heterodera glycines" spread dispersal model

"heterodera goettingiana" spread dispersal model

"heterodera hordecalis" spread dispersal model

"heterodera humuli" spread dispersal model

"heterodera mani" spread dispersal model

"heterodera riparia" spread dispersal model

"heterodera schachtii" spread dispersal model

"heterodera trifolii" spread dispersal model

"heterodera urticae" spread dispersal model

"heterodera ustinovi" spread dispersal model

"heterodera zeae" spread dispersal model

"heteronychus arator" OR "scarabaeus arator" OR "heteronychus sanctaehelenae" spread dispersal model

"heterospora chenopodii" spread dispersal model

"heterospora dimorphospora" spread dispersal model

"hirschmanniella" spread dispersal model

"hirschmanniella gracilis" spread dispersal model

"hirschmanniella loofi" spread dispersal model

"hirschmanniella oryzae" spread dispersal model

"hirschmanniella sp" spread dispersal model

"hishomonus phycitis" spread dispersal model

"homalodisca vitripennis" OR "homalodisca triquetra" OR "homalodisca coagulata" spread dispersal model

"homolodisca liturata" spread dispersal model

"hosta virus" spread dispersal model

"humulus japonicus" spread dispersal model

"hydrangea ringspot virus" spread dispersal model

"hydrilla verticillata" spread dispersal model

"hydrocotyle leucocephala" spread dispersal model

"hydrocotyle ranunculoides" OR "hydrocotyle natans" OR "hydrocotyle ranununculoides" spread dispersal model

"hydrocotyle sibthorpioides" spread dispersal model

"hydrocotyle verticillata" spread dispersal model

"hydrocotyle vulgaris" spread dispersal model

"hygroryza aristata" spread dispersal model

"hylesinus crenatus" spread dispersal model "hylobius abietis" spread dispersal model

"hylobius xiaoi" spread dispersal model

"hylurgops" spread dispersal model

"hymenoscyphus pseudoalbidus" OR "hymenoscyphus pseudoalbidus" OR "chalara fraxinea" spread dispersal model

"hypothenemus hampei" spread dispersal model

"hypothenemus obscurus" spread dispersal model

"hypoxylon mammatum" spread dispersal model

"impatiens balfourii" spread dispersal model

"impatiens capensis" spread dispersal model

"impatiens glandulifera" spread dispersal model

"impatiens necrotic spot virus" OR "insv" OR "impatiens necrotic spot tospovirus" spread dispersal model

"impatiens parviflora" spread dispersal model

"inonotus weirii" spread dispersal model

"ipomoea hederacea" spread dispersal model

"ipomoea lacunosa" spread dispersal model

"ips amitinus" spread dispersal model

"ips calligraphus" OR "ips exesus" OR "bostrichus calligraphus" OR "ips praemorsus" OR "ips ponderosae" OR "ips interstitialis" spread dispersal model

"ips cembrae" spread dispersal model

"ips confusus" OR "tomicus confusus" spread dispersal model

"ips duplicatus" spread dispersal model

"ips emarginatus" spread dispersal model

"ips grandicollis" OR "ips cacographus" OR "tomicus grandicollis" OR "ips cloudcrofti" OR "ips chagnoni" spread dispersal model

"ips hauseri" spread dispersal model

"ips integer" spread dispersal model

"ips latidens" spread dispersal model

"ips lecontei" spread dispersal model

"ips paraconfusus" spread dispersal model

"ips pini" OR "bostrichus pini" OR "ips rectus" OR "ips pallipes" OR "ips dentatus" OR "ips laticollis" OR "ips oregonis" OR "ips praefrictus" OR "ips oregoni" spread dispersal model

"ips plastographus" OR "tomicus plastographus" spread dispersal model

"ips sexdentatus" spread dispersal model

"ips spinifer" spread dispersal model

"ips subelongatus" OR "ips fallax" spread dispersal model

"ips typographus" spread dispersal model

"iresine viroid" spread dispersal model

"iris yellow spot virus" spread dispersal model

"iva axillaris" spread dispersal model

"keiferia lycopersicella" OR "gnorimoschema lycopersicella" OR "phthorimaea lycopersicella" spread dispersal model

"kuehneola uredinis" spread dispersal model

"kyllinga brevifolia" spread dispersal model

"lagarosiphon major" spread dispersal model

"laimaphelenchus penardi" spread dispersal model

"landoltia punctata" spread dispersal model

"lecanicillium acerosum" spread dispersal model

"lecanicillium aphanocladii" spread dispersal model

"lecanicillium aranearum" spread dispersal model

"lecanicillium attenuatum" spread dispersal model

"lecanicillium dimorphum" spread dispersal model

"lecanicillium flavidum" spread dispersal model

"lecanicillium fungicola" spread dispersal model

"lecanicillium fusisporum" spread dispersal model

"lecanicillium lecanii" spread dispersal model

"lecanicillium longisporum" spread dispersal model

"lecanicillium muscarium" spread dispersal model

"lecanicillium psalliotae" spread dispersal model "lecanicillium tenuipes" spread dispersal model

"lecanicillium wallacei" spread dispersal model

"leifsonia aquatica" spread dispersal model

"leifsonia kafniensis" spread dispersal model

"leifsonia pindariensis" spread dispersal model

"lemna gibba" spread dispersal model

"lemna minor" spread dispersal model

"lemna minuta" spread dispersal model

"lemna trisulca" spread dispersal model

"lemna turionifera" spread dispersal model

"lepidosaphes gloverii" spread dispersal model

"lepidosaphes ussuriensis" OR "paralepidosaphes ussuriensis" spread dispersal model

"leprosis" spread dispersal model

"leptinotarsa decemlineata" OR "chrysomela decemlineata" OR "doryphora decemlineata" OR "polygramma decemlineata" spread dispersal model

"leptocybe invasa" spread dispersal model

"leptoglossus corculus" spread dispersal model

"leptoglossus occidentalis" spread dispersal model

"leptosphaeria conoidea" spread dispersal model

"leptosphaeria derasa" spread dispersal model

"leptosphaeria doliolum" spread dispersal model

"leptosphaeria errabunda" spread dispersal model

"leptosphaeria etheridgei" spread dispersal model

"leptosphaeria macrocapsa" spread dispersal model

"leptosphaeria pedicularis" spread dispersal model

"leptosphaeria rubefaciens" spread dispersal model

"leptosphaeria sclerotioides" spread dispersal model

"leptosphaeria slovacica" spread dispersal model

"leptosphaeria sydowii" spread dispersal model

"leptosphaeria veronicae" spread dispersal model

"leptosphaerulina americana" spread dispersal model

"leptosphaerulina arachidicola" spread dispersal model

"leptosphaerulina argentinensis" spread dispersal model

"leptosphaerulina australis" spread dispersal model

"leptosphaerulina trifolii" spread dispersal model

"lettuce infectious yellows virus" OR "lettuce infectious yellows closterovirus" OR "liyv" OR "lettuce infectious yellows crinivirus" spread dispersal model

"leucaspis japonica" spread dispersal model

"leucinodes orbonalis" OR "pycnarmon discerptalis" spread dispersal model

"liberibacter africanus" OR "citrus greening bacterium" OR "liberibacter africanum" OR "liberobacter africanum" spread dispersal model

"liberibacter americanus" OR "liberobacter americanus" spread dispersal model

"liberibacter asiaticus" OR "citrus greening bacterium" OR "liberibacter asiaticum" OR "liberobacter asiaticum" spread dispersal model

"liberibacter solanacearum" OR "liberibacter solanum" OR "liberibacter psyllaurous" spread dispersal model

"limnobium laevigatum" spread dispersal model

"limnophila sessiliflora" OR "ambulia sessiliflora" spread dispersal model

"limonius californicus" spread dispersal model

"liriomyza avicenniae" spread dispersal model

"liriomyza bryoniae" spread dispersal model

"liriomyza huidobrensis" OR "liriomyza cucumifoliae" OR "agromyza huidobrensis" OR "liriomyza dianthi" OR "liriomyza langei" spread dispersal model "liriomyza sativae" OR "liriomyza guytona" OR "liriomyza minutiseta" OR "liriomyza canomarginis" OR "liriomyza munda" OR "liriomyza pullata" OR "liriomyza subpusilla" OR "liriomyza propepusilla" spread dispersal model

"liriomyza trifolii" OR "liriomyza alliovora" OR "liriomyza phaseolunata" spread dispersal model

"lissorhoptrus oryzophilus" spread dispersal model

"listronotus bonariensis" OR "hyperodes griseus" OR "neobagous setosus" OR "hyperodes bonariensis" spread dispersal model

"little cherry pathogen" spread dispersal model

"lobelia chinensis" spread dispersal model

"longidorus attenuatus" spread dispersal model

"longidorus diadecturus" spread dispersal model

"longidorus dunensis" spread dispersal model

"longidorus elongatus" spread dispersal model

"lopholeucaspis japonica" OR "leucaspis hydrangeae" OR "leucaspis japonica" OR "leucaspis japonica" spread dispersal model

"ludwigia grandiflora" OR "jussiaea michauxiana" OR "jussiaea uruguayensis" OR "jussiaea repens" OR "ludwigia clavellina" OR "ludwigia uruguayensis" OR "jussiaea grandiflora" spread dispersal model

"ludwigia peploides" OR "jussiaea californica" OR "jussiaea repens" spread dispersal model

"lupinus nootkatensis" spread dispersal model

"lupinus polyphyllus" spread dispersal model

"lygus lineolaris" spread dispersal model

"lymantria dispar" spread dispersal model

"lymantria mathura" OR "lymantria aurora" OR "porthetria mathura" OR "ocneria mathura" OR "" OR "lymantria fusca" OR "lymantria mathura" spread dispersal model

"lymantria monacha" spread dispersal model

"lysichiton americanus" spread dispersal model

"lysichiton camtschatcensis" spread dispersal model

"maconellicoccus hirsutus" OR "phenacoccus hirsutus" spread dispersal model

"macrophomina phaseolina" spread dispersal model

"macrotrophurus arbusticola" spread dispersal model

"macroventuria anomochaeta" spread dispersal model

"macroventuria wentii" spread dispersal model

"mahonia aquifolium" spread dispersal model

"malacosoma americanum" spread dispersal model

"malacosoma castrense" spread dispersal model

"malacosoma disstria" OR "malacosoma disstria" spread dispersal model

"malacosoma parallela" spread dispersal model

"marchalina hellenica" spread dispersal model

"margarodes" spread dispersal model

"margarodes prieskaensis" OR "sphaeraspis prieskaensis" spread dispersal model

"margarodes vitis" OR "sphaeraspis vitis" OR "coccionella vitis" OR "margarodes vitium" spread dispersal model

"margarodes vredendalensis" spread dispersal model

"massaria platani" spread dispersal model

"massarina eburnea" spread dispersal model

"matricaria discoidea" spread dispersal model

"matsucoccus feytaudi" spread dispersal model

"medicopsis romeroi" spread dispersal model

"megaplatypus mutatus" OR "platypus mutatus" OR "platypus plicatus" OR "platypus sulcatus" spread dispersal model

"melampsora abietis-canadensis" spread dispersal model

"melampsora aecidioides" spread dispersal model

"melampsora allii-populina" spread dispersal model

"melampsora amygdalinae" spread dispersal model

"melampsora capraearum" spread dispersal model "melampsora coleosporioides" spread dispersal model

"melampsora epiphylla" spread dispersal model

"melampsora farlowii" OR "necium farlowii" OR "chrysomyxa farlowii" spread dispersal model

"melampsora larici-epitea" spread dispersal model

"melampsora larici-populina" spread dispersal model

"melampsora laricis-pentandrae" spread dispersal model

"melampsora larici-tremulae" spread dispersal model

"melampsora magnusiana" spread dispersal model

"melampsora medusae" OR "melampsora albertensis" OR "caeoma faulliana" OR "uredo medusae" spread dispersal model

"melampsora pinitorqua" spread dispersal model

"melampsora ribesii-purpureae" spread dispersal model

"melampsora rostrupii" spread dispersal model

"melampsora salicis-albae" spread dispersal model

"melanomma pulvis-pyrius" spread dispersal model

"melanotus communis" OR "elater communis" spread dispersal model

"meloidogyne ardenensis" spread dispersal model

"meloidogyne arenaria" spread dispersal model

"meloidogyne artiellia" spread dispersal model

"meloidogyne chitwoodi" spread dispersal model

"meloidogyne duytsi" spread dispersal model

"meloidogyne enterolobii" OR "meloidogyne mayaguensis" spread dispersal model

"meloidogyne ethiopica" spread dispersal model

"meloidogyne exigua" spread dispersal model

"meloidogyne fallax" spread dispersal model

"meloidogyne graminicola" spread dispersal model

"meloidogyne hapla" spread dispersal model

"meloidogyne hispanica" spread dispersal model

"meloidogyne ichinohei" spread dispersal model

"meloidogyne incognita" spread dispersal model

"meloidogyne javanica" spread dispersal model

"meloidogyne kralli" spread dispersal model

"meloidogyne mali" spread dispersal model

"meloidogyne maritima" spread dispersal model

"meloidogyne microtyla" spread dispersal model

"meloidogyne minor" spread dispersal model

"meloidogyne naasi" spread dispersal model

"meloidogyne oryzae" spread dispersal model

"meloidogyne sasseri" spread dispersal model

"meloidogyne trifoliophila" spread dispersal model

"meloidogyne ulmi" spread dispersal model

"mesocriconema xenoplax" spread dispersal model

"metamasius hemipterus" OR "metamasius sericeus" spread dispersal model

"mexican papita viroid" spread dispersal model

"microbacterium foliorum" spread dispersal model

"microbacterium phyllosphaerae" spread dispersal model

"microsphaeropsis olivaceum" spread dispersal model

"microstegium vimineum" spread dispersal model

"mimulus guttatus" spread dispersal model

"miscanthus floridulus" spread dispersal model

"miscanthus sinensis" OR "eulalia japonica" spread dispersal model

"monarthrum fasciatum" spread dispersal model "monascostroma innumerosum" spread dispersal model

"monilinia baccarum" spread dispersal model

"monilinia demissa" spread dispersal model

"monilinia fructicola" OR "monilia fructicola" OR "sclerotinia fructicola" spread dispersal model

"monilinia fructigena" spread dispersal model

"monilinia johnsonii" spread dispersal model

"monilinia laxa" spread dispersal model

"monilinia linhartiana" spread dispersal model

"monochamus" spread dispersal model

"monochamus alternatus" OR "monochamus tesserula" spread dispersal model

"monochamus carolinensis" spread dispersal model

"monochamus clamator" spread dispersal model

"monochamus galloprovincialis" spread dispersal model

"monochamus marmorator" spread dispersal model

"monochamus mutator" OR "monochamus maculosus" spread dispersal model

"monochamus nitens" spread dispersal model

"monochamus notatus" spread dispersal model

"monochamus obtusus" spread dispersal model

"monochamus rosenmuelleri" spread dispersal model

"monochamus saltuarius" spread dispersal model

"monochamus sartor" spread dispersal model

"monochamus scutellatus" spread dispersal model

"monochamus sutor" spread dispersal model

"monochamus titillator" spread dispersal model

"mycosphaerella chrysanthemi" OR "ascochyta chrysanthemi" OR "mycosphaerella ligulicola" OR "phoma chrysanthemicola" OR "phoma ligulicola" OR "didymella ligulicola" spread dispersal model

"mycosphaerella dearnessii" OR "lecanosticta pini" OR "scirrhia acicola" OR "systremma acicola" OR "lecanosticta acicola" OR "septoria acicola" spread dispersal model

"mycosphaerella ellipsoidea" spread dispersal model

"mycosphaerella endophytica" spread dispersal model

"mycosphaerella gibsonii" OR "cercospora pini-densiflorae" OR "cercoseptoria pini-densiflorae" OR "pseudocercospora pini-densiflorae" spread dispersal model

"mycosphaerella gregaria" spread dispersal model

"mycosphaerella larici-leptolepis" spread dispersal model

"mycosphaerella laricis-leptolepidis" OR "phyllosticta laricis" OR "phoma yano-kubotae" spread dispersal model

"mycosphaerella latebrosa" spread dispersal model

"mycosphaerella pini" spread dispersal model

"mycosphaerella populicola" spread dispersal model

"mycosphaerella populorum" spread dispersal model

"mycosphaerella punctiformis" spread dispersal model

"mycosphaerella sumatrensis" spread dispersal model

"myndus crudus" spread dispersal model

"myopites stylatus" spread dispersal model

"myriophyllum alterniflorum" spread dispersal model

"myriophyllum aquaticum" spread dispersal model

"myriophyllum crispatum" spread dispersal model

"myriophyllum heterophyllum" spread dispersal model

"myriophyllum robustum" spread dispersal model

"myriophyllum spicatum" spread dispersal model

"myriophyllum tuberculatum" spread dispersal model "myriophyllum verticillatum" spread dispersal model

"nacobbus aberrans" OR "nacobbus serendipiticus bolivianus" OR "nacobbus serendipiticus" OR "anguillulina aberrans" OR "nacobbus batatiformis" spread dispersal model

"nagelus obscurus" spread dispersal model

"narcissus mosaic virus" spread dispersal model

"naturally spreading psorosis" spread dispersal model

"naupactus leucoloma" OR "graphognathus leucoloma" OR "pantomorus leucoloma" spread dispersal model

"nemapogon granella" spread dispersal model

"nematostoma parasiticum" spread dispersal model

"nemorimyza maculosa" OR "agromyza maculosa" OR "agromyza guaranitica" OR "amauromyza maculosa" OR "phytobia maculosa" spread dispersal model

"neoaliturus haematoceps" spread dispersal model

"neoaliturus tenellus" spread dispersal model

"neoceratitis cyanescens" spread dispersal model

"neodolichorhynchus lamelliferus" spread dispersal model

"neodolichorhynchus microphasmis" spread dispersal model

"neoleucinodes elegantalis" OR "leucinodes elegantalis" spread dispersal model

"neophaeosphaeria filamentosa" spread dispersal model

"neosetophoma samarorum" spread dispersal model

"neottiosporina paspali" spread dispersal model

"nigrograna mackinnonii" spread dispersal model

"nothotylenchus acris" spread dispersal model

"numonia pyrivorella" OR "acrobasis pyrivorella" OR "rhodophaea pyrivorella" OR "eurhodope pyrivorella" OR "nephopterix pyrivorella" OR "numonia pyrivora" spread dispersal model

"nysius huttoni" spread dispersal model

"odoiporus longicollis" spread dispersal model

"oemona hirta" spread dispersal model

"oerskovia turbata" spread dispersal model

"ogma menzeli" spread dispersal model

"oligonychus perditus" OR "oligonychus chamaecyparisae" spread dispersal model

"oligonychus perseae" spread dispersal model

"ophelimus maskelli" spread dispersal model

"ophiognomonia clavigignenti-juglandacearum" OR "sirococcus clavigignenti-juglandacearum" spread dispersal model

"ophiosphaerella herpotricha" spread dispersal model

"ophiostoma wageneri" OR "verticicladiella wageneri" OR "leptographium wageneri" OR "ceratocystis wageneri" spread dispersal model

"opogona sacchari" OR "opogona subcervinella" OR "tinea subcervinella" OR "alucita sacchari" spread dispersal model

"orellia falcata" spread dispersal model

"orgyia pseudotsugata" OR "hemerocampa pseudotsugata" spread dispersal model

"orthotomicus suturalis" spread dispersal model

"oxalis corniculata" spread dispersal model

"oxalis debilis" spread dispersal model

"oxalis latifolia" spread dispersal model

"oxalis pes-caprae" spread dispersal model

"palm lethal yellowing mycoplasm" spread dispersal model

"panicum capillare" spread dispersal model

"panicum dichotomiflorum" spread dispersal model

"panicum maximum" spread dispersal model

"panicum miliaceum" spread dispersal model

"panicum repens" spread dispersal model

"panicum schinzii" spread dispersal model

"pantoea stewartii" OR "pseudomonas stewartii" OR "xanthomonas stewartii" OR "pantoea stewartii" OR "aplanobacter stewartii" OR "bacterium stewartii" OR "erwinia stewartii" spread dispersal model

"papaver atlanticum" spread dispersal model

"paraconiothyrium flavescens" spread dispersal model

"paraconiothyrium fuckelii" spread dispersal model

"paraconiothyrium fuscomaculans" spread dispersal model

"paraconiothyrium lini" spread dispersal model

"paraconiothyrium maculicutis" spread dispersal model

"paraconiothyrium minitans" spread dispersal model

"paraconiothyrium tiliae" spread dispersal model

"paraleptosphaeria dryadis" spread dispersal model

"paraleptosphaeria macrospora" spread dispersal model

"paraleptosphaeria nitschkei" spread dispersal model

"paraleptosphaeria orobanches" spread dispersal model

"paraleptosphaeria praetermissa" spread dispersal model

"paraphaeosphaeria michoti" spread dispersal model

"paraphoma chrysanthemicola" spread dispersal model

"paraphoma fimeti" spread dispersal model

"paraphoma radicina" spread dispersal model

"parasaissetia nigra" spread dispersal model

"paratrichodorus anemones" spread dispersal model

"paratrichodorus nanus" spread dispersal model

"paratrichodorus pachydermus" spread dispersal model

"paratrichodorus renifer" spread dispersal model

"paratrichodorus teres" spread dispersal model

"paratylenchus bukowinensis" spread dispersal model

"paratylenchus nanus" spread dispersal model

"paratylenchus projectus" spread dispersal model

"pardalaspis cyanescens" spread dispersal model

"pardalaspis quinaria" spread dispersal model

"parthenium hysterophorus" spread dispersal model

"paspalum dilatatum" spread dispersal model

"paspalum distichum" spread dispersal model

"passalora vaginae" spread dispersal model

"paysandisia archon" OR "castnia archon" spread dispersal model

"peach mosaic virus" OR "pcmv" OR "peach mosaic closterovirus" OR "peach virus" OR "prunus virus" OR "peach american mosaic virus" OR "peach mosaic virus" OR "peach mosaic trichovirus" spread dispersal model

"peach phony rickettsia" spread dispersal model

"peach rosette mosaic virus" OR "prmv" OR "peach rosette mosaic nepovirus" spread dispersal model

"peach rosette mycoplasm" spread dispersal model

"peach rosette phytoplasma" spread dispersal model

"peach x-disease mycoplasm" spread dispersal model

"peach yellows mycoplasm" spread dispersal model

"peach yellows phytoplasma" OR "peach red suture phytoplasma" OR "peach little peach phytoplasma" spread dispersal model

"pear decline mycoplasm" spread dispersal model

"pennisetum advena" spread dispersal model

"pennisetum alopecuroides" spread dispersal model

"pennisetum setaceum" spread dispersal model

"pepino mosaic virus" OR "pepmv" OR "pepino mosaic potexvirus" spread dispersal model

"pepper chat fruit viroid" spread dispersal model "pepper mild tigre virus" spread dispersal model

"persicaria wallichii" spread dispersal model

"peyronellaea alectorolophi" spread dispersal model

"peyronellaea americana" spread dispersal model

"peyronellaea anserina" spread dispersal model

"peyronellaea arachidicola" spread dispersal model

"peyronellaea aurea" spread dispersal model

"peyronellaea australis" spread dispersal model

"peyronellaea calorpreferens" spread dispersal model

"peyronellaea coffeae-arabicae" spread dispersal model

"peyronellaea curtisii" spread dispersal model

"peyronellaea eucalyptica" spread dispersal model

"peyronellaea gardeniae" spread dispersal model

"peyronellaea glomerata" spread dispersal model

"peyronellaea lethalis" spread dispersal model

"peyronellaea musae" spread dispersal model

"peyronellaea obtusa" spread dispersal model

"peyronellaea pinodella" spread dispersal model

"peyronellaea pinodes" spread dispersal model

"peyronellaea pomorum" spread dispersal model

"peyronellaea protuberans" spread dispersal model

"peyronellaea sancta" spread dispersal model

"peyronellaea subglomerata" spread dispersal model

"peyronellaea zeae-maydis" spread dispersal model

"phaedon brassicae" spread dispersal model

"phaeocytostroma ambiguum" spread dispersal model

"phaeocytostroma megalosporum" spread dispersal model

"phaeocytostroma plurivorum" spread dispersal model

"phaeocytostroma sacchari" spread dispersal model

"phaeophleospora eugeniae" spread dispersal model

"phaeoramularia angolensis" OR "cercospora angolensis" OR "pseudocercospora angolensis" spread dispersal model

"phaeosphaeria ammophilae" spread dispersal model

"phaeosphaeria avenaria" spread dispersal model

"phaeosphaeria caricicola" spread dispersal model

"phaeosphaeria caricis" spread dispersal model

"phaeosphaeria elongata" spread dispersal model

"phaeosphaeria eustoma" spread dispersal model

"phaeosphaeria juncicola" spread dispersal model

"phaeosphaeria juncophila" spread dispersal model

"phaeosphaeria luctuosa" spread dispersal model

"phaeosphaeria nigrans" spread dispersal model

"phaeosphaeria nodorum" spread dispersal model

"phaeosphaeria oryzae" spread dispersal model

"phaeosphaeria spartinae" spread dispersal model

"phaeosphaeria spartinicola" spread dispersal model

"phaeosphaeria typharum" spread dispersal model

"phaeosphaeriopsis glauco-punctata" spread dispersal model

"pheletes californicus" OR "limonius californicus" OR "cardiophorus californicus" spread dispersal model

"phellinus weirii" OR "fomitiporia weirii" OR "inonotus weirii" OR "poria weirii" OR "phellinus sulphurascens" spread dispersal model

"phialophora cinerescens" OR "verticillium cinerescens" spread dispersal model

"phoma" spread dispersal model

"phoma acetosellae" spread dispersal model

"phoma aliena" spread dispersal model

"phoma andigena" OR "phoma andina" spread dispersal model

"phoma andina" spread dispersal model

"phoma andropogonivora" spread dispersal model

"phoma anigozanthi" spread dispersal model

"phoma aquilegiicola" spread dispersal model

"phoma arachidis-hypogaea" spread dispersal model

"phoma astragalina" spread dispersal model

"phoma aubrietiae" spread dispersal model

"phoma bellidis" spread dispersal model

"phoma bismarckii" spread dispersal model

"phoma boeremae" spread dispersal model

"phoma boerhaviae" spread dispersal model

"phoma brasiliensis" spread dispersal model

"phoma bulgarica" spread dispersal model

"phoma cajanicola" spread dispersal model

"phoma calidophila" spread dispersal model

"phoma chenopodii" spread dispersal model

"phoma chenopodiicola" spread dispersal model

"phoma clematidina" spread dispersal model

"phoma clematidis-rectae" spread dispersal model

"phoma commelinicola" spread dispersal model

"phoma complanata" spread dispersal model

"phoma costarricensis" spread dispersal model

"phoma crystallifera" spread dispersal model

"phoma dactylidis" spread dispersal model

"phoma delphinii" spread dispersal model

"phoma destructiva" spread dispersal model

"phoma dictamnicola" spread dispersal model

"phoma digitalis" spread dispersal model

"phoma dimorpha" spread dispersal model

"phoma draconis" spread dispersal model

"phoma eupatorii" spread dispersal model

"phoma eupyrena" spread dispersal model

"phoma fungicola" spread dispersal model

"phoma gentianae-sino-ornatae" spread dispersal model

"phoma glaucii" spread dispersal model

"phoma gossypiicola" spread dispersal model

"phoma haematocycla" spread dispersal model

"phoma henningsii" spread dispersal model

"phoma herbarum" spread dispersal model

"phoma herbicola" spread dispersal model

"phoma huancayensis" spread dispersal model

"phoma humicola" spread dispersal model

"phoma infossa" spread dispersal model

"phoma insulana" spread dispersal model

"phoma labilis" spread dispersal model

"phoma laundoniae" spread dispersal model

"phoma longicolla" spread dispersal model

"phoma longirostrata" spread dispersal model

"phoma macrostoma" spread dispersal model

"phoma matteuccicola" spread dispersal model

"phoma medicaginis" spread dispersal model

"phoma microchlamydospora" spread dispersal model

"phoma minor" spread dispersal model

"phoma multirostrata" spread dispersal model

"phoma nebulosa" spread dispersal model

"phoma necator" spread dispersal model

"phoma negriana" spread dispersal model

"phoma nemophilae" spread dispersal model

"phoma nigripycnidia" spread dispersal model

"phoma novae-verbascicola" spread dispersal model

"phoma omnivirens" spread dispersal model

"phoma opuntiae" spread dispersal model

"phoma paspali" spread dispersal model

"phoma pedeiae" spread dispersal model

"phoma pereupyrena" spread dispersal model

"phoma petrakii" spread dispersal model

"phoma pezizoides" spread dispersal model
"phoma piperis" spread dispersal model
"phoma piskorzii" spread dispersal model
"phoma plurivora" spread dispersal model
"phoma polemonii" spread dispersal model
"phoma poolensis" spread dispersal model
"phoma putaminum" spread dispersal model
"phoma rhei" spread dispersal model
"phoma rumicicola" spread dispersal model
"phoma ruttneri" spread dispersal model
"phoma saxea" spread dispersal model
"phoma schachtii" spread dispersal model
"phoma selaginellicola" spread dispersal model
"phoma senecionis" spread dispersal model
"phoma subherbarum" spread dispersal model
"phoma sublingam" spread dispersal model
"phoma sylvatica" spread dispersal model
"phoma syriaca" spread dispersal model
"phoma tracheiphila" OR "bakerophoma tracheiphila" OR "deuterophoma tracheiphila" spread dispersal model
"phoma tropica" spread dispersal model
"phoma versabilis" spread dispersal model
"phoma viburnicola" spread dispersal model
"phoma xanthina" spread dispersal model
"phoma zantedeschiae" spread dispersal model
"phthorimaea operculella" spread dispersal model
"phyllanthus fluitans" spread dispersal model
"phyllonorycter issikii" spread dispersal model
"phyllonorycter platani" spread dispersal model
"phyllosticta abietis" spread dispersal model
"phyllosticta minima" spread dispersal model
"phyllosticta solitaria" spread dispersal model
"phyloosticta solitaria" spread dispersal model
"phymatotrichopsis omnivora" OR "ozonium auricomum" OR "ozonium omnivorum" OR "phymatotrichum omnivorum" spread dispersal model
"phytolacca acinosa" spread dispersal model
"phytolacca americana" spread dispersal model
"phytophthora alni" spread dispersal model
"phytophthora austrocedrae" spread dispersal model
"phytophthora bisheria" spread dispersal model
"phytophthora boehmeriae" spread dispersal model
"phytophthora brassicae" spread dispersal model
"phytophthora cactorum" spread dispersal model
"phytophthora cambivora" spread dispersal model
"phytophthora capsici" spread dispersal model
"phytophthora captiosa" spread dispersal model
"phytophthora cinnamomi" spread dispersal model
"phytophthora citricola" spread dispersal model
"phytophthora citrophthora" spread dispersal model
"phytophthora colocasiae" spread dispersal model
"phytophthora cryptogea" spread dispersal model
"phytophthora drechsleri" spread dispersal model
"phytophthora erythroseptica" spread dispersal model
"phytophthora europaea" spread dispersal model
"phytophthora fallax" spread dispersal model
"phytophthora foliorum" spread dispersal model
"phytophthora fragariae" spread dispersal model
"phytophthora frigida" spread dispersal model
"phytophthora gallica" spread dispersal model
"phytophthora gonapodyides" spread dispersal model
"phytophthora hedraiandra" spread dispersal model

"phytophthora heveae" spread dispersal model

"phytophthora hibernalis" spread dispersal model

"phytophthora humicola" spread dispersal model

"phytophthora idaei" spread dispersal model

"phytophthora ilicis" spread dispersal model

"phytophthora infestans" spread dispersal model

"phytophthora insolita" spread dispersal model

"phytophthora inundata" spread dispersal model

"phytophthora ipomoeae" spread dispersal model

"phytophthora iranica" spread dispersal model

"phytophthora katsurae" spread dispersal model

"phytophthora kernoviae" spread dispersal model

"phytophthora lateralis" spread dispersal model

"phytophthora litchii" spread dispersal model

"phytophthora medicaginis" spread dispersal model

"phytophthora megakarya" spread dispersal model

"phytophthora megasperma" spread dispersal model

"phytophthora mirabilis" spread dispersal model

"phytophthora morindae" spread dispersal model

"phytophthora multivesiculata" spread dispersal model

"phytophthora multivora" spread dispersal model

"phytophthora nemorosa" spread dispersal model

"phytophthora nicotianae" spread dispersal model

"phytophthora palmivora" spread dispersal model

"phytophthora parsiana" spread dispersal model

"phytophthora phaseoli" spread dispersal model

"phytophthora pinifolia" spread dispersal model

"phytophthora pistaciae" spread dispersal model

"phytophthora plurivora" spread dispersal model

"phytophthora polonica" spread dispersal model

"phytophthora porri" spread dispersal model

"phytophthora primulae" spread dispersal model

"phytophthora pseudosyringae" spread dispersal model

"phytophthora pseudotsugae" spread dispersal model

"phytophthora psychrophila" spread dispersal model

"phytophthora quercetorum" spread dispersal model

"phytophthora quercina" spread dispersal model

"phytophthora quininea" spread dispersal model

"phytophthora ramorum" spread dispersal model

"phytophthora rosacearum" spread dispersal model

"phytophthora rubi" OR "phytophthora fragariae" spread dispersal model

"phytophthora sansomeana" spread dispersal model

"phytophthora siskiyouensis" spread dispersal model

"phytophthora sojae" spread dispersal model

"phytophthora syringae" spread dispersal model

"phytophthora tentaculata" spread dispersal model

"phytophthora trifolii" spread dispersal model

"phytophthora tropicalis" spread dispersal model

"phytophthora uliginosa" spread dispersal model "phytoplasma asteris" spread dispersal model

"phytoplasma aurantifolia" spread dispersal model

"phytoplasma australiense" spread dispersal model

"phytoplasma brasiliense" spread dispersal model

"phytoplasma fraxini" spread dispersal model

"phytoplasma mali" OR "apple witches broom phytoplasma" OR "apple proliferation phytoplasma" spread dispersal model

"phytoplasma oryzae" spread dispersal model

"phytoplasma phoenicium" spread dispersal model

"phytoplasma pini" spread dispersal model

"phytoplasma prunorum" spread dispersal model

"phytoplasma pyri" OR "pear decline phytoplasma" spread dispersal model

"phytoplasma rhamni" spread dispersal model

"phytoplasma rubi" spread dispersal model

"phytoplasma trifolii" spread dispersal model

"phytoplasma ulmi" OR "elm yellows phytoplasma" OR "elm phloem necrosis phytoplasma" spread dispersal model

"phytoplasma ziziphi" spread dispersal model

"pileolaria terebinthi" spread dispersal model

"pissodes" spread dispersal model

"pissodes castaneus" spread dispersal model

"pissodes nemorensis" OR "pissodes deodarae" OR "pissodes approximatus" OR "pissodes canadensis" spread dispersal model

"pissodes piceae" spread dispersal model

"pissodes strobi" OR "pissodes engelmanni" OR "pissodes sitchensis" spread dispersal model

"pissodes terminalis" spread dispersal model

"pistia stratiotes" spread dispersal model

"pityogenes hopkinsi" spread dispersal model

"pityophthorus juglandis" spread dispersal model

"pityophthorus setosus" spread dispersal model

"plagiostoma salicellum" spread dispersal model

"plasmopara halstedii" spread dispersal model

"platychora ulmi" spread dispersal model

"plenodomus agnitus" spread dispersal model

"plenodomus biglobosus" spread dispersal model

"plenodomus chrysanthemi" spread dispersal model

"plenodomus collinsoniae" spread dispersal model

"plenodomus confertus" spread dispersal model

"plenodomus congestus" spread dispersal model

"plenodomus enteroleucus" spread dispersal model

"plenodomus fallaciosus" spread dispersal model

"plenodomus hendersoniae" spread dispersal model

"plenodomus influorescens" spread dispersal model

"plenodomus libanotidis" spread dispersal model

"plenodomus lindquistii" spread dispersal model

"plenodomus lingam" spread dispersal model

"plenodomus lupini" spread dispersal model

"plenodomus pimpinellae" spread dispersal model

"plenodomus tracheiphilus" spread dispersal model

"plenodomus visci" spread dispersal model

"plenodomus wasabiae" spread dispersal model

"pleomassaria siparia" spread dispersal model

"pleospora betae" spread dispersal model

"pleospora calvescens" spread dispersal model

"pleospora chenopodii" spread dispersal model

"pleospora fallens" spread dispersal model

"pleospora flavigena" spread dispersal model

"pleospora halimiones" spread dispersal model

"pleospora herbarum" spread dispersal model

"pleospora incompta" spread dispersal model "pleospora typhicola" spread dispersal model

"pleurophoma pleurospora" spread dispersal model

"plum line pattern virus" spread dispersal model

"plum pox virus" OR "ppv" OR "prunus virus" OR "plum pox potyvirus" spread dispersal model

"pochonia bulbillosa" spread dispersal model

"pochonia chlamydosporia" spread dispersal model

"pochonia globispora" spread dispersal model

"pochonia goniodes" spread dispersal model

"pochonia microbactrospora" spread dispersal model

"pochonia rubescens" spread dispersal model

"pochonia suchlasporia" spread dispersal model

"polygonum perfoliatum" spread dispersal model

"polygraphus proximus" spread dispersal model

"pomacea" spread dispersal model

"pontederia cordata" spread dispersal model

"popilia japonica" spread dispersal model

"popillia japonica" spread dispersal model

"potato aucuba mosaic virus" spread dispersal model

"potato black ringspot virus" OR "tobacco ringspot virus" OR "potato andean calico virus" OR "tobacco ringspot nepovirus" OR "pbrsv" OR "potato black ringspot nepovirus" spread dispersal model

"potato deforming mosaic virus argentina" OR "pdmv" OR "potato deforming mosaic begomovirus" OR "potato deforming mosaic virus" spread dispersal model

"potato leafroll virus" spread dispersal model

"potato purple-top wilt agent" spread dispersal model

"potato spindle tuber viroid" OR "potato gothic virus" OR "tomato bunchy top viroid" OR "pstvd" OR "potato spindle tuber virus" OR "potato spindle tuber pospiviroid" spread dispersal model

"potato stolbur mycoplasm" spread dispersal model

"potato virus" OR "potato t capillovirus" OR "pvt" OR "potato t trichovirus" spread dispersal model

"potato yellow dwarf virus" OR "potato yellow dwarf rhabdovirus" OR "pydv" OR "potato yellow dwarf nucleorhabdovirus" spread dispersal model

"potato yellow vein virus" OR "pyvv" OR "potato yellow vein crinivirus" spread dispersal model

"potato yellowing virus" OR "pyv" OR "potato yellowing alfamovirus" spread dispersal model

"pratylenchoides laticauda" spread dispersal model

"pratylenchus brachyurus" spread dispersal model

"pratylenchus brzeskii" spread dispersal model

"pratylenchus coffeae" spread dispersal model

"pratylenchus convallariae" spread dispersal model

"pratylenchus crenatus" spread dispersal model

"pratylenchus fallax" spread dispersal model

"pratylenchus neglectus" spread dispersal model

"pratylenchus penetrans" spread dispersal model

"pratylenchus pratensis" spread dispersal model

"pratylenchus scribneri" spread dispersal model

"pratylenchus thornei" spread dispersal model

"pratylenchus vulnus" spread dispersal model

"premnotrypes" spread dispersal model

"premnotrypes latithorax" spread dispersal model

"premnotrypes suturicallus" spread dispersal model

"premnotrypes vorax" spread dispersal model

"preussia funiculata" spread dispersal model

"procecidochares utilis" spread dispersal model

"prunus laurocerasus" spread dispersal model "prunus necrotic ringspot virus" spread dispersal model

"prunus serotina" spread dispersal model

"pseudhalenchus minutus" spread dispersal model

"pseudocercospora" spread dispersal model

"pseudocercospora angolensis" spread dispersal model

"pseudocercospora assamensis" spread dispersal model

"pseudocercospora atromarginalis" spread dispersal model

"pseudocercospora cercidis-chinensis" spread dispersal model

"pseudocercospora chiangmaiensis" spread dispersal model

"pseudocercospora clematidis" spread dispersal model

"pseudocercospora eucalyptorum" spread dispersal model

"pseudocercospora flavomarginata" spread dispersal model

"pseudocercospora gracilis" spread dispersal model

"pseudocercospora madagascariensis" spread dispersal model

"pseudocercospora norchiensis" spread dispersal model

"pseudocercospora paraguayensis" spread dispersal model

"pseudocercospora pini-densiflorae" spread dispersal model

"pseudocercospora rhoina" spread dispersal model

"pseudocercospora robusta" spread dispersal model

"pseudocercospora sphaerulinae" spread dispersal model

"pseudocercospora subulata" spread dispersal model

"pseudocercospora tereticornis" spread dispersal model

"pseudocercospora vitis" spread dispersal model

"pseudodiplodia" spread dispersal model

"pseudomonas caryophylli" spread dispersal model

"pseudomonas cissicola" spread dispersal model

"pseudomonas solanacearum" spread dispersal model

"pseudomonas syringae" OR "pseudomonas mors-prunorum" OR "pseudomonas mors-prunorum" spread dispersal model

"pseudopityophthorus minutissimus" OR "crypturgus minutissimus" spread dispersal model

"pseudopityophthorus pruinosus" OR "pityophthorus pruinosus" OR "pityophthorus tomentosus" OR "pseudopityophthorus pulvereus" OR "pityophthorus querciperda" OR "pseudopityophthorus tropicalis" OR "pseudopityophthorus convexus" spread dispersal model

"pseudorobillarda phragmitis" spread dispersal model

"pterandrus rosa" spread dispersal model

"puccinia allii" spread dispersal model

"puccinia chrysanthemi" spread dispersal model

"puccinia cirsii" spread dispersal model

"puccinia coronata" spread dispersal model

"puccinia drabae" spread dispersal model

"puccinia graminis" spread dispersal model

"puccinia helianthi" spread dispersal model

"puccinia hemerocallidis" OR "puccinia funkiae" spread dispersal model

"puccinia horiana" spread dispersal model

"puccinia pittieriana" spread dispersal model

"puccinia recondita" spread dispersal model

"puccinia striiformis" spread dispersal model

"puccinia tanaceti" spread dispersal model

"puccinia thlaspeos" spread dispersal model

"puccinia trebouxi" spread dispersal model

"puccinia triticina" spread dispersal model

"pueraria lobata" OR "pueraria harmsii" OR "pueraria thunbergiana" OR "pueraria montana" OR "pueraria hirsuta" OR "dolichos lobatus" OR "dolichos hirsutus" OR "pachyrrhizus thunbergianus" spread dispersal model

"pueraria montana" spread dispersal model

"punctodera chalcoensis" spread dispersal model

"punctodera punctata" spread dispersal model

"punctodera stonei" spread dispersal model

"pyrenochaeta acicola" spread dispersal model

"pyrenochaeta cava" spread dispersal model

"pyrenochaeta corni" spread dispersal model

"pyrenochaeta lycopersici" spread dispersal model

"pyrenochaeta nobilis" spread dispersal model

"pyrenochaeta quercina" spread dispersal model

"pyrenochaeta unguis-hominis" spread dispersal model

"pyrenochaetopsis decipiens" spread dispersal model

"pyrenochaetopsis indica" spread dispersal model

"pyrenochaetopsis leptospora" spread dispersal model

"pyrenochaetopsis microspora" spread dispersal model

"pyrenochaetopsis pratorum" spread dispersal model

"pyrenophora phaeocomes" spread dispersal model

"pyrenophora tritici-repentis" spread dispersal model

"quadraspidiotus perniciosus" OR "aspidiotus perniciosus" OR "comstockaspis perniciosa" OR "diaspidiotus perniciosus" OR "aonidiella perniciosa" spread dispersal model

"radopholus citrophilus" spread dispersal model

"radopholus similis" OR "tylenchus granulosus" OR "tylenchus similis" OR "anguillulina similis" OR "rotylenchus similis" spread dispersal model

"ralstonia mannitolilytica" spread dispersal model

"ralstonia pickettii" spread dispersal model

"ralstonia solanacearum" OR "pseudomonas solanacearum" OR "bacterium solanacearum" OR "xanthomonas solanacearum" OR "burkholderia solanacearum" spread dispersal model

"ralstonia syzygii" spread dispersal model

"ranunculus circinatus" spread dispersal model

"raoiella indica" spread dispersal model

"raspberry leaf curl virus" OR "rlcv" OR "raspberry leaf curl nepovirus" OR "raspberry leaf curl luteovirus" spread dispersal model

"raspberry ringspot virus" OR "rprsv" OR "raspberry ringspot nepovirus" spread dispersal model

"rathayibacter iranicus" spread dispersal model

"rathayibacter rathayi" spread dispersal model

"rathayibacter tritici" spread dispersal model

"readeriella mirabilis" spread dispersal model

"reticulitermes" spread dispersal model

"rhacochlaena japonica" spread dispersal model

"rhagoletis cerasi" spread dispersal model

"rhagoletis cingulata" OR "trypeta cingulata" OR "zonosema cingulata" spread dispersal model

"rhagoletis completa" spread dispersal model

"rhagoletis fausta" OR "rhagoletis intrudens" OR "trypeta fausta" OR "spilographa fausta" OR "zonosema fausta" spread dispersal model

"rhagoletis indifferens" OR "rhagoletis cingulata" OR "rhagoletis cingulata" spread dispersal model

"rhagoletis mendax" OR "spilographa mendax" OR "zonosema mendax" spread dispersal model

"rhagoletis pomonella" OR "trypeta pomonella" OR "spilographa pomonella" OR "zonosema pomonella" spread dispersal model

"rhagoletis ramosae" spread dispersal model

"rhagoletis ribicola" spread dispersal model

"rhagoletis solanophaga" spread dispersal model

"rhagoletis suavis" spread dispersal model

"rhagoletis turpiniae" spread dispersal model

"rhagoletis zoqui" spread dispersal model "rhizoecus hibisci" OR "ripersiella hibisci" spread dispersal model

"rhizosphaera pini" spread dispersal model

"rhododendron ponticum" spread dispersal model

"rhus typhina" spread dispersal model

"rhynchophorus ferrugineus" OR "rhynchophorus signaticollis" OR "calandra ferruginea" OR "curculio ferrugineus" spread dispersal model

"rhynchophorus palmarum" OR "rhynchophorus barbirostris" OR "calandra palmarum" OR "curculio palmarum" OR "rhynchophorus cycadis" OR "rhynchophorus depressus" OR "rhynchophorus languinosus" OR "cordyle barbirostris" spread dispersal model

"ripersiella hibisci" spread dispersal model

"robinia pseudoacacia" spread dispersal model

"rosa rugosa" spread dispersal model

"rotylenchulus borealis" spread dispersal model

"rotylenchulus reniformis" spread dispersal model

"rotylenchus fallorobustus" spread dispersal model

"rotylenchus goodeyi" spread dispersal model

"rotylenchus robustus" spread dispersal model

"rotylenchus uniformis" spread dispersal model

"roussoella hysterioides" spread dispersal model

"rudbeckia laciniata" spread dispersal model

"rusticoclytus rusticus" spread dispersal model

"sagittaria latifolia" spread dispersal model

"saissetia coffeae" spread dispersal model

"saissetia nigra" spread dispersal model

"salvinia auriculata" spread dispersal model

"salvinia minima" spread dispersal model

"salvinia molesta" spread dispersal model

"salvinia natans" spread dispersal model

"salvinia oblongifolia" spread dispersal model

"saperda candida" spread dispersal model

"satsuma dwarf virus" OR "sdv" OR "citrus mosaic virus" OR "satsuma dwarf nepovirus" OR "satsuma dwarf nepovirus" OR "satsuma dwarf sadwavirus" spread dispersal model

"sauertylenchus maximus" spread dispersal model

"scaphoideus luteolus" spread dispersal model

"scirrhia acicola" spread dispersal model

"scirrhia pini" spread dispersal model

"scirtothrips aurantii" OR "scirtothrips acaciae" spread dispersal model

"scirtothrips citri" OR "euthrips citri" spread dispersal model

"scirtothrips dorsalis" OR "anaphothrips andreae" OR "heliothrips minutissimus" OR "neophysopus fragariae" OR "anaphothrips dorsalis" OR "scirtothrips dorsalis" OR "scirtothrips dorsalis" spread dispersal model

"scirtothrips perseae" spread dispersal model

"scolecobasidium arenarium" spread dispersal model

"scolytus amygdali" spread dispersal model

"scolytus morawitzi" OR "eccoptogaster morawitzi" spread dispersal model

"scolytus multistriatus" spread dispersal model

"scolytus schevyrewi" spread dispersal model

"scolytus ventralis" spread dispersal model

"scuttelonema brachyurus" spread dispersal model

"scyphophorus acupunctatus" spread dispersal model

"selenophoma linicola" spread dispersal model

"selenophoma mahoniae" spread dispersal model

"senecio inaequidens" spread dispersal model

"septoria abeliceae" spread dispersal model

"septoria chrysanthemella" spread dispersal model

"septoria citri" spread dispersal model

"septoria cucurbitacearum" spread dispersal model

"septoria lycopersici" spread dispersal model

"septoria malagutii" spread dispersal model

"septoria matricariae" spread dispersal model "septoria obesa" spread dispersal model

"septoria populi" spread dispersal model

"sesbania punicea" spread dispersal model

"setomelanomma holmii" spread dispersal model

"setophoma sacchari" spread dispersal model

"setophoma terrestris" spread dispersal model

"setosphaeria monoceras" spread dispersal model

"sicyos angulatus" spread dispersal model

"simplicillium lamellicola" spread dispersal model

"simplicillium lanosoniveum" spread dispersal model

"simplicillium obclavatum" spread dispersal model

"sirex ermak" OR "paururus ermak" spread dispersal model

"sirococcus conigenus" spread dispersal model

"solanum carolinense" spread dispersal model

"solanum elaeagnifolium" spread dispersal model

"solanum rostratum" spread dispersal model

"solanum triflorum" spread dispersal model

"solidago canadensis" spread dispersal model

"solidago gigantea" spread dispersal model

"solidago nemoralis" spread dispersal model

"sorghum halepense" spread dispersal model

"spartina anglica" spread dispersal model

"sphaeropsis visci" spread dispersal model

"spiroplasma citri" spread dispersal model

"spodoptera eridania" OR "xylomyges eridania" OR "prodenia eridania" OR "laphygma eridania" spread dispersal model

"spodoptera exigua" spread dispersal model

"spodoptera frugiperda" OR "laphygma frugiperda" OR "caradrina frugiperda" spread dispersal model

"spodoptera littoralis" OR "prodenia littoralis" OR "hadena littoralis" spread dispersal model

"spodoptera litura" OR "prodenia litura" spread dispersal model

"sporormiella minima" spread dispersal model

"squash leaf curl virus" OR "squash leaf curl geminivirus" OR "slcv" OR "squash leaf curl bigeminivirus" OR "squash leaf curl begomovirus" spread dispersal model

"stagonospora foliicola" spread dispersal model

"stagonospora neglecta" spread dispersal model

"stagonosporopsis actaeae" spread dispersal model

"stagonosporopsis ajacis" spread dispersal model

"stagonosporopsis andigena" spread dispersal model

"stagonosporopsis artemisiicola" spread dispersal model

"stagonosporopsis astragali" spread dispersal model

"stagonosporopsis caricae" spread dispersal model

"stagonosporopsis crystalliniformis" spread dispersal model

"stagonosporopsis cucurbitacearum" spread dispersal model

"stagonosporopsis dennisii" spread dispersal model

"stagonosporopsis dorenboschii" spread dispersal model

"stagonosporopsis heliopsidis" spread dispersal model

"stagonosporopsis hortensis" spread dispersal model

"stagonosporopsis ligulicola" spread dispersal model

"stagonosporopsis loticola" spread dispersal model

"stagonosporopsis lupini" spread dispersal model

"stagonosporopsis oculo-hominis" spread dispersal model

"stagonosporopsis rudbeckiae" spread dispersal model

"stagonosporopsis trachelii" spread dispersal model "stagonosporopsis valerianellae" spread dispersal model

"stegophora ulmea" OR "gnomonia ulmea" OR "cylindrosporella ulmea" OR "gloeosporium ulmeum" OR "asteromella ulmea" OR "sphaeria ulmea" OR "dothidella ulmea" OR "lambro ulmea" OR "gloeosporium ulmicola" OR "gloeosporium ulmicolum" spread dispersal model

"stenocarpella macrospora" OR "diplodia macrospora" OR "macrodiplodia zeae" OR "macrodiplodia macrospora" OR "stenocarpella zeae" spread dispersal model

"stenocarpella maydis" OR "diplodia maydis" OR "sphaeria maydis" OR "sphaeria zeae" OR "diplodia zeae-maydis" OR "macrodiplodia zeae" OR "dothiora zeae" OR "diplodia zeae" OR "hendersonia zeae" spread dispersal model

"sternochetus mangiferae" OR "acryptorhynchus mangiferae" OR "cryptorhynchus mangiferae" spread dispersal model

"stolbur phytoplasma" OR "potato stolbur phytoplasma" OR "grapevine bois noir phytoplasma" OR "classical stolbur phytoplasma" OR "phytoplasma solani" OR "maize redness phytoplasma" spread dispersal model

"strauzia longipennis" OR "straussia longipennis" spread dispersal model

"strawberry crinkle virus" spread dispersal model

"strawberry latent c virus" OR "stlcv" OR "strawberry latent c rhabdovirus" spread dispersal model

"strawberry latent ringspot virus" spread dispersal model

"strawberry mild yellow edge virus" spread dispersal model

"strawberry vein banding virus" OR "strawberry virus" OR "svbv" OR "strawberry vein banding caulimovirus" spread dispersal model

"strawberry witches broom mycoplasm" spread dispersal model

"strobilomya viaria" spread dispersal model

"strobilomyia viaria" OR "lasiomma viarium" OR "lasiomma melaniola" OR "strobilomyia melaniola" spread dispersal model

"subanguina radicicola" spread dispersal model

"subplenodomus apiicola" spread dispersal model

"subplenodomus drobnjacensis" spread dispersal model

"subplenodomus valerianae" spread dispersal model

"subplenodomus violicola" spread dispersal model

"sunflower chlorotic mottle virus" spread dispersal model

"symphoricarpus albus" spread dispersal model

"synchytrium endobioticum" OR "synchytrium solani" OR "chrysophlyctis endobiotica" spread dispersal model

"tachypterellus quadrigibbus" spread dispersal model

"tanzanian lethal decline phytoplasma" OR "phytoplasma cocostanzaniae" spread dispersal model

"tatter leaf virus" spread dispersal model

"tecia solanivora" OR "scrobipalpopsis solanivora" spread dispersal model

"tellima grandiflora" spread dispersal model

"tetranychus evansi" spread dispersal model

"tetropium abietis" spread dispersal model

"tetropium castaneum" spread dispersal model

"tetropium gabrieli" spread dispersal model

"tetropium gracilicorne" spread dispersal model

"thaumastocoris peregrinus" spread dispersal model

"thaumatotibia leucotreta" OR "argyroploce leucotreta" OR "cryptophlebia leucotreta" OR "argyroploce batrachopa" OR "enarmonia batrachopa" spread dispersal model

"thaumetopoea pityocampa" spread dispersal model

"thecaphora alsinearum" spread dispersal model

"thecaphora amaranthi" spread dispersal model "thecaphora cerastii" spread dispersal model

"thecaphora hennenea" spread dispersal model

"thecaphora italica" spread dispersal model

"thecaphora melandrii" spread dispersal model

"thecaphora saponariae" spread dispersal model

"thecaphora solani" OR "angiosorus solani" spread dispersal model

"thrips flavus" spread dispersal model

"thrips major" spread dispersal model

"thrips meridionalis" spread dispersal model

"thrips nigropilosus" spread dispersal model

"thrips palmi" OR "thrips gossypicola" OR "thrips leucadophilus" OR "thrips clarus" OR "thrips gracilis" OR "chloethrips aureus" spread dispersal model

"thrips tabaci" spread dispersal model

"thyridaria rubronotata" spread dispersal model

"tilletia indica" OR "neovossia indica" spread dispersal model

"tobacco ringspot virus" OR "nicotiana virus 12" OR "trsv" OR "tobacco ringspot nepovirus" spread dispersal model

"tobacco streak ilarvirus" OR "tobacco streak virus" OR "tsvp" spread dispersal model

"tomato apical stunt viroid" OR "tasvd" OR "tomato apical stunt pospiviroid" spread dispersal model

"tomato black ring virus" spread dispersal model

"tomato chlorosis virus" OR "tomato chlorosis closterovirus" OR "tocv" OR "tomato chlorosis crinivirus" spread dispersal model

"tomato chlorotic dwarf viroid" spread dispersal model

"tomato chocolate virus" spread dispersal model

"tomato infectious chlorosis virus" OR "ticv" OR "tomato infectious chlorosis closterovirus" OR "tomato infectious chlorosis crinivirus" spread dispersal model

"tomato marchitez virus" spread dispersal model

"tomato mottle virus" OR "florida tomato virus" OR "tomato mottle geminivirus" OR "tmov" OR "tomato mottle bigeminivirus" OR "tomato mottle begomovirus" spread dispersal model

"tomato planta macho viroid" spread dispersal model

"tomato ringspot virus" OR "winter peach mosaic virus" OR "peach yellow bud mosaic virus" OR "blackberry himalaya mosaic virus" OR "torsv" OR "nicotiana virus 13" OR "grapevine yellow vein virus" OR "tomato ringspot nepovirus" spread dispersal model

"tomato spotted wilt virus" OR "tswv" OR "tomato spotted wilt tospovirus" spread dispersal model

"tomato torrado virus" spread dispersal model

"tomato yellow leaf curl sardinia virus" OR "tomato yellow leaf curl sardinia begomovirus" spread dispersal model

"tomato yellow leaf curl virus" OR "tomato yellow leaf curl geminivirus" OR "tomato leaf curl geminivirus" OR "tomato yellow leaf curl bigeminivirus" OR "tylcv" OR "tomato leaf curl bigeminivirus" OR "tomato yellow leaf curl begomovirus" spread dispersal model

"toxicodendron radicans" spread dispersal model

"toxoptera citricida" spread dispersal model

"toxoptera citricidus" OR "aphis aeglis" OR "paratoxoptera argentiniensis" OR "aphis tavaresi" OR "aphis citricidus" OR "toxoptera citricida" OR "toxoptera citricola" OR "toxoptera tavaresi" OR "aphis nigricans" OR "myzus citricidus" OR "toxoptera aphoides" spread dispersal model

"toxotrypana curvicauda" spread dispersal model

"tranzschelia discolor" spread dispersal model

"trechispora brinkmannii" spread dispersal model

"trematophoma" spread dispersal model

"trematosphaeria pertusa" spread dispersal model

"trialeurodes ricini" spread dispersal model

"trialeurodes vaporariorum" spread dispersal model

"tribolium castaneum" spread dispersal model "trichodorus cylindricus" spread dispersal model

"trichodorus primitivus" spread dispersal model

"trichodorus similis" spread dispersal model

"trichodorus sparsus" spread dispersal model

"trichodorus variopapillatus" spread dispersal model

"trichodorus viruliferus" spread dispersal model

"trichoferus campestris" spread dispersal model

"trichoferus fasciculatus" spread dispersal model

"trichoferus griseus" spread dispersal model

"trichoferus holosericeus" spread dispersal model

"trioza erytreae" OR "spanioza erythreae" OR "trioza erythreae" OR "spanioza merwei" OR "trioza merwei" spread dispersal model

"trogoderma granarium" OR "trogoderma khapra" OR "trogoderma affrum" spread dispersal model

"trophurus imperialis" spread dispersal model

"tulip virus" spread dispersal model

"turanoclytus namanganensis" spread dispersal model

"tuta absoluta" OR "phthorimaea absoluta" OR "gnorimoschema absoluta" OR "scrobipalpula absoluta" OR "scrobipalpuloides absoluta" OR "gnorimoschema absoluta" spread dispersal model

"tylenchorhynchus dubius" spread dispersal model

"tylenchorhynchus leviterminalis" spread dispersal model

"tylenchorhynchus teeni" spread dispersal model

"tylenchulus semipenetrans" spread dispersal model

"tylolaimophorus typicus" spread dispersal model

"unaspis citri" OR "chionaspis citri" OR "prontaspis citri" OR "dinaspis veitchi" spread dispersal model

"unaspis euonymi" spread dispersal model

"unaspis yanonensis" spread dispersal model

"uromyces trifolii-repentis" spread dispersal model

"vaccinium angustifolium" spread dispersal model

"vaccinium corymbosum" spread dispersal model

"venturia nashicola" spread dispersal model

"verbesina encelioides" spread dispersal model

"verticillium alboatrum" spread dispersal model

"verticillium albo-atrum" spread dispersal model

"verticillium biguttatum" spread dispersal model

"verticillium dahliae" spread dispersal model

"verticillium leptobactrum" spread dispersal model

"viteus vitifoliae" OR "dactylosphaera vastatrix" OR "dactylosphaera vitifoliae" OR "phylloxera vitifoliae" OR "daktulosphaira vitifoliae" OR "phylloxera vastatrix" OR "rhizaphis vastatrix" OR "dactylosphaera vitifolii" OR "foaiella vitifolii" OR "peritymbia vitifolii" OR "peritymbia vitisana" OR "phylloxera vitifolii" OR "peritymbia vastatrix" OR "phylloxera pemphigoides" OR "pemphigus vitifoliae" OR "daktulosphaira vitifoliae" OR "daktulosphaira vitifoliae" spread dispersal model

"watermelon silver mottle virus" OR "wmsmov" OR "watermelon silver mottle tospovirus" spread dispersal model

"westerdykella capitulum" spread dispersal model

"westerdykella minutispora" spread dispersal model

"westerdykella ornata" spread dispersal model

"western x disease phytoplasma" OR "peach western x phytoplasma" OR "peach yellow leafroll phytoplasma" OR "peach x disease phytoplasma" OR "phytoplasma pruni" spread dispersal model

"witches broom" spread dispersal model

"wojnowicia hirta" spread dispersal model "xanthomonas" spread dispersal model

"xanthomonas alangii" spread dispersal model

"xanthomonas albilineans" spread dispersal model

"xanthomonas alfalfae" spread dispersal model

"xanthomonas arboricola" OR "xanthomonas corylina" OR "phytomonas corylina" OR "xanthomonas campestris" spread dispersal model

"xanthomonas argemones" spread dispersal model

"xanthomonas axonopodis" OR "xanthomonas citri" OR "xanthomonas campestris" OR "xanthomonas campestris" OR "phytomonas citri" OR "xanthomonas citri" OR "xanthomonas citri" OR "pseudomonas citri" spread dispersal model

"xanthomonas betae" spread dispersal model

"xanthomonas campestris" spread dispersal model

"xanthomonas citri" spread dispersal model

"xanthomonas codiaei" spread dispersal model

"xanthomonas cucurbitae" spread dispersal model

"xanthomonas cynarae" spread dispersal model

"xanthomonas eucalypti" spread dispersal model

"xanthomonas fragariae" spread dispersal model

"xanthomonas hortorum" spread dispersal model

"xanthomonas hyacinthi" spread dispersal model

"xanthomonas ionidii" spread dispersal model

"xanthomonas laureliae" spread dispersal model

"xanthomonas lawsoniae" spread dispersal model

"xanthomonas leeana" spread dispersal model

"xanthomonas melonis" spread dispersal model

"xanthomonas oryzae" OR "pseudomonas oryzae" OR "xanthomonas kresek" OR "xanthomonas itoana" OR "xanthomonas campestris" OR "xanthomonas translucens" spread dispersal model

"xanthomonas perforans" spread dispersal model

"xanthomonas physalidis" spread dispersal model

"xanthomonas pisi" spread dispersal model

"xanthomonas populi" spread dispersal model

"xanthomonas sacchari" spread dispersal model

"xanthomonas syngonii" spread dispersal model

"xanthomonas theicola" spread dispersal model

"xanthomonas thirumalacharii" spread dispersal model

"xanthomonas translucens" OR "xanthomonas translucens" OR "xanthomonas translucens" OR "xanthomonas campestris" OR "xanthomonas translucens" OR "xanthomonas translucens" OR "xanthomonas translucens" OR "pseudomonas translucens" OR "xanthomonas campestris" spread dispersal model

"xanthomonas tribuli" spread dispersal model

"xanthomonas vasicola" spread dispersal model

"xanthomonas vesicatoria" OR "pseudomonas exitiosa" OR "pseudomonas vesicatoria" spread dispersal model

"xanthomonas viticola"

spread dispersal model

"xanthomonas vitistrifoliae" spread dispersal model

"xiphinema americanum" OR "tylencholaimus americanus" OR "xiphinema americanum" spread dispersal model

"xiphinema brevicollum" spread dispersal model

"xiphinema bricolense" spread dispersal model

"xiphinema californicum" spread dispersal model

"xiphinema chambersi" spread dispersal model "xiphinema coxi" spread dispersal model

"xiphinema diffusum" spread dispersal model

"xiphinema diversicaudatum" spread dispersal model

"xiphinema incognitum" spread dispersal model

"xiphinema index" spread dispersal model

"xiphinema pachtaicum" spread dispersal model

"xiphinema rivesi" spread dispersal model

"xiphinema vuittenezi" spread dispersal model

"xyleborinus andrewesi" spread dispersal model

"xyleborinus saxesenii" spread dispersal model

"xyleborus glabratus" spread dispersal model

"xylella fastidiosa" OR "peach phony agent" OR "xylella fastidiosa" OR "citrus variegated chlorosis agent" OR "prunus virus" OR "grapevine pierce's disease agent" OR "peach virus" spread dispersal model

"xyloclytus altaicus" spread dispersal model

"xylophilus ampelinus" OR "xanthomonas ampelina" OR "erwinia vitivora" spread dispersal model

"xylosandrus compactus" spread dispersal model

"xylosandrus crassiusculus" OR "xyleborus crassiusculus" spread dispersal model

"xylosandrus germanus" spread dispersal model

"xylotrechus altaicus" OR "xyloclytus altaicus" spread dispersal model

"xylotrechus antilope" spread dispersal model

"xylotrechus arvicola" spread dispersal model

"xylotrechus namanganensis" OR "xylotrechus namangensis" spread dispersal model

"xylotrechus stebbingi" spread dispersal model

"xyphon fulgida" spread dispersal model

"yucatan lethal decline phytoplasma" spread dispersal model

"zaprionus indianus" spread dispersal model

Appendix F. Number of times that each search term was found in Web of Knowledge results

Table 22: The number of times each search term (excluding individual species names) was found in the title or abstract of the results of the Web of Knowledge search.

Category	Search term	# of WoK results containing the term
Pests	weed*	3528
Pests	fung*	1812
Pests	invasive	1206
Pests	disease	1045
Pests	aphid*	960
Pests	pathogen*	877
Pests	insect*	871
Pests	bacteri*	855
Pests	pest	732
Pests	mite	691
Pests	*virus*	617
Pests	herbivor*	454
Pests	parasit*	443
Pests	fly	371
Pests	beetle	314
Pests	alien	298
Pests	moth	233
Pests	coleoptera*	177
Pests	competitor	165
Pests	lepidoptera*	140
Pests	nematod*	106
Pests	diptera*	83
Pests	hymenoptera*	80
Pests	*hopper	75
Pests	*wasp	71
Pests	acari*	66
Pests	snail	60
Pests	non*native	45
Pests	hemiptera*	41
Pests	*bug	37
Pests	gastropod*	34
Pests	caterpillar	26
Pests	thrip	25
Pests	slug	21
Pests	thysanoptera*	16

Category	Search term	# of WoK results containing the term
Pests	oomyc*	14
Pests	phytoplasm*	11
Pests	cicad*	11
Pests	sawfly	5
Pests	*viroid	4
Pests	gasteropod*	0
Plants	herb*	6516
Plants	plant	3097
Plants	mate	2351
Plants	pea	1358
Plants	seed	1014
Plants	tree	885
Plants	crop	884
Plants	herb	792
Plants	pear	717
Plants	date	670
Plants	grass*	645
Plants	nut	558
Plants	root	481
Plants	tea	366
Plants	beet	344
Plants	fruit	305
Plants	bay	256
Plants	wheat	211
Plants	oat	197
Plants	*corn	193
Plants	corn	193
Plants	shrub	190
Plants	rice	173
Plants	potato	154
Plants	sage	149
Plants	bean	148
Plants	fig	124
Plants	pulse	118
Plants	vine	116

Category	Search term	# of WoK results containing the term
Plants	lime	108
Plants	tomato	105
Plants	maize	92
Plants	sugar	88
Plants	brassica*	84
Plants	cotton	70
Plants	tuber	70
Plants	apple	69
Plants	grape	69
Plants	plum	67
Plants	citrus	65
Plants	cane	62
Plants	gramin*	61
Plants	forb	58
Plants	*berry	58
Plants	cereal	55
Plants	barley	52
Plants	palm	52
Plants	oilseed	49
Plants	legume	45
Plants	clove	38
Plants	orange	34
Plants	swede	33
Plants	sprout	32
Plants	vegetable	32
Plants	cucumber	31
Plants	pepper	29
Plants	rye	28
Plants	chestnut	27
Plants	strawberry	23
Plants	lupin	22
Plants	banana	21
Plants	sunflower	21
Plants	cabbage	20
Plants	carrot	20
Plants	cherry	20
Plants	bulb	19
Plants	melon	19
Plants	mustard	18
Plants	olive	18

Category	Search term	# of WoK results containing the term
Plants	sorghum	18
Plants	cucurbit	17
Plants	mace	16
Plants	marrow	16
Plants	cassava	15
Plants	cowpea	15
Plants	peach	15
Plants	peanut	15
Plants	juniper	14
Plants	lettuce	14
Plants	radish	14
Plants	squash	13
Plants	grapefruit	12
Plants	mint	12
Plants	coconut	11
Plants	hops	11
Plants	cactus	10
Plants	rape*seed	10
Plants	turnip	10
Plants	chickpea	9
Plants	coffee	9
Plants	eggplant	9
Plants	garlic	9
Plants	onion	9
Plants	cauliflower	8
Plants	laurel	8
Plants	yam	8
Plants	flax	7
Plants	millet	7
Plants	papaya	7
Plants	spinach	7
Plants	almond	6
Plants	anise	6
Plants	apricot	6
Plants	bamboo	6
Plants	cassia	6
Plants	cocoa	6
Plants	lemon	6
Plants	mango	6
Plants	pome	6

Category	Search term	# of WoK results containing the term
Plants	kiwi	5
Plants	lentil	5
Plants	thyme	5
Plants	asparagus	4
Plants	cress	4
Plants	dill	4
Plants	hazelnut	4
Plants	leek	4
Plants	nectarine	4
Plants	pineapple	4
Plants	poppy	4
Plants	pumpkin	4
Plants	salad	4
Plants	walnut	4
Plants	watermelon	4
Plants	chive	3
Plants	cumin	3
Plants	currant	3
Plants	hawthorn	3
Plants	hibiscus	3
Plants	mandarin	3
Plants	persimmon	3
Plants	plantain	3
Plants	raspberry	3
Plants	soya	3
Plants	artichoke	2
Plants	avocado	2
Plants	borage	2
Plants	broccoli	2
Plants	buckthorn	2
Plants	cashew	2
Plants	celery	2
Plants	citron	2
Plants	guava	2
Plants	hemp	2
Plants	kale	2
Plants	mulberry	2
Plants	okra	2
Plants	parsley	2
Plants	pistachio	2
Plants	pomegranate	2
Plants	purslane	2
Plants	rocket	2
Plants	spice	2
Plants	taro	2
Plants	angelica	1
Plants	arbutus	1
Plants	aubergine	1
Plants	carambola	1
Plants	chervil	1
Plants	cinnamon	1
Plants	clementine	1
Plants	collard	1
Plants	endive	1
Plants	fennel	1
Plants	ginger	1
Plants	kaki	1
Plants	kapok	1
Plants	kumquat	1
Plants	linden	1
Plants	linseed	1
Plants	oregano	1
Plants	pecan	1
Plants	pepino	1
Plants	rosemary	1
Plants	scorzonera	1
Plants	sesame	1
Plants	tamarind	1
Plants	tangerine	1
Plants	tarragon	1
Plants	teff	1
Plants	triticale	1
Plants	ugli	1
Plants	water*cress	1
Plants	allspice	0
Plants	arrowroot	0
Plants	azarole	0
Plants	balm	0
Plants	basil	0
Plants	beetroot	0

Category	Search term	# of WoK results containing the term
Plants	bergamot	0
Plants	bilimbi	0
Plants	borecole	0
Plants	buckwheat	0
Plants	calabrese	0
Plants	camomile	0
Plants	canistel	0
Plants	caper	0
Plants	caraway	0
Plants	cardamom	0
Plants	cardoon	0
Plants	carob	0
Plants	celeriac	0
Plants	cherimoya	0
Plants	chickling*vetch	0
Plants	chicory	0
Plants	chinotto	0
Plants	chokeberry	0
Plants	coriander	0
Plants	cornsalad	0
Plants	courgette	0
Plants	curcuma	0
Plants	damson	0
Plants	dasheen	0
Plants	dewberry	0
Plants	durian	0
Plants	eddoe	0
Plants	fenugreek	0
Plants	filbert	0
Plants	flageolet	0
Plants	gherkin	0
Plants	ginseng	0
Plants	glassworth	0
Plants	gooseberry	0
Plants	greengage	0
Plants	grumichama	0
Plants	guanabana	0
Plants	hempseed	0
Plants	horseradish	0
Plants	hyssop	0

Category	Search term	# of WoK results containing the term
Plants	jackfruit	0
Plants	jambolan	0
Plants	jasmine	0
Plants	kiwano	0
Plants	kohlrabi	0
Plants	liquorice	0
Plants	lollo*rosso	0
Plants	loquat	0
Plants	lovage	0
Plants	lychee	0
Plants	macadamia	0
Plants	mangetout	0
Plants	marjoram	0
Plants	medlar	0
Plants	mirabelle	0
Plants	mizuna	0
Plants	mountain*ash	0
Plants	nutmeg	0
Plants	oilfruit	0
Plants	oysterplant	0
Plants	pak*choi	0
Plants	palmfruit	0
Plants	palmoil	0
Plants	parsnip	0
Plants	passion*fruit	0
Plants	patisson	0
Plants	pe-tsai	0
Plants	peppermint	0
Plants	pine*nut	0
Plants	pomelo	0
Plants	pomerac	0
Plants	pulasan	0
Plants	quince	0
Plants	radicchio	0
Plants	rambutan	0
Plants	rhubarb	0
Plants	rooibos	0
Plants	rose*hip	0
Plants	safflower	0
Plants	saffron	0

Category	**Search term**	**# of WoK results containing the term**
Plants	sallowthorn	0
Plants	salsify	0
Plants	sapote	0
Plants	savory	0
Plants	scarole	0
Plants	shaddock	0
Plants	shallot	0
Plants	sorrel	0
Plants	soursop	0
Plants	spelt	0
Plants	sweet*cicely	0
Plants	sweetsop	0
Plants	tai*goo*choi	0
Plants	tangelo	0
Plants	tannia	0
Plants	treeberry	0
Plants	turmeric	0
Plants	valerian	0
Plants	vanilla	0
Plants	wineberry	0
Plants	witloof	0
Spread	dispers*	2512
Spread	spread*	2099
Spread	invasion	1502
Spread	movement*	1182
Spread	diffus*	1104
Spread	colonis*	804
Modelling	model*	6584
Modelling	simulat*	1959

Appendix G. Representative studies re-examined in the fitness evaluation

Table 23: The ten most representative studies assigned to each cluster. During the fitness evaluation, the fitness criteria in Table 12 were evaluated for each of these studies.

Cluster	Ten most representative studies
1	Blenis PV, Chang KF, Hiratsuka Y (1993) Spore dispersal gradients and disease gradients of Western Gall Rust. *Canadian Journal of Forest Research-Revue Canadienne De Recherche Forestiere,* **23**, 2481-2486.
	Brock MT, Weinig C, Galen C (2005) A comparison of phenotypic plasticity in the native dandelion *Taraxacum ceratophorum* and its invasive congener *T-officinale*. *New Phytologist,* **166**, 173-183.
	Dauer JT, Mortensen DA, Vangessel MJ (2007) Temporal and spatial dynamics of long-distance *Conyza canadensis* seed dispersal. *Journal of Applied Ecology,* **44**, 105-114.
	Ferrandino FJ, Elmer WH (1996) Septoria leaf spot lesion density on trap plants exposed at varying distances from infected tomatoes. *Plant Disease,* **80**, 1059-1062.
	Jung C (2005) Some evidences of aerial dispersal of twospotted spider mites from an apple orchard into a soybean field. *Journal of Asia-Pacific Entomology,* **8**, 279-283.
	Laranjeira FF, Barbosa CJ, Santos-Filho HP, Gonçalves TF, Nickel O (2006) Progress, spread and natural transmission of Bahia bark scaling of citrus in Brazil. *Annals of Applied Biology,* **148**, 187-195.
	Mundt CC, Ahmed HU, Finckh MR, Nieva LP, Alfonso RF (1999) Primary disease gradients of bacterial blight of rice. *Phytopathology,* **89**, 64-67.
	Paulitz TC, Dutilleul P, Yamasaki SH, Fernando WGD, Seaman WL (1999) A generalized two-dimensional Gaussian model of disease foci of head blight of wheat caused by *Gibberella zeae*. *Phytopathology,* **89**, 74-83.
	Skarpaas O, Silverman EJ, Jongejans E, Shea K (2011) Are the best dispersers the best colonizers? Seed mass, dispersal and establishment in *Carduus* thistles. *Evolutionary Ecology,* **25**, 155-169.
	Travadon R, Bousset L, Saint-Jean S, Brun H, Sache I (2007) Splash dispersal of *Leptosphaeria maculans* pycnidiospores and the spread of blackleg on oilseed rape. *Plant Pathology,* **56**, 595-603.
2	Bendor TK, Metcalf SS, Fontenot LE, Sangunett B, Hannon B (2006) Modeling the spread of the Emerald Ash Borer. *Ecological Modelling,* **197**, 221-236.
	Beukema SJ, Robinson DCE (2004) Modelling Mountain Pine in the Chilcotin using the Westwide Pine Beetle Model. Vancouver, Canada, ESSA Technologies Ltd.
	Colbach N (2009) How to model and simulate the effects of cropping systems on population dynamics and gene flow at the landscape level: example of oilseed rape volunteers and their role for co-existence of GM and non-GM crops. *Environmental Science and Pollution Research,* **16**, 348-360.
	Gilligan CA, Truscott JE, Stacey AJ (2007) Impact of scale on the effectiveness of disease control strategies for epidemics with cryptic infection in a dynamical landscape: an

Cluster	Ten most representative studies
	example for a crop disease. *Journal of the Royal Society Interface,* **4**, 925-934. Gonzalez-Andujar JL, Perry JN, Moss SR (1999) Modeling effects of spatial patterns on the seed bank dynamics of *Alopecurus myosuroides*. *Weed Science,* **47**, 697-705. Leon-Cortes JL, Lennon JJ, Thomas CD (2003) Ecological dynamics of extinct species in empty habitat networks. 2. The role of host plant dynamics. *Oikos,* **102**, 465-477. Lô-Pelzer E, Bousset L, Jeuffroy MH, Salam MU, Pinochet X, Boillot M, Aubertot JN (2010) SIPPOM-WOSR: A Simulator for Integrated Pathogen POpulation Management of phoma stem canker on Winter OilSeed Rape. I. Description of the model. *Field Crops Research,* **118**, 73-81. Mercader RJ, Siegert NW, Liebhold AM, Mccullough DG (2011) Simulating the effectiveness of three potential management options to slow the spread of emerald ash borer (*Agrilus planipennis*) populations in localized outlier sites. *Canadian Journal of Forest Research-Revue Canadienne De Recherche Forestiere,* **41**, 254-264. Skelsey P, Rossing WaH, Kessel GJT, Van Der Werf W (2010) Invasion of *Phytophthora infestans* at the landscape level: How do spatial scale and weather modulate the consequences of spatial heterogeneity in host resistance? *Phytopathology,* **100**, 1146-1161. Stanaway MA (2011) Hierarchical Bayesian models for estimating the extent of plant pest invasions.
3	Bolker BM, Pacala SW (1999) Spatial moment equations for plant competition: Understanding spatial strategies and the advantages of short dispersal. *American Naturalist,* **153**, 575-602. Brown DH, Hastings A (2003) Resistance may be futile: dispersal scales and selection for disease resistance in competing plants. *Journal of Theoretical Biology,* **222**, 373-388. Chaianunporn T, Hovestadt T (2012) Evolution of dispersal in metacommunities of interacting species. *Journal of Evolutionary Biology,* **25**, 2511-2525. Eppstein MJ, Molofsky J (2007) Invasiveness in plant communities with feedbacks. *Ecology Letters,* **10**, 253-263. Hartvigsen G, Levin S (1997) Evolution and spatial structure interact to influence plant-herbivore population and community dynamics. *Proceedings of the Royal Society B-Biological Sciences,* **264**, 1677-1685. Korniss G, Caraco T (2005) Spatial dynamics of invasion: the geometry of introduced species. *Journal of Theoretical Biology,* **233**, 137-150. Mitteldorf J, Pepper J (2009) Senescence as an adaptation to limit the spread of disease. *Journal of Theoretical Biology,* **260**, 186-195. Muller-Landau HC, Levin SA, Keymer JE (2003) Theoretical perspectives on evolution of long-distance dispersal and the example of specialized pests. *Ecology,* **84**, 1957-1967. Park AW, Gubbins S, Gilligan CA (2001) Invasion and persistence of plant parasites in a

Cluster	Ten most representative studies
	spatially structured host population. *Oikos,* **94**, 162-174.
	Vuilleumier S, Buttler A, Perrin N, Yearsley JM (2011) Invasion and eradication of a competitively superior species in heterogeneous landscapes. *Ecological Modelling,* **222**, 398-406.
4	Aylor DE (1999) Biophysical scaling and the passive dispersal of fungus spores: relationship to integrated pest management strategies. *Agricultural and Forest Meteorology,* **97**, 275-292.(a)
	Gharekhani G (2009) Modeling population dynamics and dispersion of codling moth *Cydia pomonella* L.(Lepidoptera, Tortricidae). Doctoral thesis. Faculty of Agricultural Sciences at the University of Hohenheim, Stuttgart, Germany.
	Harrison S, Hastings A, Strong DR (2005) Spatial and temporal dynamics of insect outbreaks in a complex multitrophic system: tussock moths, ghost moths, and their natural enemies on bush lupines. *Annales Zoologici Fennici,* **42**, 409-419.
	Kareiva PM (1983) Local movement in herbivorous insects: applying a passive diffusion model to mark-recapture field experiments. *Oecologia,* **57**, 322-327.
	Puche H, Weissling TJ, Schnell R, Epsky ND, Heath RR (2005) Estimating dispersal rate of the silky cane weevil (Coleoptera : Curculionidae). *Journal of Applied Entomology,* **129**, 293-299.
	Tyson RC, Wilson JB, Lane WD (2011) Beyond diffusion: Modelling local and long-distance dispersal for organisms exhibiting intensive and extensive search modes. *Theoretical Population Biology,* **79**, 70-81.
	Yamamura K (2002) Dispersal distance of heterogeneous populations. *Population Ecology,* **44**, 93-101.
	Yang XS, Madden LV, Brazee RD (1991) Application of the diffusion equation for modeling splash dispersal of point-source pathogens. *New Phytologist,* **118**, 295-301.
	Zawolek MW (1993) Shaping a focus - wind and stochasticity. *Netherlands Journal of Plant Pathology,* **99**, 241-255.
5	Fennell M, Murphy JE, Armstrong C, Gallagher T, Osborne B (2012) Plant Spread Simulator: A model for simulating large-scale directed dispersal processes across heterogeneous environments. *Ecological Modelling,* **230**, 1-10.
	Fennell M, Murphy JE, Gallagher T, Osborne B (2013) Simulating the effects of climate change on the distribution of an invasive plant, using a high resolution, local scale, mechanistic approach: challenges and insights. *Global Change Biology,* **19**, 1262-1274.
	Hester S, Cacho O (2012) Optimization of search strategies in managing biological invasions: a simulation approach. *Human and Ecological Risk Assessment,* **18**, 181-199.
	Muirhead JR, Leung B, Van Overdijk C, Kelly DW, Nandakumar K, Marchant KR, Macisaac HJ (2006) Modelling local and long-distance dispersal of invasive emerald ash borer *Agrilus planipennis* (Coleoptera) in North America. *Diversity*

Cluster	Ten most representative studies
	and Distributions, **12**, 71-79. Niggemann M, Jetzkowitz J, Brunzel S, Wichmann MC, Bialozyt R (2009) Distribution patterns of plants explained by human movement behaviour. *Ecological Modelling*, **220**, 1339-1346. Pergl J, Müllerová J, Perglová I, Herben T, Pyšek P (2011) The role of long-distance seed dispersal in the local population dynamics of an invasive plant species. *Diversity and Distributions*, **17**, 725-738. Peterson AT, Scachetti-Pereira R, Hargrove WW (2004) Potential geographic distribution of *Anoplophora glabripennis* (Coleoptera : Cerambycidae) in North America. *American Midland Naturalist*, **151**, 170-178. Pitt JPW, Kriticos DJ, Dodd MB (2011) Temporal limits to simulating the future spread pattern of invasive species: *Buddleja davidii* in Europe and New Zealand. *Ecological Modelling*, **222**, 1880-1887. Pitt JPW, Worner SP, Suarez AV (2009) Predicting Argentine ant spread over the heterogeneous landscape using a spatially explicit stochastic model. *Ecological Applications*, **19**, 1176-1186. Starrfelt J, Kokko H (2010) Parent-offspring conflict and the evolution of dispersal distance. *American Naturalist*, **175**, 38-49.
6	Bertschinger L, Keller ER, Gessler C (1995) Development of Epivit, a simulation-model for contact-transmitted and aphid-transmitted potato viruses. *Phytopathology*, **85**, 801-814. Ferrari MJ, Bjørnstad ON, Partain JL, Antonovics J (2006) A gravity model for the spread of a pollinator-borne plant pathogen. *American Naturalist*, **168**, 294-303. Gottwald TR, Gibson GJ, Garnsey SM, Irey M (1999) Examination of the effect of aphid vector population composition on the spatial dynamics of citrus tristeza virus spread by stochastic modeling. *Phytopathology*, **89**, 603-608. Lloyd M (1991) Computer analysis of the shape of spread of epidemics on a grid. *Mathematical Biosciences*, **107**, 289-297. Marion G, Gibson G, Renshaw E (2003) Estimating likelihoods for spatio-temporal models using importance sampling. *Statistics and Computing*, **13**, 111-119. Pethybridge SJ, Madden LV (2003) Analysis of spatiotemporal dynamics of virus spread in an Australian hop garden by stochastic modeling. *Plant Disease*, **87**, 56-62. Pethybridge SJ, Madden LV, Griggs J, Wilson CR (2004) Species composition and abundance of aphids in Australian hop gardens and their impact on spatiotemporal patterns of Carlavirus epidemics. *Plant Pathology*, **53**, 498-507. Takasu F (2009) Individual-based modeling of the spread of pine wilt disease: vector beetle dispersal and the Allee effect. *Population Ecology*, **51**, 399-409. Xu XM, Ridout MS (2000) Stochastic simulation of the spread of race-specific and race-nonspecific aerial fungal pathogens in cultivar mixtures. *Plant Pathology*, **49**, 207-218. Xu XM, Ridout MS (2001) Effects of prevailing wind direction on spatial statistics of plant

Cluster	Ten most representative studies
	disease epidemics. *Journal of Phytopathology-Phytopathologische Zeitschrift*, **149**, 155-166.
7	Aylor DE, Schmale DG, Iii, Shields EJ, Newcomb M, Nappo CJ (2011) Tracking the potato late blight pathogen in the atmosphere using unmanned aerial vehicles and Lagrangian modeling. *Agricultural and Forest Meteorology*, **151**, 251-260. Dillon ML, Fitt GP, Hamilton JG, Rochester WA (1996) A simulation model of wind-driven dispersal of *Helicoverpa* moths. *Ecological Modelling*, **86**, 145-150. Hopkinson RF, Soroka JJ (2010) Air trajectory model applied to an in-depth diagnosis of potential diamondback moth infestations on the Canadian Prairies. *Agricultural and Forest Meteorology*, **150**, 1-11. Isard SA, Barnes CW, Hambleton S *et al.* (2011) Predicting soybean rust incursions into the north american continental interior using crop monitoring, spore trapping, and aerobiological modeling. *Plant Disease*, **95**, 1346-1357. Leskinen M, Markkula I, Koistinen J *et al.* (2011) Pest insect immigration warning by an atmospheric dispersion model, weather radars and traps. *Journal of Applied Entomology*, **135**, 55-67. Miao J, Wu YQ, Gong ZJ, He YZ, Duan Y, Jiang YL (2013) Long-distance wind-borne dispersal of *Sitodiplosis mosellana* Géhin (Diptera:Cecidomyiidae) in Northern China. *Journal of Insect Behavior*, **26**, 120-129. Otuka A, Watanabe T, Suzuki Y, Matsumura M, Furuno A, Chino M (2005) Real-time prediction system for migration of rice planthoppers *Sogatella furcifera* (Horváth) and *Nilaparvata lugens* (Stål) (Homoptera: Delphacidae). *Applied Entomology and Zoology*, **40**, 221-229. Otuka A, Watanabe T, Suzuki Y *et al.* (2006) A migration analysis of *Sogatella furcifera* (Horvath) (Homoptera : Delphacidae) using hourly catches and a three-dimensional simulation model. *Agricultural and Forest Entomology*, **8**, 35-47. Pan Z, Yang XB, Pivonia S, Xue L, Pasken R, Roads J (2006) Long-term prediction of soybean rust entry into the continental United States. *Plant Disease*, **90**, 840-846. Savage D, Barbetti MJ, Macleod WJ, Salam MU, Renton M (2012) Seasonal and diurnal patterns of spore release can significantly affect the proportion of spores expected to undergo long-distance dispersal. *Microbial Ecology*, **63**, 578-585.
8	Caplat P, Nathan R, Buckley YM (2012) Seed terminal velocity, wind turbulence, and demography drive the spread of an invasive tree in an analytical model. *Ecology*, **93**, 368-377. Ellner SP, Schreiber SJ (2012) Temporally variable dispersal and demography can accelerate the spread of invading species. *Theoretical Population Biology*, **82**, 283-298. Garnier A, Pivard S, Lecomte J (2008) Measuring and modelling anthropogenic secondary seed dispersal along roadverges for feral oilseed rape. *Basic and Applied Ecology*, **9**, 533-541. Kot M, Lewis MA, Van Den Driessche P (1996) Dispersal data and the spread of invading

Cluster	Ten most representative studies
	organisms. *Ecology*, **77**, 2027-2042. Mahdjoub T, Menu F (2008) Prolonged diapause: A trait increasing invasion speed? *Journal of Theoretical Biology,* **251**, 317-330. Marchetto KM, Jongejans E, Shea K, Isard SA (2010) Plant spatial arrangement affects projected invasion speeds of two invasive thistles. *Oikos,* **119**, 1462-1468. Neubert MG, Kot M, Lewis MA (2000) Invasion speeds in fluctuating environments. *Proceedings of the Royal Society B: Biological Sciences,* **267**, 1603-1610. Robinet C, Kehlenbeck H, Kriticos DJ *et al.* (2012) A suite of models to support the quantitative assessment of spread in pest risk analysis. *Plos One,* **7**. Skarpaas O, Shea K (2007) Dispersal patterns, dispersal mechanisms, and invasion wave speeds for invasive thistles. *American Naturalist*, **170**, 421-430. Wingen LU, Brown JKM, Shaw MW (2007) The population genetic structure of clonal organisms generated by exponentially bounded and fat-tailed dispersal. *Genetics,* **177**, 435-448.

(a): Paper presents two models in the same cluster.

GLOSSARY

Dispersal	The active or passive process by which a propagule of a species moves through space (Cousens et al., 2008).
Generic model	A model developed based on features of plant-pest interactions that are shared across a broad spectrum of different pest and host taxa.
Plant pest	Any species, strain or biotype of plant, animal or pathogenic agent injurious to plants or plant products (IPPC, 2010).
Quantitative model	A mathematical or algorithmic representation of the physiology, demography or population dynamics of an organism in space and/or time.
Specific model	A model developed with special regard to the biology of a particular plant pest, its host and the location and environment where their interactions occur.
Spread	Expansion of the geographical distribution of a pest through dispersal (IPPC, 2010).