Supplementary Information for the following article:

Title: Effects of modelling choices on early invasive risk assessments: lessons from the psyllid vectors of Citrus Huanglongbing

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Supplementary Material 1: List of studies that apply SDMs to the top 20 quarantine pests in Europe.

Full references with their corresponding DOIs are in the reference list at the end. In modelling algorithms, when there was only one or two models used, we specified which ones. Ensemble models include any combination of at least 3 models into a single prediction. Some of the publications were not accessible to us. In those cases, we extracted the information from the abstract whenever possible, and the missing values were marked as "Inaccessible" in the table below.

Species	Modelling algorithms	Performance index	Source of the presence data	Reference
Agrilus anxius Gory, 1841	Maxent	AUC	GBIF + field data	Fløe et al., 2015
Agrilus planipennis Fairmaire, 1888	Maxent	AUC	GBIF + field data	Fløe et al., 2015
Agrilus planipennis Fairmaire, 1888	Maxent	AUC & Omission rate	GBIF + Scientific articles + field data	Dang et al., 2021
Agrilus planipennis Fairmaire, 1888	Maxent	AUC	GBIF + Emerald Ash Borer Informative Network + Scientific articles	Meshkova et al., 2023
Anoplophora chinensis Forster, 1771	Maxent	AUC	Cannot Access	L. Zhang et al., 2025
Anoplophora chinensis Forster, 1771	Maxent	AUC	GBIF + iNaturalist + Scientific articles	Alramadan et al., 2025
Anoplophora chinensis Forster, 1771	Climex	None	CABI + Scientific articles	Ge et al., 2014
Anoplophora chinensis Forster, 1771	Maxent, Climex and Ensemble model (Maxent + Climex)	AUC	CABI + field data + Scientific articles	Zhou et al., 2022
Anoplophora chinensis Forster, 1771	Maxent	AUC, TSS, Kappa & Mobility-oriented parity	GBIF + Scientific articles	Zhou et al., 2023
Aromia bungii Faldermann, 1835	Ensemble model (GAM	AUC, TSS, Kappa, Boyce index	GBIF + iNaturalist	Ruzzier et al., 2025

	+ GBM + RF + Maxent)			
Aromia bungii Faldermann, 1835	Maxent	AUC	GBIF + iNaturalist + field data + Scientific articles +grey literature	L. Zhang et al., 2024
Candidatus liberibacter africanus	Maxent	AUC, TSS, Boyce index	Articles + GBIF + official reports	Godefroid, 2023
Candidatus liberibacter africanus	Climex	None	GBIF + Scientific articles + EPPO + CABI	Aidoo, Souza, da Silva, Santana Junior, Picanco, Kyerematen, et al., 2022
Candidatus liberibacter africanus	Maxent	AUC	GBIF + official reports + EPPO	Benhadi-Marin et al., 2022
Candidatus liberibacter africanus	Climex	None	GBIF + Scientific articles + EPPO + CABI	Souza et al., 2024
Candidatus liberibacter africanus	Ensemble model	None	CABI + EPPO + field data	Ajene, Khamis, van Asch, Pietersen, Rasowo, et al., 2020
Candidatus liberibacter africanus	Ensemble model	AUC	Online databases + Scientific articles + expert communication	Shimwela et al., 2016
Candidatus liberibacter africanus	Maxent	AUC	GBIF + scientific literature + natural museum dataset	Espinosa-Zaragoza et al., 2021
Candidatus liberibacter africanus	Maxent	AUC	Field data	Aidoo et al., 2019
Candidatus liberibacter africanus	Maxent	AUC	GBIF	Benhadi-Marin et al., 2020
Candidatus liberibacter africanus	Maxent	AUC	GBIF + CABI + EPPO + Scientific articles	Aidoo, Souza, da Silva, Santana Junior, Picanco, Osei-Owusu, et al., 2022
Candidatus liberibacter asiaticus	Climex	None	GBIF + Scientific articles	Souza et al., 2023
Candidatus liberibacter asiaticus	Maxent	AUC	GBIF + EPPO + Scientific articles	R. Wang, Yang, et al., 2020
Candidatus liberibacter asiaticus	Maxent	AUC	GBIF + EPPO + Scientific articles	R. Wang et al., 2019
Candidatus liberibacter asiaticus	Maxent	AUC	Field data + official data	You et al., 2024

Candidatus liberibacter asiaticus	Maxent	AUC	GBIF + CABI + EPPO + Scientific articles	Aidoo et al., 2023
Candidatus liberibacter asiaticus	Maxent	AUC	Field data	Alonso-Hernandez et al., 2024
Candidatus liberibacter asiaticus	Ensemble model	AUC	Inaccessible	Narouei-Khandan et al., 2016
Candidatus liberibacter asiaticus	Maxent	AUC	Field data	Ajene, Khamis, van Asch, Pietersen, Seid, et al., 2020
Candidatus liberibacter asiaticus	Maxent	AUC	GBIF + field data + Scientific articles	Aidoo, Souza, da Silva, Santana Jr, Picanço, Kyerematen, et al., 2022
Xylella fastidiosa	Ensemble model	AUC & TSS	Scientific Scientific articles + grey literature	Godefroid et al., 2019
Xylella fastidiosa	Maxent	AUC & Boyce index	Field data	Cruaud et al., 2018
Xylella fastidiosa	Maxent	AUC & TSS	Official dataset	Bosso, Di Febbraro, et al., 2016
Xylella fastidiosa	Maxent	AUC & TSS	Official dataset	Bosso, Russo, et al., 2016
Xylella fastidiosa	GAM	AUC & TSS	Official dataset	Godefroid et al., 2022
Xylella fastidiosa	Maxent	AUC & Continuous Boyce index	GBIF + Scientific articles	Rossi & Rasplus, 2023
Xylella fastidiosa	Maxent	AUC	Official dataset	Romero Fernandez, 2020
Phyllosticta citricarpa	Climex	None	Expert communication + official dataset	Paul et al., 2005
Phyllosticta citricarpa	Climex	None	Field data + reports	Yonow et al., 2013
Anoplophora glabripennis	Ensemble model (biomod2) & Maxent	AUC, TSS, Kappa, Schoener's D index, Jaccard index, Sørensen-	GBIF + iNaturalist + field data + CABI + GISD + Scientific articles + grey literature	Ding et al., 2025

		Dice similarity coefficient		
Anoplophora glabripennis	Climex	None	GBIF + CABI + EPPO + Scientific articles	Zhou et al., 2021
Anoplophora glabripennis	Maxent	AUC	GBIF + Scientific articles + news reports + quarantine websites	Q.C. Zhang et al., 2022
Anoplophora glabripennis	GARP	Chi-square test	Field data	Peterson et al., 2004
Anoplophora glabripennis	Maxent	AUC & Boyce	Field data	Shatz et al., 2016
Anoplophora glabripennis	Maxent	AUC + TSS	GBIF + iNaturalist + Scientific articles + field data	L. Zhang et al., 2024
Anoplophora glabripennis	Climex	None	Plant Host Official Dataset	Shim et al., 2020
Anoplophora glabripennis	Ensemble model (Maxent + Climex)	AUC, AICc & Omission rate	GBIF + CABI + Scientific articles	Byeon et al., 2021
Anoplophora glabripennis	Mahalanobis Typicality	Boyce index	Field data	Shatz et al., 2013
Anoplophora glabripennis	Climex	None	Scienfic Scientific articles	MacLeod et al., 2002
Anthonomus eugenii	Maxent	AUC	GBIF + CABI + Official dataset + iNaturalist + BoldSystems + Scientific articles	Q. Li et al., 2025
Anthonomus eugenii	Ensemble model (GAM, GBM, GLM, RF & Maxent)	AUC & TSS	GBIF + BoldSystems + Scientific articles	P. Wang et al., 2025
Popillia japonica Newman, 1838	Ensemble model	AUC & TSS	iNaturalist	Della Rocca & Milanesi, 2022b
Popillia japonica Newman, 1838	Climex	None	GBIF + EPPO + CERIS + Scientific articles	Kistner-Thomas, 2019
Popillia japonica Newman, 1838	INLA	AUC & TSS	iNaturalist	Della Rocca & Milanesi, 2022a

Popillia japonica Newman, 1838	Climex, Maxent & Ensemble (Climex + Maxent)	AUC	GBIF + iNaturalist + Scientific articles	Zhu et al., 2023
Popillia japonica Newman, 1838	Climex	None	Inaccessible	Allsopp, 1996
Popillia japonica Newman, 1838	Maxent	AUC, Omission rates	GBIF + Scientific articles	Zhu et al., 2017
Popillia japonica Newman, 1838	Random Forests	AUC, Sensitivity, Continuous Boyce index	Citizen science platforms + field data	Borner et al., 2023
Bactrocera dorsalis Hendel	Climex	None	Field data + museum database + Scientific articles	De Villiers et al., 2016
Bactrocera dorsalis Hendel	Climex	None	EPPO + Scientific articles	Stephens et al., 2007
Bactrocera dorsalis Hendel	Maxent	AUC	GBIF + CABI + Scientific articles	Dong et al., 2022
Bactrocera dorsalis Hendel	Maxent	AUC	Field data	Magagula et al., 2015
Bactrocera dorsalis Hendel	Climex	None	Inaccessible	Wang, JunWei et al., 2010
Bactrocera dorsalis Hendel	Maxent, Climex and Ensemble (Maxent + Climex)	AUC + TSS	GBIF + Scientific articles	Ullah, Zhang, Gul, Hafeez, Desneux, & Qin, 2023
Bactrocera dorsalis Hendel	Climex	None	Inaccessible	Hou, 2005
Bactrocera dorsalis Hendel	Maxent	AUC + TSS	Scientific articles + Expert communication	Hill & Terblanche, 2014
Bactrocera dorsalis Hendel	Maxent + Bioclim + Domain + Garp (separate)	AUC + Kappa	GBIF + CABI + Scientific articles	Xia et al., 2024
Bactrocera dorsalis Hendel	Maxent	AUC	GBIF + Scientific articles	A. Wang et al., 2022

Bactrocera dorsalis Hendel	Climex	None	Unclear data origin, likely field data or scientific articles	Kim et al., 2020
Bactrocera dorsalis Hendel	Climex	None	CABI	Sridhar et al., 2014
Bactrocera dorsalis Hendel	Maxent	AUC	GBIF + CABI + Scientific articles	Qin et al., 2019
Bactrocera zonata	ILCYM - Insect Life cycle	None	Unclear	Choudhary et al., 2021
Bactrocera zonata	Climex	AUC	Articles + CABI + EPPO	Ni et al., 2012
Bactrocera zonata	Maxent	AUC	GBIF + CABI + Scientific articles	Zingore et al., 2020
Bactrocera zonata	Climex, Maxent & Ensemble (Climax + Maxent)	AUC	GBIF + EPPO + Scientific articles	Ullah, Zhang, Gul, Hafeez, Desneux, Qin, et al., 2023
Bactrocera zonata	Maxent	AUC	Field data	Mahmoud et al., 2020
Rhagoletis pomonella Walsh, 1867	Climex	None	EPPO + Scientific articles	Geng et al., 2011
Rhagoletis pomonella Walsh, 1867	Maxent and Climex	AUC, Omission rates, AICc	GBIF + Scientific articles	Kumar et al., 2016
Rhagoletis pomonella Walsh, 1867	Maxent & BRT	AUC	GBIF + Scientific articles	Godefroid et al., 2015
Dendrolimus sibiricus Chetverikov, 1908	Climex	None	Scientific articles	Möykkynen, Timo & Pukkala, Timo, 2014
Spodoptera frugiperda	Maxent	AUC	GBIF	Znidarsic et al., 2024
Spodoptera frugiperda	Climex	None	GBIF + iNaturalist + ASCAN	Weinberg et al., 2022
Spodoptera frugiperda	Maxent	AUC	GBIF + CABI + Scientific articles + grey literature	Jiang et al., 2022

Spodoptera frugiperda	Maxent	AUC	GBIF + CABI + Scientific articles	R. Wang, Jiang, et al., 2020
Spodoptera frugiperda	Maxent	AUC	GBIF + CPC + Scientific articles	J. Fan et al., 2020
Spodoptera frugiperda	Maxent	AUC	GBIF + CPC	Baloch et al., 2020
Spodoptera frugiperda	Maxent	TSS	GBIF + Scientific articles	Liu et al., 2020
Spodoptera frugiperda	Ensemble model	AUC & TSS	GBIF + CABI + Scientific articles + official dataset	H. Zhao et al., 2023
Spodoptera frugiperda	Maxent	AUC, TSS, Kappa	GBIF + field data	S. Fan et al., 2020
Spodoptera frugiperda	Maxent	AUC	GBIF + CABI + Scientific articles	Zacarias, 2020
Spodoptera frugiperda	Climex	None	GBIF + Plantwise + Scientific articles	Ramirez-Cabral et al., 2017
Spodoptera frugiperda	Ensemble model	AUC & TSS	GBIF + CABI + Scientific articles + expert communication	Early et al., 2018
Spodoptera frugiperda	Maxent	AUC	GBIF	Karuppannasamy et al., 2024
Spodoptera frugiperda	Maxent	AUC	GBIF + CABI + field data + Scientific articles	Barkessa et al., 2024
Spodoptera frugiperda	Maxent	AUC	GBIF + FAO	Abdel-Rahman et al., 2023
Spodoptera frugiperda	Maxent	AUC	Field data	Cokola et al., 2020
Thaumatotibia leucotreta Meyrick	Maxent	AUC	GBIF + CABI + EPPO	X. Li et al., 2022
Thaumatotibia leucotreta Meyrick	Ensemble model	Kappa, AUC, TSS, Correlation coefficients and Correct Classificaiton R	GBIF + CABI + EPPO	X. Li et al., 2023

Bactericera cockerelli Sulc, 1909	Maxent	AUC, Bayesian information criterion, Omission rate	GBIF + EPPO + report	Wan et al., 2020
Bactericera cockerelli Sulc, 1909	Climex	None	GBIF, EPPO, CABI, Scientific articles	Suwandharathne et al., 2023
Bursaphelenchus xylophilus	GARP	None	Official dataset	Y.-H. Chen, 2009
Bursaphelenchus xylophilus	Maxent	AUC	Official dataset	Ouyang et al., 2022
Bursaphelenchus xylophilus	Maxent	AUC	GBIF + CABI + Official websites + Articles	Xiao et al., 2024
Bursaphelenchus xylophilus	Maxent	Inaccessible	Inaccessible	J. Zhao et al., 2023
Bursaphelenchus xylophilus	Maxent	AUC	Field data + Articles + Official dataset	Gao, Liu, Li, et al., 2023
Bursaphelenchus xylophilus	Maxent	AUC	GBIF + Articles + CABI + Official dataset	Gao, Liu, Zhao, et al., 2023
Bursaphelenchus xylophilus	Maxent	AUC	Field data	H. Li et al., 2022
Bursaphelenchus xylophilus	Maxent	AUC	Scientific Articles	Hirata et al., 2017
Bursaphelenchus xylophilus	Maxent & Climex	AUC	Official dataset	L. Chen et al., 2024
Bursaphelenchus xylophilus	Maxent	AUC	GBIF, official dataset	Tang et al., 2021
Bursaphelenchus xylophilus	Maxent	AUC	Official dataset	J. Wang et al., 2023
Bursaphelenchus xylophilus	Maxent	AUC	EPPO + Articles + Grey literature	Estay et al., 2014
Bursaphelenchus xylophilus	Maxent	AUC	Official websites + Grey literature + Scientific articles	Ikegami & Jenkins, 2018

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Supplementary Material 2: Details on Data, Model, Assessment, and Prediction following the ODMAP protocol recommended in Zurell et al., (2020) for SDMs.

Overview

We used an ensemble modelling approach applied to presence-only data, largely adapted from Valavi et al., (2022), using the 5 modelling methods and settings that were identified in that study as performing the best when combined. Scripts had already been adapted by Meynard et al., (2023) to use the most up-to-date packages, particularly since rgdal has been abandoned. Environmental layers were downloaded from Chelsa (Karger et al., 2017) and up-scaled to a coarser resolution 20 times that of the original, which corresponds to 10 min resolution (roughly 18 km at the equator). Scripts applied here are therefore a re-adaptation from this last publication, and can be found in the archive: https://tinyurl.com/yc29szae.

Authorship

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- Title: Effects of modelling choices on invasive species risk assessment using species distribution models: lessons from the psyllid vectors of Citrus Huanglongbing
- DOI:

Model objective

- Model objective: Forecast and transfer
- Target output: Potential habitat suitability for invasive species introduction

Taxon

- (i) Huanglongbing disease, (ii) insect psyllid vectors, and (iii) insect parasitoid of the vectors

Location

- Global

Scale of Analysis

- Spatial extent (Long/Lat): Longitude 90º E - 90º W, Latitude 90º S - 90º N
- Spatial resolution: 10 min resolution (approximately 18 km resolution)
- Temporal extent: Period of climate normals (1981-2010)
- Temporal resolution: three decades
- Boundary: Natural

Biodiversity data

- Observation type: field survey, literature search, citizen science and standardized monitoring

- Response data type: Presence-only

Type of Predictors

- Predictor types: Climatic Variables (BioClim), extracted from Chelsa V2.1 released in 24-05-2021 (Karger et al., 2017).

Conceptual model / Hypotheses

- Different key choices in SDM modelling can have different and relevant impacts in early risk assessments, not only in terms of performance, but also in terms of identification of areas at risk and management recommendations. We focus on choices that can be improved in early risk assessments to identify the lower-effort / higher gain strategies: improving occurrence data quality, native versus native and invaded calibration range, single modelling algorithm (MaxEnt) versus ensemble modelling, variable selection and background versus pseudo-absence points. Secondly, we compared standard statistical metrics based on whole-range performance (AUC, TSS, Boyce), with a statistics that focuses on the confirmed occurrences in the invaded range (invasion false negative rate = iFNR). Finally, we used a index of range overlap (Jaccard index) to evaluate whether small and large differences in the performance statistics are reflected in large differences in the predicted areas at risk.

Assumptions

- We used classic SDM strategies, therefore the same assumptions apply: that the occurrences used as input are correct and represent the range of environmental conditions that the species can occupy; that there is niche conservatism across the full range.

SDM Algorithms

- Algorithms: SDMs were fitted using five different algorithms, as recommended in (Valavi et al., 2022): MaxEnt, generalised additive models (GAM), LASSO, boosted regression trees (BRT), and random forests (RF).

- Model complexity: varied depending on the algorithm, but settings correspond to those recommended in (Valavi et al., 2022).

- Ensemble modelling: we combined the five SDMs to ensemble SDM predictions, using the average.

Workflow

- We ran the 7 different SDM modelling strategies (REF, DEF, OCC, NAT, BACK, AUTO, MAX, see Table S2.1 below), each with a different combination of modelling choices regarding data quality, model calibration range, background or pseudo-absence points handling, variable selection, and modelling algorithms.

- We performed 5 cross validations for each modelling strategy, repeating the SDMs using geographical data partitioning using the package blockCV (Valavi et al., 2019).

Software

- Software: QGIS, R, Packages: Stars, Terra
- Data availability: all data needed to run the scripts is available in an archive https://tinyurl.com/yc29szae
- Code availability: all scripts needed to replicate the modelling are available in the same archive as the data https://tinyurl.com/yc29szae

Data

Biodiversity data

- Taxon names: *Liberibacter africanus, Trioza erytreae, Tamarixia dryi, Psyllaephagus pulvinatus, Liberibacter asiaticus, Liberibacter americanus, Diaphorina citri, Tamarixia radiata, Diaphorencyrtus aligarhensis.*
- Taxonomic reference system: for *Diaphorina citri*: Kuwayama, 1908; and for *Trioza erytreae*: Del Guercio, 1918.

  Full references:

  Kuwayama Sh. 1908 - Die Psylliden Japans. I. Transactions of the Sapporo Natural History Society 2: 149-189.

  Del Guercio G. 1918 - Note ed osservazioni di entomologia agraria. Il cecidio delle foglie del limone ed il suo cecidozoo in Eritrea. Agricultura Coloniale 1918: 167-169.
- Ecological level: Species
- Data source: Species occurrence data extracted from GBIF, INaturalist, EPPO, scientific literature, public official monitoring reports or data repositories and from contact with experts. Detailed information in Supplementary Material S3.
- Scaling & Sample size: The occurrence dataset was up-scaled to match the spatial resolution of the environmental layers (10 min resolution). For each grid cell, the species was recorded as present if one or more occurrence points were recorded inside the cell. Two different occurrence datasets were used (Supplementary Material S3) to illustrate modelling choices regarding data extraction and cleaning. After up-scaling, this results in the following number of occurrences: (1) basic GBIF dataset - 241 total occurrences, with 177 occurrences for *D. citri* and 64 occurrences for *T. erytreae*; (2) high-quality dataset - 1198 total occurrences (843 for *D. citri* & 355 for *T. erytreae*).
- Mask: Antarctica and the oceans were removed from our projections; the rest of the globe is included.
- Absence data collection: no absence data was collected.

- Pseudo-absence and background data: 10,000 background data points were first randomly placed within a 1,000 km buffer around occurrence points (this means that the extent of the background also varied, for example if we limited occurrence to native-only versus native + invaded) at the resolution of the environmental layers (i.e. there cannot be two background points in the same grid cell). All modelling strategies using background data used this random sample (Table S2.1), which is intended to represent the long-term (multiple generation) accessible area (Barve et al., 2011). For modelling strategies using pseudo-absences, we eliminated from the background points those that were too close (< 100km) from confirmed presences. This was intended to represent population dispersal distances, therefore eliminating from the potential background sampling the areas that are deemed within reach from confirmed occurrences. Pseudo-absences were therefore background points located more than 100 km from any recorded occurrence, but within a 1,000 km radius.

- Errors and biases: details on data compilation and cleaning can be found in Supplementary Material S3. The basic GBIF dataset has all the classic biases described for broadly available occurrence data (Zizka et al., 2020). In the high-quality dataset we dedicated a significant effort to eliminate incorrect occurrences (placed in areas where local psyllid experts had no knowledge of its introduction for example, or where a photographic record showed a misidentification), and to add records in areas that are already well-known because of the economic damages caused by HLB.

Data partitioning

- Selection of training data: we adopted a fivefold spatial cross-validation approach to measure model predictive performance. The species distribution range was divided into 10 x10 spatial blocks using the "blockCV" R package (Valavi et al., 2019). We assigned the 100 blocks to five folds via 50 iterations for a balanced fold assignment.

- Training data: in a spatial five-fold cross-validation, one spatial block is left out for validation, while the other four are used for training. There were five blocks, each used in turn as training or validation.

- Validation data: see explanation above.

- Test data: we did not have an independent test dataset.

- Statistics: for model performance, we used different complementary model performance metrics based on all occurrences (native and invaded range, depending on what was used in the calibration): AUC, TSS, Boyce, Kappa, sensitivity, specificity, false negative rate, invasive false negative rate. Additionally, we calculated the Jaccard index (Jaccard, 1908) comparing the projected range for each modelling strategy to a reference modelling strategy.

Environmental data/Predictor variables

- Predictor variables: Climatic data (1980-2010): bio1 - Average Annual Mean Temperature; bio2 - Average Mean Diurnal Range (Mean of monthly (max temp - min temp)); bio3 = Average Isothermality; bio4 = Average Temperature Seasonality; bio5 = Max Temperature of Warmest Month; bio6 = Average Min Temperature of Coldest Month; bio7 = Average Temperature Annual Range; bio8 = Average Mean Temperature

of Wettest Quarter; bio9 = Average Mean Temperature of Driest Quarter; bio10 = Average Mean Temperature of Warmest Quarter; bio11 = Average Mean Temperature of Coldest Quarter; bio12 = Average Annual Precipitation; bio13 = Average Precipitation of Wettest Month; bio14 = Average Precipitation of Driest Month; bio15 = Average Precipitation Seasonality (Coefficient of Variation); bio16 = Average Precipitation of Wettest Quarter; bio17 = Average Precipitation of Driest Quarter; bio18 = Precipitation of Warmest Quarter; bio19 = Precipitation of Coldest Quarter; GDD0 = Growing degree days at 0°C; GDD5 = Growing degree days at 5°C; GDD10 = Growing degree days at 10°C; NPP = Net Primary Productivity

- Data sources: data was extracted from Chelsa Climate (Karger et al., 2017), available at: https://chelsa-climate.org/downloads

- Spatial resolution: The original data was at 30 arc seconds resolution (1km^2 at the equator), but was up-scaled to a resolution 20 times coarser (10 min resolution, roughly 18 km at the equator).

- Extent of raw data: -180, -90, 180, 84

- Coordinate reference system: EPSG:4326 - WGS 84

- Temporal extent: Period of climate data (1981-2010)

- Temporal resolution: Single time period, 30 years averaged

- Data processing: We up-scaled by 20 the raw environmental data (30 arc seconds) to match the model's resolution (10 min resolution). For the upscaling process, we calculated the mean value of the cells using a resampling. Oceans and Antarctica were removed using the continents boundary vector map "countriesHigh" from the R package rworldxtra (http://www.naturalearthdata.com/downloads/10m-cultural-vectors/)

Model:

Table S2.1: Types of models that we compared. The first two model types are opposite alternatives: (1) The simple default model (DEF), represents the easiest and simplest options that are often used in early risk assessments; (2) The reference model (REF), represents the higher standard model; models (3) to (7) use the same calibration details as in the reference model, except for the one characteristic that is highlighted: (3) use of the low quality input occurrence dataset (OCC), (4) native-only occurrences during calibration (NAT); (5) use of background points instead of pseudo-absences (BACK); (6) use of automated variable selection instead of pre-determined variables (AUTO); (7) and use of MaxEnt alone instead of ensemble modelling (MAX). All modelling details can be found in the methods section and scripts.

Model Type	Modelling Strategies
(1) Default (DEF)	Standard cleaning of publicly available dataset (GBIF only), only native occurrences used for calibration, use of default background points, automated variable selection, Maxent-only

(2) Reference (REF)	High quality dataset (thorough cleaning and consultation with taxonomic experts), all available occurrences are used in calibration (native + invaded), use of pseudo-absences, Pre-selected variables, ensemble modelling following Valavi et al 2022
(3) Basic Occurrence dataset (OCC)	**Standard cleaning of publicly available dataset (GBIF only)**, all available occurrences used, use of pseudo-absences, Pre-selected variables, ensemble modelling
(4) Native only calibration area (NAT)	High quality dataset, **native-only occurrences used**, use of pseudo-absences,Pre-selected variables, ensemble modelling
(5) Background points (BACK)	High quality dataset, all available occurrences used, **use of background points**, Pre-selected variables, ensemble modelling
(6) Automated Variable Selection (AUTO)	High quality dataset, all available occurrences used, use of background points, **automated variable selection**, ensemble modelling
(7) Maxent only (MAX)	High quality dataset, all available occurrences used, use of background points, Pre-selected variables, **Maxent-only**

<Quantification of Novelty>

Model

Predetermined Variables

We started with the list of variables presented in "environmental predictors" above. However, all modelling strategies, except the one with automated variable selection (AUTO), used a subset of predetermined biologically relevant predictor variables identified by (i) scanning the literature for the bioclimatic variables most associated with the studied species (Aidoo, Souza, da Silva, Santana Jr, et al., 2022; Aidoo, Souza, da Silva, Santana Junior, et al., 2022; Godefroid, 2023), and (ii) including at least one variable representing the average, seasonality, and extremes (e.g., in the coldest quarter, in the driest quarter) of both temperature and precipitation.

Based on these criteria, we selected the following variables: Temperature Seasonality (Bio4), Minimum Temperature of Coldest Month (Bio6), Mean Temperature of Wettest Quarter (Bio8), Mean Temperature of Warmest Quarter (Bio10), Precipitation of Driest Month (Bio14), Precipitation Seasonality (Bio15), Precipitation of Warmest Quarter (Bio18), and Precipitation of Coldest Quarter (Bio19). Pairwise correlations among these variables were assessed within the calibration range of each modeling strategy (REF, OCC, NAT). For both species, Bio4 was removed due to high correlation with (-0.89 and -0.78 respectively for *D. citri* and *T. erytreae*) (Spearman $r > 0.7$) (Supplementary Material S4).

For the AUTO modelling strategy, the "data snooping" procedure (Dormann et al., 2013) was applied to GAM, following Meynard et al., (2017). This approach identifies the most informative predictors from the full set of environmental variables, reducing potential biases in model calibration (Supplementary Material S4).

Model settings

Relative data weight was calculated for each data point, to take into account the uneven number of occurrences and absence points. The weight values (weight_col) were calculated so that the sum of each class would be the same, bringing the weight of presences and pseudo-absences/background data to 50% for each category (Barbet-Massin et al., 2012; Valavi et al., 2022). The other settings follow in general Valavi et al., (2022), with a few exceptions. Most notably, we limited the complexity of GAM models using a maximum number of knots for each smooth term of k = 4; and we changed the background / pseudo-absence strategy, as explained in the different alternative modelling strategies. Below are details for each modelling algorithm.

1. GAM (Generalized Additive Model)

Library: mgcv

Function: gam

Formula: occ ~ s(bio6, k=4) + s(bio19, k=4) + s(bio8, k=4) + s(bio14, k=4) + s(bio15, k=4) + s(bio18, k=4) + s(bio10, k=4)

Family: binomial

Weights: data[[weight_col]]; 50% weight for all occurrences

2. BRT (Boosted Regression Trees)

Package: gbm

Function: gbm.step()

Predictors: Environmental variables (e.g. "bio6", "bio19", "bio8", "bio14", "bio15", "bio18", "bio10")

Response Variable: Occurrences

Family: "bernoulli"

Site Weights: data[[weight_col]]; 50% weight for all occurrences

Tree Complexity: 5

Learning Rate: 0.001

Number of Trees: 50

Cross-validation Folds: 4

Maximum Trees: 10,000

3. LASSO (Least Absolute Shrinkage and Selection Operator)

Quadratic Transformation Applied to Predictors

Function: cv.glmnet()

Response Variable: Occurrence

Family: "binomial"

Alpha: 1 (LASSO penalty)

Weights: data[[weight_col]]; 50% weight for all occurrences

Standardization: TRUE

Predictor Matrix: sparse.model.matrix(~. -1)

4. Random Forest

Formula: occ ~ bio6 + bio19 + bio8 + bio14 + bio15 + bio18 + bio10

Number of Trees (ntree): 1000

Sampling Strategy:

Presence (occ == 1) and Background (occ == 0) balanced

sampsize = c("0" = prNum, "1" = prNum)

Sampling Replacement: TRUE

5. Maxent

Library: dismo

Function: maxent()

Predictors: Environmental variables (e.g. "bio6", "bio19", "bio8", "bio14", "bio15", "bio18", "bio10")

Presence Weights: ifelse(data$occ == 1, 100, maxent_weight)

Cross-validation Folds: k = 5

Train-Test Splitting Based on Folds

Evaluation Function: evaluate()

Prediction Applied to Raster Stack<Model settings (extrapolation)

6. Final Ensemble Model

Mean of Predictions from all 5 models:

Model estimates

<Coefficients>

Model selection - model averaging - ensembles

Model selection: Ensemble of models using the average of predicted probabilities for all 5 modelling algorithms.

Analysis and Correction of non-independence

No autocorrelation analysis. MESS was carried out, not presented here.

Threshold selection

For threshold value (when needed to calculate TSS and other statistics), the optimal.thresholds() function from the PresenceAbsence R package was used to determine the presence-absence classification threshold. The method that maximizes sensitivity plus specificity was applied.

For mapping in figure 6, we also used quantiles based on the confirmed occurrences along the the reference model's output predicted values. For example, the lower 5% quantile contains 5% of the occurrences in the lowest predicted values. This lower 5% quantile therefore contains occurrences that are in rather marginal habitats for the species. This allowed defining the following risk categories based on other quantiles: 0-5% - no risk; 5-25% low risk; 25-50% medium risk; 50-75% high risk; 75-100% very high risk (Figure 6 in the manuscript). As seen in this figure, the optimal threshold defined above follows a similar distribution that the 5% quantile threshold, although some differences can be seen in specific areas.

Assessment

Performance statistics

For accessing the model's performance we used the following statistics: AUC, TSS, Kappa, Sensitivity, Specificity, BOYCE index, False Negative rate (FNR), Invasive False Negative rate and Jaccard index (Table S2.2). Many of these follow exactly the same pattern, so we only present results for AUC, TSS and Boyce in the main text, along with FNR in the invasion range, and Jaccard.

Table S2.2: Description and range of the different performance metrics.

Metric	**Description**	**Range**	**Key Use Case**
AUC	Measures overall discrimination ability	0 - 1	Model evaluation independent of a threshold

TSS	Balances sensitivity & specificity	-1 to 1	Optimizing threshold selection
Kappa	Accounts for chance agreement.	-1 to 1	Evaluating classification reliability.
Sensitivity	Measures ability to detect presence.	0 - 1	Important in conservation (avoiding false negatives).
Specificity	Measures ability to detect absence.	0 - 1	Avoiding false positives in risk assessments.
Boyce Index	Presence-only model validation.	-1 to 1	SDM model evaluation for presence-only data.
False Negative Rate (FNR)	Proportion of missed presences.	0 - 1	Avoiding underestimation of species distribution.
Invasive False Negative Rate (IFNR)	FNR specific to invasive species.	0 - 1	Avoiding underestimation species invasive ability
Jaccard Index	Measures agreement in binary classification.	0 - 1	Comparing predicted distributions between different model outputs

Plausibility check

Response shapes: Check plausibility of the relations of the ecological variables, in comparison with field knowledge, experts and the bibliography.

Expert judgement: Resulting maps observation

Prediction

Prediction output

Raw predictions in the range of probabilities (0-1); reclassified as 0 or 1 if presence-absence predictions required.

Uncertainty quantification

See different modelling strategies explored in Table S2.1.

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Supplementary Material 3: Occurrence Points, Data Retrieval and Cleaning

Here we wanted to compare a basic occurrence dataset, quickly compiled and cleaned using standard procedures, with a more invested dataset complemented through an in-depth search and consultation with global and local psyllid experts. We also took advantage of a few well-known highly specific interactions to compile this dataset. Since both species of interest transmit very specific variants of HLB and have obligate parasites species which are themselves highly specific, we also used occurrence data for the HLB variants and the parasitoids, as strong indicators of the presence of one or the other psyllid species (see below).

Two occurrence datasets of the insect vectors were compiled: (1) the basic occurrence dataset; (2) and a high-quality dataset. For both datasets, the occurrence records of the two insect vectors of the HLB disease worldwide, were searched. This included the three known bacteria strains responsible for the HLB disease (*Candidatus L. africanus*, *Candidatus L. asiaticus* and *Candidatus L. americanus*), the two known associated vector species *(T. erytreae* and *D. citri)*, and four predominant and specialized parasitoid species: *Tamarixia dryi*, (Urbaneja-Bernat et al., 2019), and *Psyllaephagus pulvinatus* (Pérez-Rodríguez et al., 2019), parasitoids of *T. erytreae*; *Tamarixia radiata* (Hoddle & Pandey, 2014) and *Diaphorencyrtus aligarhensis* (Bistline-East et al., 2015), parasitoids of *D. citri*. For each vector species, the corresponding presence records of associated bacteria strain or parasitoid species were merged together into a single dataset of the vector species occurrence.

For the basic occurrence dataset, we downloaded the occurrences, using only the public dataset GBIF: the Global Biodiversity Information Facility, (2024) (Available from http://www.gbif.org, accessed on 18 January of 2024). A total of 3,459 records were extracted (750 for *T. erytreae* and 2,709 for *D. citri*).

This preliminary dataset was cleaned using standard procedures by eliminating occurrences with obvious geographic coordinates errors (e.g. reported high degree of uncertainty, mismatch of coordinates and reported region, coordinates calculated from the region's centroid, coordinates located in the sea), and eliminating duplicates. The occurrence data was then up-scaled by aggregating occurrence records inside the same grid cells at the same resolution than the environmental layers used during the modelling (10 min resolution, ~18 km), which reduced the data to a total of 241 occurrences (64 for *T. erytreae* and 177 for *D. citri*) (Fig.S3.1).

For the high-quality dataset, occurrence records were extracted from the following publicly available datasets: GBIF: the Global Biodiversity Information Facility (2024) (Available from http://www.gbif.org, accessed on 18/01/2024); iNaturalist (Available from https://www.inaturalist.org/, accessed on 18/01/2024); EPPO Global Database (Available from https://gd.eppo.int/, accessed on 18/01/2024); The Commonwealth Agricultural Bureau International (Available from https://www.cabi.org/, accessed on 18/01/2024In addition, we used monitoring data from the websites of the Province of Galicia (available from https://mediorural.xunta.gal/es/temas/agricultura/sanidad-vegetal/organismos-nocivos-de-cuarentena, accessed 18/01/2024); the Portuguese Directorate General of Food and Veterinary Medicine (available from https://www.dgav.pt/plantas/conteudo/sanidade-vegetal/inspecao-fitossanitaria/informacao-fitossanitaria/trioza-erytreae/, , accessed on 18/01/2024). Additionally, we performed extensive and detailed bibliographic research to find occurrence records from all types of scientific literature and official reports on a global scale. For the literature search, we used Google, Web of Science, Google Scholar and Scielo, and we included texts in English, Spanish, Portuguese and French. Additionally, we contacted various

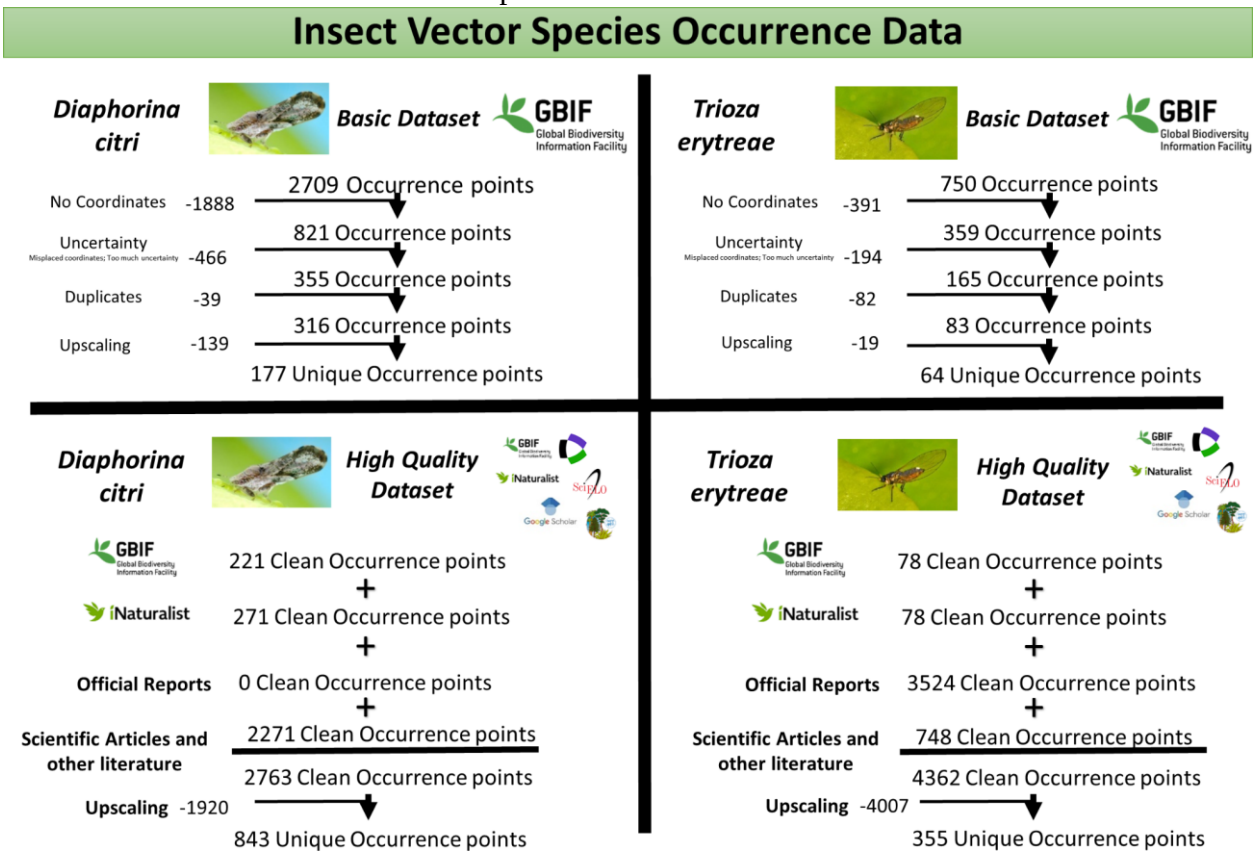
researchers for additional help in data retrieval and validation, including authors of previous papers where their own dataset included records we could not verify. We also contacted several local experts in South America, where there were few publications that included precise occurrence records, despite the fact that HLB is well known to occur in the region.

This dataset also underwent an intensive data cleaning process. This included removing records with no coordinates, points with high precision error (over 10km) and records with coordinates extracted from a country's centroid. Records with no coordinates, but with a specified location, were not removed if the location (e.g city) was small enough to maintain the required precision (less than 10km radius). For these cases, the centroids of the location were used. In addition, all points were checked for coordinate placement errors using QGIS by plotting them on a world map, with expert assistance. The reference of each record was traced back to its original source, to verify the reliability of every record. Finally, duplicate occurrence points were removed. Errors found included country's centroids as occurrence points, such as for T. erytreae in the center of Spain and for D. citri in Madagascar. Other errors included a misidentification found for a D. citri record in Cyprus, T. erytreae records in South Africa mistakenly introduced as D. citri, and nonsensical records such as D. citri in the Chilean altiplano.

After cleaning, we had a total of 7,125 records (4,362 for *T. erytreae* and 2,763 for *D. citri*). To match the large scale used in our models, the occurrence data was upscaled by aggregating occurrence records within the same cells of the model (20x20), which reduced to total occurrence points to 1,198 points (355 for *T. erytreae* and 843 for *D. citri*) (Fig.S3.1).

Note that the occurrence dataset, which includes the two vector species and HLB global occurrences, is available in the archive https://tinyurl.com/yc29szae, including the accession numbers, DOIs or other source links for each record.

Figure S3.1 – Graphical representation of the occurrence data extraction and cleaning process of the two datasets for the two vector species.



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Supplementary Material 4: Description of predictors used in the different modelling strategies for both species.

Only those selected in one of the modelling efforts are included in this table.

Variable Selection	Species	Environmental Variables Used
Pre-determined predictors	Both	**Bio6** - Min Temperature of Coldest Month (°C); **Bio8** - Mean Temperature of Wettest Quarter (°C); **Bio10** - Mean Temperature of Warmest Quarter (°C); **Bio14** - Precipitation of Driest Month (°C); **Bio15** - Precipitation Seasonality (%); **Bio18** - Precipitation of Warmest Quarter (mm); **Bio19** - Precipitation of Coldest Quarter (mm)
Automated Variable Selection (AUTO)	*Trioza erytreae*	**Bio1** - Annual Mean Temperature; **Bio2** - Mean Diurnal Range (°C); **Bio4** - Temperature Seasonality (°C); **Bio5** - Max Temperature of Warmest Month (°C); **Bio11** - Mean Temperature of Coldest Quarter (°C); **Bio13** - Precipitation of Wettest Month (mm); **Bio14** - Precipitation of Driest Month (mm); **Bio15** - Precipitation Seasonality (%); **Bio18** - Precipitation of Warmest Quarter (mm); **Bio19** - Precipitation of Coldest Quarter (mm)
	Diaphorina citri	**Bio1** - Annual Mean Temperature (°C); **Bio2** - Mean Diurnal Range (°C); **Bio5** - Max Temperature of Warmest Month (°C); **Bio11** - Mean Temperature of Coldest Quarter (°C); **Bio15** - Precipitation Seasonality (%); **Bio16** - Precipitation of Wettest Quarter (mm); **Bio17** - Precipitation of Driest Quarter (mm); **Bio18** - Precipitation of Warmest Quarter (mm); **Bio19** - Precipitation of Coldest Quarter (mm)