

Article

Using Species Distribution Models (SDMs) to Estimate the Suitability of European Mediterranean Non-Native Area for the Establishment of *Toumeyella Parvicornis* (Hemiptera: Coccidae)

Nicolò Di Sora ^{1,†} , Roberto Mannu ^{2,†} , Luca Rossini ^{1,3,*} , Mario Contarini ^{1,*}, Diego Gallego ⁴ 
and Stefano Speranza ¹ 

¹ Dipartimento di Scienze Agrarie e Forestali, Università degli Studi della Tuscia, Via San Camillo de Lellis snc, 01100 Viterbo, Italy

² Dipartimento di Agraria, Università degli Studi di Sassari, Viale Italia 39A, 07100 Sassari, Italy

³ Service d'Automatique et d'Analyse des Systèmes, Université Libre de Bruxelles, v. F.D. Roosevelt 50, CP 165/55, 1050 Brussels, Belgium

⁴ Department of Ecology, University of Alicante, Carretera San Vicente del Raspeig s/n, 03690 San Vicente del Raspeig, Alicante, Spain

* Correspondence: luca.rossini@unitus.it (L.R.); contarini@unitus.it (M.C.)

† These authors contributed equally to this work.

Simple Summary: Predicting species distribution is a fundamental step for setting up opportune control actions. The suitability of the environment for the establishment of the species is even more important in case of invasive insects, such as *Toumeyella parvicornis* (Hemiptera, Coccidae). This species is a soft scale insect native to North America recently introduced in Italy and in France, where it established and spread, causing harmful infestations on stone pine (*Pinus pinea* L.) plants. Some aspects of its biology, such as the several overlapped generations and the high fecundity, may contribute to make it a successful invasive species when in a suitable environment. This is supported by the observations carried out in Central Italy, where the climate and environmental conditions seem suitable for the species to develop. To prevent further spread across the Mediterranean basin, it would be helpful to identify the most suitable areas by considering bioclimatic variables, as is commonly carried out in case of invasive species. We prepared potential pest distribution maps of European areas by utilizing Species Distribution Models. This information adds further detail to the report recently published by the European Food Safety Authority (EFSA). The areas with the highest suitability for the species are located along the coasts, where most Mediterranean pines occur. This correspondence suggests a high risk of widespread dispersal and provides useful information for implementing management strategies of this damaging pest.

Abstract: The pine tortoise scale, *Toumeyella parvicornis*, is an insect native to the Nearctic region that is able to infest several *Pinus* species. It can cause weakening, defoliation and, at high infestation levels, tree death. After its first report in Italy in 2015, the pest spread rapidly over the surrounding areas and was reported in France in 2021. Due to the threat that this pest poses to pine trees, the suitability of European Mediterranean basin areas for *T. parvicornis* at different spatial scales was estimated by constructing species distribution models (SDMs) using bioclimatic variables. Our results showed that several coastal areas of the Mediterranean basin area could be suitable for *T. parvicornis*. Based on performance assessment, all the SDMs tested provided a good representation of the suitability of European Mediterranean non-native area for *T. parvicornis* at different spatial scales. In particular, most of the areas with a medium or high level of suitability corresponded to the geographical range of distribution of different *Pinus* spp. in Europe. Predicting the suitability of European Mediterranean areas for *T. parvicornis* provides a fundamental tool for early detection and management of the spread of this pest in Europe.

Keywords: pine tortoise scale; alien species; stone pine; species distribution models; biological invasion



Citation: Di Sora, N.; Mannu, R.; Rossini, L.; Contarini, M.; Gallego, D.; Speranza, S. Using Species Distribution Models (SDMs) to Estimate the Suitability of European Mediterranean Non-Native Area for the Establishment of *Toumeyella Parvicornis* (Hemiptera: Coccidae). *Insects* **2023**, *14*, 46. <https://doi.org/10.3390/insects14010046>

Academic Editor: Andrés Millán

Received: 2 December 2022

Revised: 23 December 2022

Accepted: 30 December 2022

Published: 3 January 2023



Copyright: © 2023 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

1. Introduction

The pine tortoise scale, *Toumeyella parvicornis* (Cockerell) (Hemiptera: Coccidae), is a sap-sucking insect infesting several species belonging to *Pinus* genera (Pinaceae) [1,2]. The insect mainly lives on the crown [1], and adult females (Figure 1) tend to colonize more small twigs than needles [3,4]. *Toumeyella parvicornis* generally overwinters as fertilized adult females [5] and are able to complete at least 1–2 generations per year in its native range [1]. Nymphs develop to the adult stages through three instars in female individuals and four in males. Adults exhibit a marked sexual dimorphism with wingless females. Except for the first preimaginal stage, usually defined as “crawler”, *T. parvicornis* is sessile [2,6].



Figure 1. *Toumeyella parvicornis* adult female.

Toumeyella parvicornis originates from the Nearctic region, where it was first described in Florida [7] and then reported in the northern part of the USA [7–10], in Canada [11], and in Mexico [12]. In recent years, *T. parvicornis* has been established in other countries outside its native area, including the Turks and Caicos Islands [2], Puerto Rico [13], and Europe [14]. The first report of this insect in Europe was in Italy [14], where the first outbreak was documented on *Pinus pinea* L. trees in the Campania region. Recently, *T. parvicornis* has rapidly spread throughout Italy [4,15], and in 2021, it was reported in France [15].

The rapid expansion of the pine tortoise scale in Europe is generating serious concerns throughout the scientific community. In fact, *T. parvicornis* attacks cause substantial weakening and defoliation of pine trees that can lead to tree death when severe infestations occur [16]. *Toumeyella parvicornis* populations, which may rapidly reach a high density, increase the risk of accidental branch falls, representing a great concern for citizens' safety and health in urban green areas. In addition, *T. parvicornis* produces a large amount of honeydew, which can disturb urban park users especially in urban environments [16], where pine trees often have a fundamental historical and architectural value [4,17,18], since it covers structures and monuments. The implementation of monitoring strategies is of fundamental importance mainly because pine trees are very common in urban areas, where control actions can be strongly limited by European laws even when pest infestations can endanger the safety of citizens [19].

Although *Pinus banksiana* Lamb represents the main host of *T. parvicornis* in the Nearctic region [11,20], this insect can develop on different *Pinus* species in non-native areas. For instance, in the Turks and Caicos Islands, the Caribbean pine [*Pinus caribaea* var. *bahamensis* (Grisebach) W. H. Barrett & Golfari] is the primary host of this pest [2], whereas in Europe

the stone pine (*Pinus pinea* L.) is its main host [6]. *Pinus pinaster* Aiton showed low susceptibility to pine tortoise scale, whereas *Pinus halepensis* Mill. was apparently not susceptible to its infestations [6].

Among different statistical and mathematical tools, Species Distribution Models (SDMs) represent the most widely used tool in the research field of ecology and conservation biology to assess the potential distribution of a species. In particular, SDMs facilitate our understanding of species-environment relationships and estimate species potential distribution also in areas where the species has not been observed yet [21–23].

Although SDMs do not report any information about the temporal dynamics of the diffusion of a species [24], they are widely used to make projections about the suitability of different geographical environments to invasive alien species [25–29], also in the case of small sample size [30].

Identifying the most suitable areas for an invasive species could actively support local authorities, technicians, and communities in defining the areas at risk for invasion and where surveillance should be improved. For this reason, the aim of this work was to estimate the potential suitability of European Mediterranean non-native areas for *T. parvicornis*. In particular, different SDM approaches were used to identify the potential spread of the pine tortoise scale in Italy and Europe on the basis of known distribution and bioclimatic variables. The comparison between different SDMs aimed to provide a better scenario of the potential distribution of this species in European Mediterranean areas.

2. Materials and Methods

2.1. Occurrence Records and Bioclimatic Variables

Geographic coordinates for *T. parvicornis* occurrences in Mediterranean Europe were obtained from literature and in Central Italy by direct monitoring in stone pine growing-areas. In particular, reports from the Regional Plant Protection Services of the Campania region [available at <http://agricoltura.regione.campania.it/> (accessed on 1 December 2022)] and the European and Mediterranean Plant Protection Organization (EPPO) database [15] were used to extract the occurrences of pine tortoise scale in Central Italy and Southern France, respectively. In Central Italy, records of *T. parvicornis* were also acquired by monitoring stone pine growing-areas and trees in urban parks of the Lazio region from December 2021 to January 2022. At first, sampling sites representing *P. pinea* growing-areas and urban trees were randomly chosen from a distribution map available for the Lazio region [31], and from the Google Earth software [available from <https://earth.google.com/web/> (accessed on 1 December 2022)]. At each selected location, *T. parvicornis* infestations were assessed by visually inspecting the trees for typical symptoms (i.e., presence of black mold on the crown, plant deterioration, yellowish and desiccated needles as shown in Figure 2). A monocular scope at 40× magnification was used to detect the insect on symptomatic plants, whereas needles and branches on the ground were examined to assess the presence of *T. parvicornis* adults and/or molting residuals. A total of 52 and 53 occurrence records for *T. parvicornis* were found in Italy and Europe, respectively (Supplementary materials Table S1).

2.2. Bioclimatic Variables

Nineteen bioclimatic variables were obtained from the WorldClim Global Climate Database (version 1.4) [<http://www.worldclim.org> (accessed on 1 December 2022)] as georeferenced raster files [32]. Georeferenced images with a spatial resolution of 30 arc-sec (~1 km²) and 2.5 arc-min (~4.5 km²) were used for modelling *T. parvicornis* potential distribution in Italy and Europe, respectively. Prior to the analysis, raster images were clipped to cover the same fixed area using QGIS software (version 3.24) [available at <http://qgis.org> (accessed on 1 December 2022)]. Multicollinearity among the bioclimatic variables was tested at a spatial resolution of 30 arc-sec (~1 km²) using the Pearson's correlation coefficients in order to remove the highly correlated variables ($R^2 > 0.80$ or $R^2 < -0.80$) before running the models (Supplementary materials Table S2). The multicollinearity tests led us to select only nine bioclimatic variables (Table 1).



Figure 2. Symptoms on *Pinus pinea* plants infested by *Toumeyella parvicornis*: dying tree (**up**) and infested twig with adult females, honeydew, and mold (**bottom**).

Table 1. List of bioclimatic variables considered for modelling. Variables used in the Species Distribution Models (SDMs) are reported in bold.

Variable	Description
BIO01	Annual Mean Temperature
BIO02	Mean Diurnal Temperature Range [Mean of monthly (max temp–min temp)]
BIO03	Isothermality (BIO02/BIO07) ($\times 100$)
BIO04	Temperature Seasonality (standard deviation $\times 100$)
BIO05	Max Temperature of Warmest Month
BIO06	Min Temperature of Coldest Month
BIO07	Temperature Annual Range (BIO05–BIO06)
BIO08	Mean Temperature of Wettest Quarter
BIO09	Mean Temperature of Driest Quarter
BIO10	Mean Temperature of Warmest Quarter
BIO11	Mean Temperature of Coldest Quarter
BIO12	Annual Precipitation
BIO13	Precipitation of Wettest Month
BIO14	Precipitation of Driest Month
BIO15	Precipitation Seasonality (Coefficient of Variation)

Table 1. Cont.

Variable	Description
BIO16	Precipitation of Wettest Quarter
BIO17	Precipitation of Driest Quarter
BIO18	Precipitation of Warmest Quarter
BIO19	Precipitation of Coldest Quarter

2.3. Species Distribution Modelling

Four different algorithms were used to estimate the potential distribution of *T. parvicornis* in Italy and Europe: Generalized Linear Model (GLM), Multivariate Adaptive Regression Splines (MARS), Random Forest (RF), and MaxEnt [33,34]. The models were implemented using the biomod2 package [35] in R software (version 4.1.3) [36].

The GLM, MARS and RF algorithms need pseudo-absence records in addition to occurrence points. Therefore, 1000 pseudo-absence records, located at least 500 m apart from the occurrence points, were generated. This process was repeated 3 times, thus obtaining three different datasets of pseudo-absences for each algorithm. The default model settings in biomod2 were used for fitting GLM, MARS, and RF algorithms.

The MaxEnt algorithm can be applied considering presence-only records instead of presence-absence data [37], which implies the use of complex nonlinear functions [38]. Model complexity can be controlled by a set of parameters named Feature Classes (FCs) and Regularization Multiplier (RM). The FCs aim to improve model fitting [38] and consist of a transformation of the original predictor variables that can be used either separately or in combination [i.e., linear (L), quadratic (Q), hinge (H), product (P), and threshold (T)], whereas the RM aims to reduce overfitting [39].

Parameterization in MaxEnt is necessary as models fitted with default settings often lead to skewed projections if compared to the parametrized models [39–42]. For this reason, twenty different models were fitted by considering 4 FC combinations (L, LQ, LQH, H) and RM values ranging from 1 to 5. All the recorded occurrences available and 1000 randomly positioned background points were used for model fitting. The model best fitting the data was selected based on the Akaike's Information Criterion with a small sample size correction (AICc) [43], which reflects both model goodness-of-fit and complexity [44]. Conventionally, the lowest AICc value indicates the best fitting model for the dataset considered [44,45]. Parameterization was carried out using the ENMeval package [45] in R software.

2.4. Model Evaluation and Predictions

For all the tested models, 80% of the data was used for calibration, whereas the remaining 20% was used for performance tests, as conventionally applied for SDM application and modelling [29,46,47].

Model performance was evaluated by considering the Area Under the Curve (AUC), the Receiver Operating Characteristic (ROC), and the True Statistical Skill (TSS). In short, AUC measures the discrimination capacity between presences and absences and ranges from 0 to 1. Values of AUC higher than 0.8 and 0.9 indicate good and excellent performances, respectively [48–51]. The TSS measures the classification accuracy of a model with respect to a threshold value and ranges between -1 and 1. TCC values of -1 and 1 indicate no correspondence and complete correspondence between observations and predictions, respectively [52].

Finally, the distribution probabilities obtained by the models were projected using QGIS software to visually evaluate the suitability level of European countries for *T. parvicornis* development. The variables with the greatest contributions to the distribution of *T. parvicornis* were conventionally divided in "classes of suitability" that ranged from

“very low” to “very high” suitability (S), as follows: $S < 0.2$ = very low, $0.2 \leq S < 0.4$ = low, $0.4 \leq S < 0.6$ = intermediate, $0.6 \leq S < 0.8$ = high, and $S \geq 0.8$ = very high.

3. Results

3.1. Habitat Suitability for *T. parvicornis* in Italy

The results of the contribution weights of bioclimatic variables in estimating the suitability of Italian areas for *T. parvicornis* varied with the model involved. The bioclimatic variables influencing the most the distribution of *T. parvicornis* in Italy were BIO01 (i.e., annual mean temperature) and BIO12 (i.e., annual precipitation) for the GLM model, BIO01 and BIO03 (i.e., isothermality) for the MARS model, BIO03 and BIO01 for the RF model, and BIO01 and BIO15 (i.e., precipitation seasonality) for the MaxEnt model (Table 2).

Table 2. Relative contribution of each bioclimatic variable to Generalized Linear Model (GLM), Multivariate Adaptive Regression Splines (MARS) model, MaxEnt model, and Random Forest (RF) model to estimate the suitability of Italy for *Toumeyella parvicornis*.

Bioclimatic Variable ¹	GLM	MARS	MaxEnt	RF
BIO01	19.74%	32.30%	33.12%	26.47%
BIO02	6.40%	4.61%	3.07%	1.76%
BIO03	10.18%	20.37%	14.17%	32.35%
BIO04	6.05%	1.23%	5.14%	1.47%
BIO08	12.96%	2.65%	7.36%	5.59%
BIO09	5.77%	11.54%	3.66%	5.29%
BIO12	16.12%	2.21%	12.55%	7.06%
BIO15	12.18%	17.92%	16.56%	10.88%
BIO19	10.60%	7.17%	4.38%	9.12%

¹ See Table 1 for acronyms.

Assessment of SDMs performance when determining the areas suitable to *T. parvicornis* in Italy was based on the AUC and TSS values. All models provided excellent performances considering that AUC values were higher than 0.93, indicating a strong capability to predict the potential distribution of *T. parvicornis* in Italy. However, the RF model (AUC = 0.99 ± 0.01 ; TSS = 0.96 ± 0.04) had the best performance compared to the other tested models (MARS: AUC = 0.97 ± 0.02 , TSS = 0.93 ± 0.05 ; MaxEnt: AUC = 0.96 ± 0.05 , TSS = 0.90 ± 0.10 ; GLM: AUC = 0.96 ± 0.07 , TSS = 0.90 ± 0.10).

Model predictions for the Italian Peninsula are shown in Figure 3. Despite the observed differences, both in the weight of bioclimatic variables and in predictive power, no specific differences in prediction of the most suitable area for *T. parvicornis* were identified among the tested SDMs. The potential *T. parvicornis* distribution area was mainly concentrated around the coastal areas of Lazio, Campania, and Toscana regions (Figure 3). Moreover, high suitability areas were found in the Sardinia region by GLM, MARS, and MaxEnt models, whereas only the GLM model predicted a high suitability area in the middle of Puglia and Calabria regions.

Larger differences among the model predictions concerned the lower-suitability areas (Figure 3) where the MARS model extended the potential distribution more than the other models. On the contrary, the potential distribution estimated by the RF model was quite restricted.

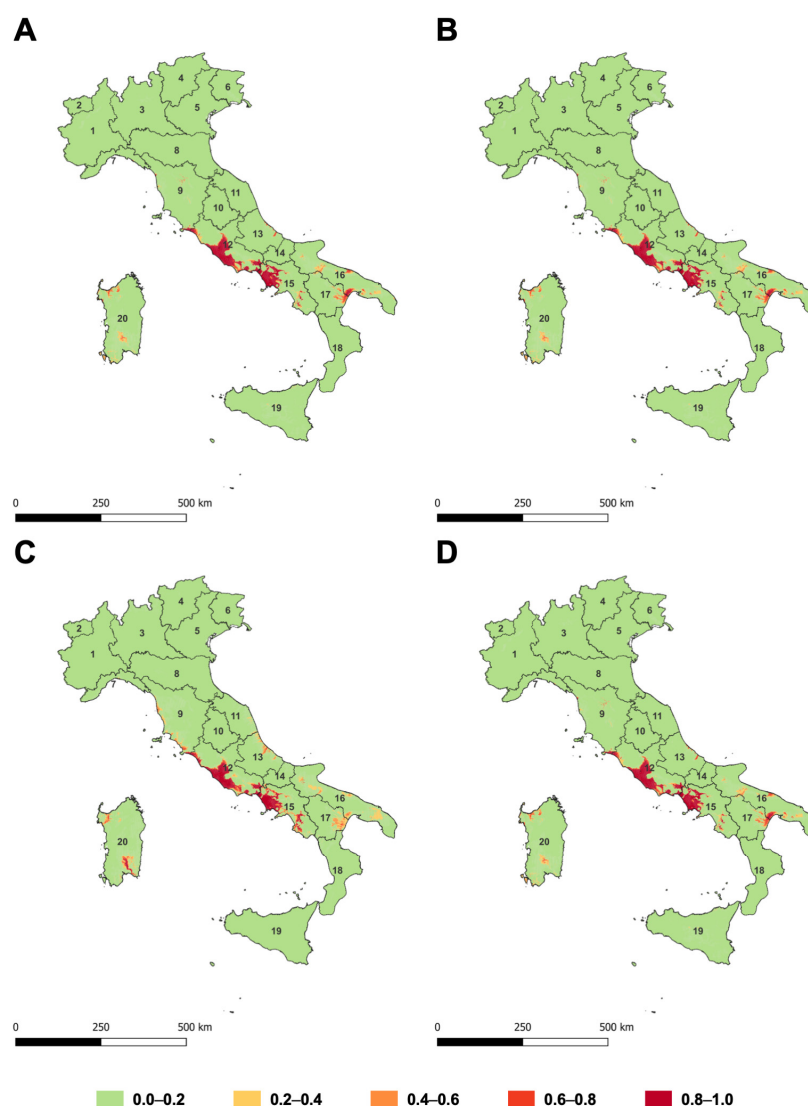


Figure 3. Distribution of suitable areas for *Toumeyella parvicornis* in Italy based on bioclimatic variables using Generalized Linear Model (GLM) (A), Multivariate Adaptive Regression Splines (MARS) model (B), MaxEnt model (C), and Random Forest (RF) model (D). Different colours indicate “classes of suitability” (green = very low; yellow = low; light orange = intermediate; dark orange = high; red = very high). Numbers in maps refer to Italian administrative regions (1 = Piemonte; 2 = Valle d’Aosta; 3 = Lombardia; 4 = Trentino Alto Adige; 5 = Veneto; 6 = Friuli Venezia Giulia; 7 = Liguria; 8 = Emilia Romagna; 9 = Toscana; 10 = Umbria; 11 = Marche; 12 = Lazio; 13 = Abruzzo; 14 = Molise; 15 = Campania; 16 = Puglia; 17 = Basilicata; 18 = Calabria; 19 = Sicilia; 20 = Sardegna).

3.2. Habitat Suitability for *T. parvicornis* in European Mediterranean Area

As already noted for Italy, the contribution of bioclimatic variables in estimating the most suitable areas for *T. parvicornis* in European Mediterranean area was different among the models tested. The BIO01 (i.e., annual mean temperature) and BIO19 (i.e., precipitation of the coldest quarter) variables were the most important variables affecting the distribution of *T. parvicornis* for the GLM and MARS models (Table 3). The bioclimatic variables contributing the most to the projections in the MaxEnt model were BIO15 (i.e., precipitation seasonality) and BIO19, whereas those contributing the most in the RF model were BIO01 and BIO19. Among all the bioclimatic variables considered, BIO02 (i.e., mean diurnal temperature range) and BIO04 (i.e., temperature seasonality) showed limited contribution to estimate the potential species distribution (Table 3).

Table 3. Relative contribution of each bioclimatic variable to Generalized Linear Model (GLM), Multivariate Adaptive Regression Splines (MARS) model, MaxEnt model, and Random Forest (RF) model to estimate the suitability of Mediterranean Europe for *Toumeyella parvicornis*.

Bioclimatic Variable ¹	GLM	MARS	MaxEnt	RF
BIO01	35.73%	35.13%	2.88%	15.64%
BIO02	8.44%	14.39%	10.20%	1.82%
BIO03	3.49%	2.86%	14.94%	4.73%
BIO04	6.36%	1.77%	2.64%	15.27%
BIO08	3.54%	0.64%	11.28%	11.27%
BIO09	6.49%	11.62%	6.66%	12.73%
BIO12	11.36%	2.27%	15.42%	12.00%
BIO15	4.49%	12.30%	20.76%	9.09%
BIO19	20.09%	19.02%	15.24%	17.45%

¹ See Table 1 for acronyms.

Based on AUC and TSS, the MARS model best represented the dataset available (AUC = 0.98 ± 0.03 ; TSS = 0.96 ± 0.06), followed by GLM (AUC = 0.97 ± 0.04 ; TSS = 0.94 ± 0.07), MaxEnt (AUC = 0.97 ± 0.03 ; TSS = 0.94 ± 0.07), and RF (AUC = 0.97 ± 0.03 ; TSS = 0.94 ± 0.07), which showed very similar values.

A visual description of the results is provided in Figure 4. As already observed in the Italian projections, the most suitable areas to *T. parvicornis* in European Mediterranean area were concentrated in the coastal zone (Figure 2). Considering the overall model predictions, the most suitable areas were the Tyrrhenian Sea coast of Italy, the French Riviera, and the Balkan coast of the Adriatic Sea. In addition, a relevant extension of the potential distribution predicted by the models was in the north-western area of the Iberian Peninsula covering both Portugal and Spain. Unlike the other models, GLM and MARS indicated highly suitable areas for *T. parvicornis* along the eastern coast of Spain as well.

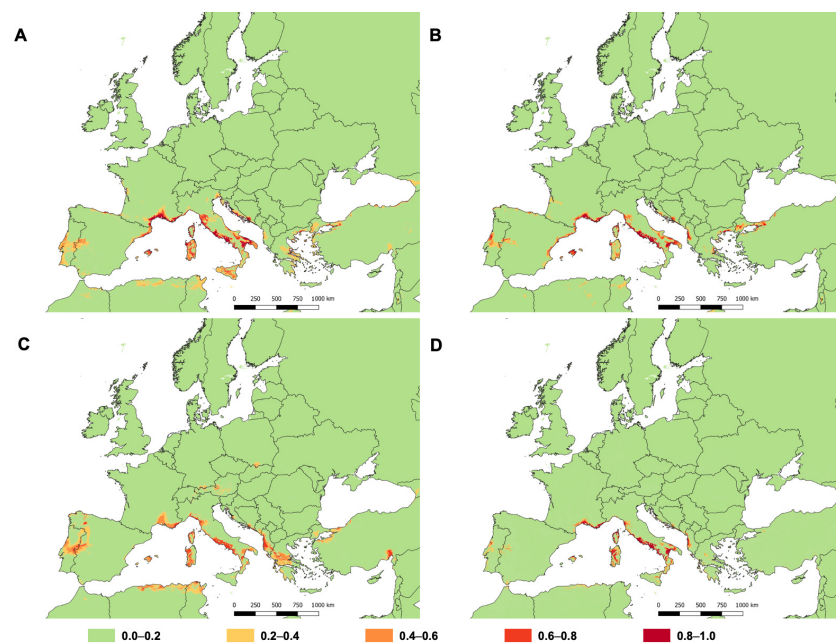


Figure 4. Distribution of suitable areas for *Toumeyella parvicornis* in Mediterranean Europe based on bioclimatic variables using Generalized Linear Model (GLM) (A), Multivariate Adaptive Regression Splines (MARS) model (B), MaxEnt model (C), and Random Forest (RF) model (D). Different colours indicate “classes of suitability” (green = very low; yellow = low; light orange = intermediate; dark orange = high; red = very high).

4. Discussion

The recent detection of *T. parvicornis* in Italy and in France has raised a serious concern about the potential diffusion of this pest across the European continent, including the Mediterranean area. Our study estimated for the first time the most suitable areas where the species may potentially spread in the next few years using a species distribution modelling approach. SDMs are a powerful and widely used tool to predict the areas where a species may potentially develop and spread [29,53–57]. All the tested models demonstrated good accuracies to estimating the suitability of Mediterranean European countries for *T. parvicornis*, and variability in accuracies were exclusively due to differences in fitting functions between regression-based (e.g., GLM, MARS) and nonparametric models (e.g., RF) [42].

Based on our study, the annual mean temperature played a fundamental role in explaining the projections of habitat suitability for *T. parvicornis* in Italy, especially in the GLM, MARS, and MaxEnt models. This information is of fundamental importance in the framework of a climate change scenario, as already stated for other pest species infesting agricultural and forest environments, such as *Philaenus spumarius* L. (Hemiptera: Aphrophoridae) [57], *Lobesia botrana* (Denis & Schiffermüller) (Lepidoptera: Tortricidae) [58], and *Tuta absoluta* (Meyrick) (Lepidoptera: Gelechiidae) [59]. Our results are also in line with the findings of Solhjoui-Fard et al. [60] and Yan et al. [61], where the annual mean temperature was the variable best explaining the potential distribution of *Ferrisia virgata* (Cockerell) (Hemiptera: Pseudococcidae), *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae), *Apodiphus amygdali* (Germar) (Hemiptera: Pentatomidae), *Adelphocoris lineolatus* (Goeze) (Hemiptera: Miridae), and *Thrips palmi* Karny (Thysanoptera: Thripidae).

A secondary variable that is worth mentioning for Italy is isothermality, which was the best explanatory variable according to the RF model. This variable is strictly related to the maritime areas, given that it evaluates the thermal gap between summer and winter temperatures [62]. Areas characterized by warmer winters, which Italian maritime areas normally have, may favor the development of *T. parvicornis* by leading this species to have more generations than in places with colder winters. In fact, this phenomenon has been already observed for other alien species, such as *Nezara viridula* (Linnaeus) (Hemiptera: Pentatomidae) and *Hyphantria cunea* (Drury) (Lepidoptera: Erebiidae) [63–67], and may also occur with *T. parvicornis*.

The European scenario outputs provided more extensive projections than the ones obtained that only considered Italy. In fact, the GLM and MARS models confirmed that temperature was the main explanatory variable at European Mediterranean spatial scale, whereas MaxEnt and RF considered precipitation seasonality and precipitation of the coldest quarter, respectively, as the best ones. Precipitation seasonality is a relevant variable, above all, in the coastal areas featured by rainfall anomalies during the seasons [62] and where the pest is already present (e.g., France). However, strong precipitation during summer, when the *T. parvicornis* activity is higher, may act as a natural control of preimaginal stages (i.e., the crawler). In fact, intense rainfall can kill the young instars and the mobile stages of this insect or carry them away from the host plant [16], as already observed for other species such as *Dactylopius opuntiae* (Cockerell) (Hemiptera: Dactylopiidae), *Quadricarifer punctatella* (Motschulsky) (Lepidoptera: Notodontidae), and *Eriogaster lanestris* (Linnaeus) (Lepidoptera: Lasiocampidae) [68–70]. In contrast, precipitation of the coldest quarter is a variable that may affect the overwintering capacity of the pest. In fact, strong rainfall in winter may mechanically remove the overwintering individuals from the host plant, thus influencing de facto the abundance of the population of the subsequent spring [71].

Our findings are also in line with Bragard et al. [5], who found that European countries have suitable features for the development of this pest, using the World distribution of Köppen–Geiger climate types present in the areas where *T. parvicornis* occurred as a method to predict the potential distribution of the insect.

The main host species of *T. parvicornis* occurring in Europe is *P. pinea*. This plant species has a low genetic diversity [72–74], which may favor the spread of this insect. In fact, a lower genetic diversity may indicate similar susceptibility among the plants to the pest, above all where extensive monocultures of *Pinus* species are present. This aspect has been already observed in intensive monoculture fields where a low genetic diversity of the plants resulted in a higher susceptibility to both biotic and abiotic stresses [75–77].

Stone and maritime pines are an essential element of cities in Italy [78] and coastal landscapes of many other Mediterranean countries such as France. Therefore, *T. parvicornis* may potentially change the aesthetic of many places if no prompt actions are carried out. Aesthetics is not the only element that may be impaired by the pest activity because *T. parvicornis* infestations may represent a serious concern where stone pines are cultivated for pinenut production, especially in some widely extended areas of Spain, Portugal, and France. Therefore, the interpretation of SDMs' projections cannot ignore the host plant distribution. From this point of view, our results are in line with the suggestion provided by the European Food Safety Authority [5], indicating that *T. parvicornis* has the potential to establish throughout the Europe wherever suitable hosts occur. In fact, the most suitable areas for *T. parvicornis* in European Mediterranean countries estimated by SDMs overlapped with the distribution of *P. pinea* and *P. pinaster* (Figure 5), which were recognized as the main hosts in newly invaded areas in Europe [6].

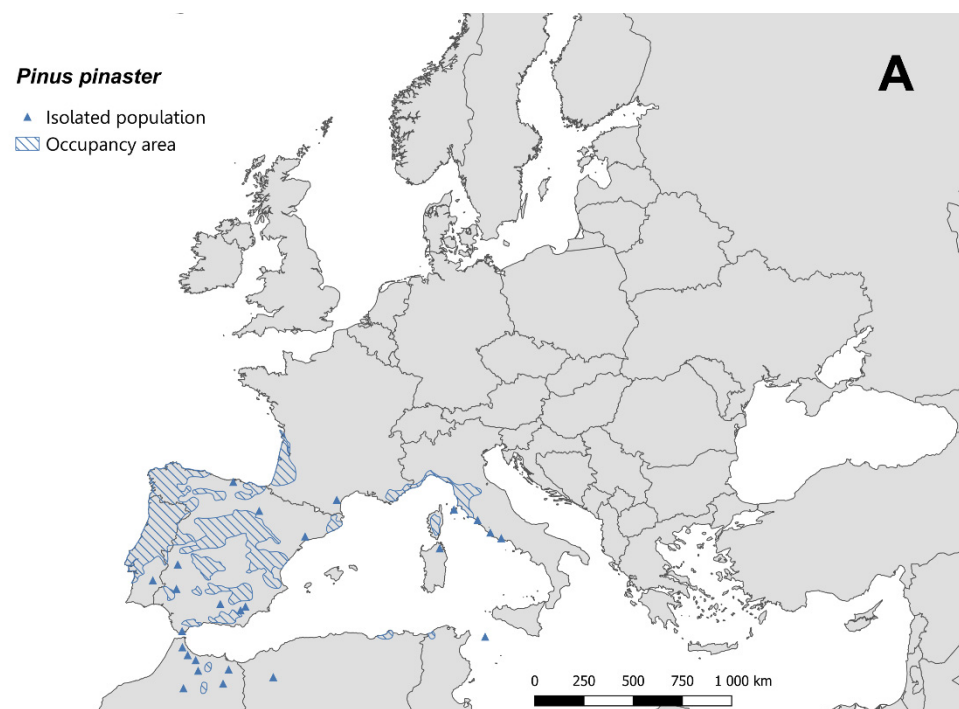


Figure 5. Cont.

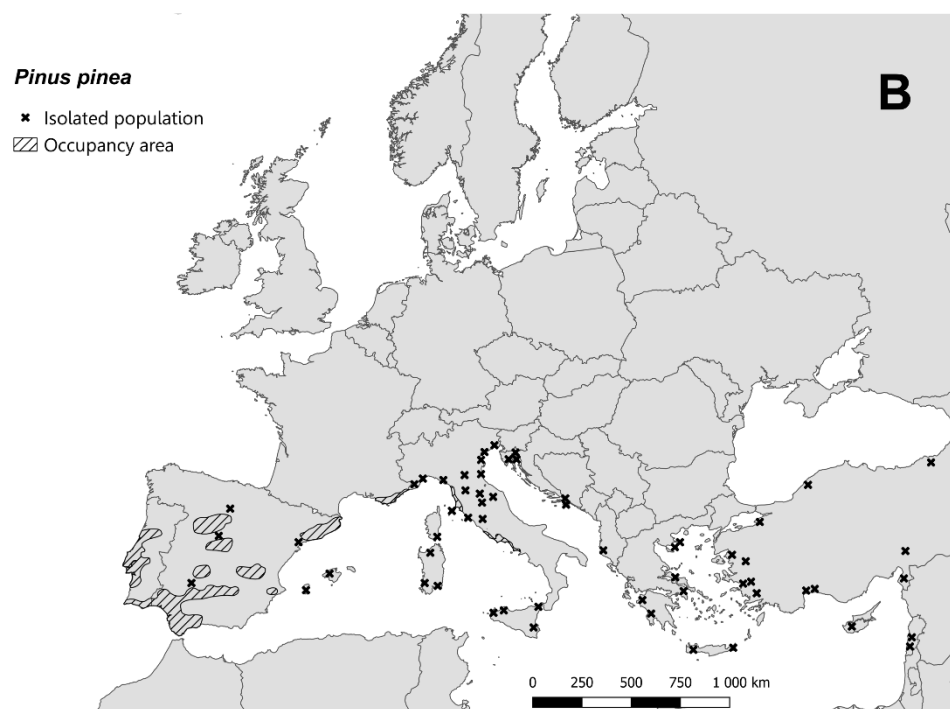


Figure 5. Distribution of (A) *Pinus pinaster* and (B) *Pinus pinea* in Europe following Caudullo et al. [79].

In this regard, based on the information available on the distribution of the main host plant species in Italy and Mediterranean Europe, we analyzed where the potential spread of *T. parvicornis* is more likely to occur, among the areas indicated by the SDMs outputs of our study. In Mediterranean countries, most *Pinus* species are in coastal areas [79], where the model outputs suggested a high suitability for the pest diffusion. In the Italian Peninsula, the most infested areas cover the Lazio and Campania regions, where stone pines grow in both natural and urban environments. In addition, first detections have been recently reported also along the Adriatic coast, particularly in the Abruzzo and Puglia regions [15,80]. According to the model outputs, particular attention should be given to the extensive stone pine forests of Emilia Romagna, where *T. parvicornis* may aggravate the ongoing deleterious activity of *Crisicoccus pini* (Kuwana) (Hemiptera: Pseudococcidae), another invasive pest infesting the same host plant [81,82]. Similarly, Tuscany is another Italian region extensively covered with stone pines where the pest has been recently detected [83] and where the model outputs indicated a high suitability for the pest diffusion. Hence, all these Italian regions should be strictly monitored to promptly reduce the diffusion of *T. parvicornis* given the extensive presence of host plants and the high suitability indicated by our results.

A different scenario concerns Sardinia, where *T. parvicornis* has not been detected yet but stone and maritime pines are widely diffused [84,85], above all in the southern part of the region. In this case, careful monitoring of imported pine plants and wood is fundamental to prevent the introduction of this pest in the island.

Although *T. parvicornis* is an oligophagous species strictly related to a restricted pool of host plants, it has several characteristics of an ideal invasive species. In fact, small size, parthenogenetic reproduction, and high adaptability to new environments are features generally associated with highly invasive pests [86]. Moreover, the reduced size (up to 5 mm for adults) of *T. parvicornis* makes the detection of the infested plants, especially adult plants, very difficult and promotes its diffusion by wind. In addition to being small, the Italian and European climate conditions seem to play a fundamental role in its diffusion. For instance, in North America *T. parvicornis* has one generation per year [1,87], whereas in warmer areas several overlapped generations were observed [2,6].

Considering the distribution of both *P. pinea* and *P. pinaster* in Europe and our SDMs outputs, we hypothesize that the Iberian Peninsula may be another highly suitable area

to *T. parvicornis*, given the extensive presence of the host plant [88,89]. Extensive pine forests and plantations are present in Portugal and Spain [79], where they are considered a precious source of biodiversity [90]. However, pine forests of the Iberian Peninsula are often subjected to abiotic stresses such as fires [91,92], and biotic adversities, such as the pine wood nematode *Bursaphelenchus xylophilus* Nickle (1981) [93,94] or bark beetle species belonging to the *Tomicus* genus [95,96]. Even though it has not been proven yet, it is likely that *T. parvicornis* could be more aggressive towards plants already affected by other adversities.

Obtaining a complete and detailed potential distribution map of *T. parvicornis* for different regions would be of fundamental importance, above all to construct prompt monitoring and control strategies. An early control strategy would avoid some dangerous conditions, as already observed in the Turks and Caicos Islands, where *T. parvicornis* dramatically reduced the range of native *Pinus caribaea* var. *bahamensis* [2]. Besides the short-term actions that could be performed based on the results of this study, a secondary aspect would be relevant for a long-term scenario. Therefore, we hypothesize that a slight increase of the annual mean temperature may dramatically extend the suitable areas. In fact, our predictions were based on actual climate conditions (years 1970–2000) because we aimed to understand the potential spread of the pest in the next few years. The same analysis presented in our work could be performed in further studies by considering a climate change scenario, as already carried out for other insect pest species [97,98].

In conclusion, we believe that the scenario presented in this work could allow technicians and local authorities to focus on the most susceptible areas to *T. parvicornis*, thus helping them to manage properly this injurious pest in Mediterranean European area.

Supplementary Materials: The following supporting material can be downloaded at: <https://www.mdpi.com/article/10.3390/insects14010046/s1>, Table S1: List of records used to estimate the suitability of European Mediterranean non-native area for *Toumeyella parvicornis* using Species Distribution Models (SDMs); Table S2: Results of Pearson's correlation analysis among bioclimatic variables at a spatial resolution of 30 arc-sec (~1 km²).

Author Contributions: Conceptualization, N.D.S., R.M., L.R., M.C., D.G. and S.S.; methodology, N.D.S., R.M. and L.R.; software, N.D.S. and R.M.; validation, N.D.S.; formal analysis, R.M.; investigation, N.D.S. and R.M.; resources, M.C., D.G. and S.S.; data curation, N.D.S. and R.M.; writing—original draft preparation, N.D.S., R.M. and L.R.; writing—review and editing, N.D.S., R.M., L.R., M.C., D.G. and S.S.; visualization, N.D.S. and R.M.; supervision, M.C., D.G. and S.S.; project administration, S.S.; funding acquisition, S.S. All authors have read and agreed to the published version of the manuscript.

Funding: N.D.S. is funded by the Lazio Region (Agriculture Department) and the Università degli Studi della Tuscia (Italy). The research was carried out in the frame of the Italian MIUR (Ministry for Education, University and Research) initiative 'Department of Excellence' (Law 232/2016). L.R. and R.M. are funded by MUR (Italian Ministry of University and Research) in the framework of the European Social Funding REACT-EU—National Program for Research and Innovation 2014–2020.

Data Availability Statement: The data associated with this publication, as well as the R script to reproduce the results, are publicly available at <https://github.com/lucaros1190/SDM-Toumeyella> (accessed on 1 December 2022).

Acknowledgments: This work is in loving memory of Enrico Chiarot, dear colleague and friend who spent much of his energies in saving the stone pine trees of the city of Rome. The authors acknowledge Ana Helena Dias Francesconi for revising the manuscript and Simone Menegoni for the support during field activities.

Conflicts of Interest: The authors declare no conflict of interest.

References

- Hamon, A.; Williams, M. *The Soft Scale Insects of Florida (Homoptera: Coccoidea: Coccidae)*; Florida Department of Agriculture and Consumer Services, Division of Plant Industry: Gainesville, Florida, 1984; Volume 11.
- Malumphy, C.; Hamilton, M.A.; Manco, B.N.; Green, P.W.C.; Sanchez, M.D.; Corcoran, M.; Salamanca, E. *Toumeyella parvicornis* (Hemiptera:Coccidae), causing severe decline of *Pinus caribaea* var. *bahamensis* in the Turks and Caicos Islands. *Source Fla. Entomol.* **2012**, *95*, 113–119. [[CrossRef](#)]
- Orr, L.W. Agricultural experiment station studies on natural vs. artificial control of the pine tortoise scale. *Univ. Minn. Agric. Exp. Stn.* **1931**, 1–21.
- Di Sora, N.; Rossini, L.; Contarini, M.; Chiarot, E.; Speranza, S. Endotherapeutic treatment to control *Toumeyella parvicornis* Cockerell infestations on *Pinus pinea* L. *Pest Manag. Sci.* **2022**, *78*, 2443–2448. [[CrossRef](#)]
- Bragard, C.; Baptista, P.; Chatzivassiliou, E.; Di Serio, F.; Gonthier, P.; Jaques Miret, J.A.; Fejer Justesen, A.; Magnusson, C.S.; Milonas, P.; Navas-Cortes, J.A.; et al. Pest categorisation of *Toumeyella parvicornis*. *EFSA J.* **2022**, *20*, e07146. [[CrossRef](#)] [[PubMed](#)]
- Garonna, A.; Foscari, A.; Russo, E.; Jesu, G.; Somma, S.; Cascone, P.; Guerrieri, E. The spread of the non-native pine tortoise scale *Toumeyella parvicornis* (Hemiptera: Coccidae) in Europe: A major threat to *Pinus pinea* in Southern Italy. *Iforest—Biogeosci. For.* **2018**, *11*, 628–634. [[CrossRef](#)]
- Cockerell, T.D.A.; Quaintance, A.L. New and little-known Coccidae from Florida. *Psyche A J. Entomol.* **1897**, *8*, 89–91. [[CrossRef](#)]
- Stimmel, J.F. Pine tortoise scale, *Toumeyella parvicornis* (Cockerell) (Homoptera: Coccidae). *Regul. Hortic.* **1984**, *10*, 23–24.
- Clarke, S.R.; DeBarr, G.L.; Liu, T.X. Contact toxicities of five pyrethroid and four organophosphorous insecticide to toumeyella parvicornis (Cockerell) crawlers. *Can. Entomol.* **1992**, *124*, 563–564. [[CrossRef](#)]
- Cooper, D.D.; Cranshaw, W.S. Seasonal biology and associated natural enemies of two *Toumeyella* spp. in Colorado. *Southwest. Entomol.* **2004**, *29*, 39–45.
- Bradley, G.A. Effect of *Formica obscuripes* (Hymenoptera: Formicidae) on the predator-prey relationship between *Hyperaspis congressis* (Coleoptera: Coccinellidae) and *Toumeyella numismaticum* (Homoptera: Coccidae). *Can. Entomol.* **1973**, *105*, 1113–1118. [[CrossRef](#)]
- Myartseva, S.N.; Ruiz Cancino, E. Annotated Checklist of the Aphelinidae (Hymenoptera: Chalcidoidea) of México. *Folia Entomol. Mex.* **2000**, *109*, 7–33.
- Segarra-Carmona, A.E.; Cabrera-Asencio, I. *Toumeyella parvicornis* (Cockerell) (Hemiptera: Coccoidea: Coccidae): A new invasive pest of pine trees in Puerto Rico. *J. Agric. Univ. Puerto Rico* **2010**, *94*, 175–177. [[CrossRef](#)]
- Garonna, A.P.; Scarpato, S.; Vicinanza, F.; Espinosa, B. First report of *Toumeyella parvicornis* (Cockerell) in Europe (Hemiptera: Coccidae). *Zootaxa* **2015**, *3949*, 142–146. [[CrossRef](#)]
- EPPO. Available online: <https://gd.eppo.int/taxon/TOUMPA/distribution/IT> (accessed on 1 December 2022).
- Servizio Fitosanitario Nazionale Protezione delle Piante, *Toumeyella parvicornis*. Available online: <https://www.protezionedellepiante.it/emergenze-fitosanitarie/toumeyella-parvicornis/> (accessed on 1 December 2022).
- Bernetti, G. *Selvicoltura speciale*; Unione tipografico-editrice Torinese, Ed.; Unione Tipografico-Editrice Torinese: Torino, Italy, 1995.
- Ciancio, O.; Travaglini, D.; Bianchi, L.; Mariotti, B. La gestione delle pinete litoranee di pino domestico: Il caso dei tomboli di Cecina. In Proceedings of the III Congresso Nazionale Selvicoltura, Taormina, Italy, 16–19 October 2008; pp. 156–162.
- Mannu, R.; Torres-Vila, L.M.; Olivieri, M.; Lentini, A. When a threatened species becomes a threat: A key to reading the habitats directive based on occurrence and distribution of *Cerambyx cerdo* L. in Mediterranean urban and peri-urban areas. *Insect Conserv. Divers.* **2021**, *14*, 730–735. [[CrossRef](#)]
- Rabkin, F. Studies on the Biology of the Manitoba Jack Pine Scale *Toumeyella* Sp.(Coccidae Homoptera). Master's Thesis, University of Manitoba, Winnipeg, MB, Canada, 1939.
- Guisan, A.; Zimmermann, N.E. Predictive habitat distribution models in ecology. *Ecol. Modell.* **2000**, *135*, 147–186. [[CrossRef](#)]
- Guisan, A.; Thuiller, W. Predicting species distribution: Offering more than simple habitat models. *Ecol. Lett.* **2005**, *8*, 993–1009. [[CrossRef](#)]
- Elith, J.; Leathwick, J.R. Species distribution models: Ecological explanation and prediction across space and time. *Annu. Rev. Ecol. Evol. Syst.* **2009**, *40*, 677–697. [[CrossRef](#)]
- Rossini, L.; Bono Rosselló, N.; Contarini, M.; Speranza, S.; Garone, E. Modelling ectotherms' populations considering physiological age structure and spatial motion: A novel approach. *Ecol. Inform.* **2022**, *70*, 101703. [[CrossRef](#)]
- Jeschke, J.M.; Strayer, D.L. Usefulness of bioclimatic models for studying climate change and invasive species. *Ann. N. Y. Acad. Sci.* **2008**, *1134*, 1–24. [[CrossRef](#)]
- Wang, X.Y.; Huang, X.L.; Jiang, L.Y.; Qiao, G.X. Predicting potential distribution of chestnut phylloxerid (Hemiptera: Phylloxeridae) based on GARP and Maxent ecological niche models. *J. Appl. Entomol.* **2010**, *134*, 45–54. [[CrossRef](#)]
- Wang, F.; Wang, D.; Guo, G.; Zhang, M.; Lang, J.; Wei, J. Potential distributions of the invasive barnacle scale *Ceroplastes cirripediformis* (Hemiptera: Coccidae) under climate change and implications for its management. *J. Econ. Entomol.* **2021**, *114*, 82–89. [[CrossRef](#)]
- Sung, S.; Kwon, Y.S.; Lee, D.K.; Cho, Y. Predicting the potential distribution of an invasive species, *Solenopsis invicta* Buren (Hymenoptera: Formicidae), under climate change using species distribution models. *Entomol. Res.* **2018**, *48*, 505–513. [[CrossRef](#)]
- Tang, J.; Li, J.; Lu, H.; Lu, F.; Lu, B. Potential distribution of an invasive pest, *Euplatypus parallelus*, in China as predicted by Maxent. *Pest Manag. Sci.* **2019**, *75*, 1630–1637. [[CrossRef](#)]

30. Pearson, R.G.; Raxworthy, C.J.; Nakamura, M.; Townsend Peterson, A. Predicting species distributions from small numbers of occurrence records: A test case using cryptic geckos in Madagascar. *J. Biogeogr.* **2006**, *34*, 102–117. [[CrossRef](#)]
31. Chirici, C.; Fattori, F.; Cutolo, C.; Tufano, T.; Corona, C.; Barbati, B.; Blasi, B.; Copiz, C.; Rossi, R.; Biscontini, B.; et al. La realizzazione della carta delle formazioni naturali e semi-naturali e della carta forestale su basi tipologiche della regione Lazio. *For. J. Silv. For. Ecol.* **2014**, *11*, 65. [[CrossRef](#)]
32. Fick, S.E.; Hijmans, R.J. WorldClim 2: New 1-km spatial resolution climate surfaces for global land areas. *Int. J. Climatol.* **2017**, *37*, 4302–4315. [[CrossRef](#)]
33. Gong, Z.; Zhang, Y. What is it you really want of me? generalized reward learning with biased beliefs about domain dynamics. In Proceedings of the AAAI Conference on Artificial Intelligence, New York, NY, USA, 3 April 2020; Volume 34, pp. 2485–2492.
34. Kou, J.; Wang, T.; Yu, F.; Sun, Y.; Feng, C.; Shao, X. The moss genus didymodon as an indicator of climate change on the tibetan plateau. *Ecol. Indic.* **2020**, *113*, 106204. [[CrossRef](#)]
35. Thuiller, W.; Georges, D.; Engler, R.; Breiner, F. Package ‘Biomod2’. Ensemble Platform for Species Distribution Modeling. 2016. Available online: <https://cran.r-project.org/web/packages/biomod2/biomod2.pdf> (accessed on 1 December 2022).
36. R Development Core Team. *R: A Language and Environment for Statistical Computing*; R Foundation for Statistical Computing: Vienna, Austria, 2022.
37. Phillips, S.; Anderson, R.; Schapire, R. Maximum entropy modeling of species geographic distributions. *Ecol. Modell.* **2006**, *190*, 231–259. [[CrossRef](#)]
38. Elith, J.; Graham, C.H.; Anderson, R.P.; Dudík, M.; Ferrier, S.; Guisan, A.; Hijmans, R.J.; Huettmann, F.; Leathwick, J.R.; Lehmann, A.; et al. Novel methods improve prediction of species’ distributions from occurrence data. *Ecography* **2006**, *29*, 129–151. [[CrossRef](#)]
39. Merow, C.; Smith, M.J.; Silander, J.A. A practical guide to MaxEnt for modeling species’ distributions: What it does, and why inputs and settings matter. *Ecography* **2013**, *36*, 1058–1069. [[CrossRef](#)]
40. Shcheglovitova, M.; Anderson, R.P. Estimating optimal complexity for ecological niche models: A jackknife approach for species with small sample sizes. *Ecol. Modell.* **2013**, *269*, 9–17. [[CrossRef](#)]
41. Radosavljevic, A.; Anderson, R.P. Making better maxent models of species distributions: Complexity, overfitting and evaluation. *J. Biogeogr.* **2014**, *41*, 629–643. [[CrossRef](#)]
42. Valavi, R.; Guillera-Aroita, G.; Lahoz-Monfort, J.J.; Elith, J. Predictive performance of presence-only species distribution models: A benchmark study with reproducible code. *Ecol. Monogr.* **2022**, *92*, e01486. [[CrossRef](#)]
43. Anderson, D.R.; Burnham, K.P. Avoiding pitfalls when using information-theoretic methods. *J. Wildl. Manag.* **2002**, *66*, 912–918. [[CrossRef](#)]
44. Warren, D.L.; Seifert, S.N. Ecological Niche Modeling in Maxent: The importance of model complexity and the performance of model selection criteria. *Ecol. Appl.* **2011**, *21*, 335–342. [[CrossRef](#)]
45. Muscarella, R.; Galante, P.J.; Soley-Guardia, M.; Boria, R.A.; Kass, J.M.; Uriarte, M.; Anderson, R.P. ENMeval: An R Package for conducting spatially independent evaluations and estimating optimal model complexity for Maxent ecological niche models. *Methods Ecol. Evol.* **2014**, *5*, 1198–1205. [[CrossRef](#)]
46. Kumar, S.; Graham, J.; West, A.M.; Evangelista, P.H. Using district-level occurrences in maxent for predicting the invasion potential of an exotic insect pest in India. *Comput. Electron. Agric.* **2014**, *103*, 55–62. [[CrossRef](#)]
47. Lozano, V.; Marzioletti, F.; Carranza, M.L.; Chapman, D.; Branquart, E.; Dološ, K.; Große-Stoltenberg, A.; Fiori, M.; Capece, P.; Brundu, G. Modelling *Acacia saligna* invasion in a large mediterranean island using PAB factors: A Tool for implementing the european legislation on invasive species. *Ecol. Indic.* **2020**, *116*, 106516. [[CrossRef](#)]
48. Elith, J.; Kearney, M.; Phillips, S. The art of modelling range-shifting species. *Methods Ecol. Evol.* **2010**, *1*, 330–342. [[CrossRef](#)]
49. Freitas, F.F.; Khosa, C.K.; Sanz, V. Exploring the standard model EFT in VH production with machine learning. *Phys. Rev. D* **2019**, *100*, 035040. [[CrossRef](#)]
50. Dakhil, M.A.; Xiong, Q.; Farahat, E.A.; Zhang, L.; Pan, K.; Pandey, B.; Olatunji, O.A.; Tariq, A.; Wu, X.; Zhang, A.; et al. Past and future climatic indicators for distribution patterns and conservation planning of temperate coniferous forests in Southwestern China. *Ecol. Indic.* **2019**, *107*, 105559. [[CrossRef](#)]
51. Engelhardt, E.K.; Neuschulz, E.L.; Hof, C. Ignoring biotic interactions overestimates climate change effects: The potential response of the spotted nutcracker to changes in climate and resource plants. *J. Biogeogr.* **2020**, *47*, 143–154. [[CrossRef](#)]
52. Allouche, O.; Tsoar, A.; Kadmon, R. Assessing the accuracy of species distribution models: Prevalence, kappa and the true skill statistic (TSS). *J. Appl. Ecol.* **2006**, *43*, 1223–1232. [[CrossRef](#)]
53. Sobek-Swant, S.; Kluza, D.A.; Cuddington, K.; Lyons, D.B. Potential distribution of emerald ash borer: What can we learn from ecological niche models using Maxent and GARP? *For. Ecol. Manag.* **2012**, *281*, 23–31. [[CrossRef](#)]
54. Alaniz, A.J.; Carvajal, M.A.; Vergara, P.M. Giants are coming? predicting the potential spread and impacts of the giant asian hornet (*Vespa mandarinia*, Hymenoptera:Vespidae) in the USA. *Pest Manag. Sci.* **2021**, *77*, 104–112. [[CrossRef](#)]
55. Li, X.; Xu, D.; Jin, Y.; Zhuo, Z.; Yang, H.; Hu, J.; Wang, R. Predicting the current and future distributions of *Brontispa longissima* (Coleoptera: Chrysomelidae) under climate change in China. *Glob. Ecol. Conserv.* **2021**, *25*, e01444. [[CrossRef](#)]
56. Early, R.; Rwomushana, I.; Chipabika, G.; Day, R. Comparing, evaluating and combining statistical species distribution models and CLIMEX to forecast the distributions of emerging crop pests. *Pest Manag. Sci.* **2022**, *78*, 671–683. [[CrossRef](#)]

57. Godefroid, M.; Morente, M.; Schartel, T.; Cornara, D.; Purcell, A.; Gallego, D.; Moreno, A.; Pereira, J.A.; Fereres, A. Climate tolerances of *Philaenus spumarius* should be considered in risk assessment of disease outbreaks related to *Xylella fastidiosa*. *J. Pest Sci.* **2022**, *95*, 855–868. [CrossRef]
58. Ponti, L.; Gutierrez, A.; Boggia, A.; Neteler, M. Analysis of grape production in the face of climate change. *Climate* **2018**, *6*, 20. [CrossRef]
59. Ponti, L.; Gutierrez, A.P.; de Campos, M.R.; Desneux, N.; Biondi, A.; Neteler, M. Biological invasion risk assessment of *Tuta absoluta*: Mechanistic versus correlative methods. *Biol. Invasions* **2021**, *23*, 3809–3829. [CrossRef]
60. Solhjoui-Fard, S.; Sarafrazi, A.; Minbashi Moeini, M.; Ahadiyat, A. Predicting habitat distribution of five heteropteran pest species in Iran. *J. Insect Sci.* **2013**, *13*, 116. [CrossRef] [PubMed]
61. Yan, Y.; Wang, Y.C.; Feng, C.C.; Wan, P.H.M.; Chang, K.T.T. Potential distributional changes of invasive crop pest species associated with global climate change. *Appl. Geogr.* **2017**, *82*, 83–92. [CrossRef]
62. O'Donnell, M.; Ignizio, D. Bioclimatic predictors for supporting ecological applications in the conterminous United States. *U.S. Geol. Surv. Data Ser.* **2012**, *691*, 10.
63. Kiritani, K. Predicting impacts of global warming on population dynamics and distribution of arthropods in Japan. *Popul. Ecol.* **2006**, *48*, 5–12. [CrossRef]
64. Musolin, D.L. Insects in a warmer world: Ecological, physiological and life-history responses of true bugs (Heteroptera) to climate change. *Glob. Chang. Biol.* **2007**, *13*, 1565–1585. [CrossRef]
65. Gomi, T.; Nagasaka, M.; Fukuda, T.; Hagihara, H. Shifting of the life cycle and life-history traits of the fall webworm in relation to climate change. *Entomol. Exp. Appl.* **2007**, *125*, 179–184. [CrossRef]
66. Walther, G.R.; Roques, A.; Hulme, P.E.; Sykes, M.T.; Pyšek, P.; Kühn, I.; Zobel, M.; Bacher, S.; Botta-Dukát, Z.; Bugmann, H.; et al. Alien species in a warmer world: Risks and opportunities. *Trends Ecol. Evol.* **2009**, *24*, 686–693. [CrossRef]
67. Robinet, C.; Roques, A. Direct impacts of recent climate warming on insect populations. *Integr. Zool.* **2010**, *5*, 132–142. [CrossRef]
68. Moran, V.C.; Hoffmann, J.H.; Basson, N.C.J. The effects of simulated rainfall on cochineal insects (Homoptera: Dactylopiidae): Colony composition and survival on cactus cladodes. *Ecol. Entomol.* **1987**, *12*, 51–60. [CrossRef]
69. Kamata, N.; Igarashi, Y. Influence of rainfall on feeding behavior, growth, and mortality of larvae of the beech caterpillar, *Quadralcarifera punctatella* (Motschulsky) (Lep., Notodontidae). *J. Appl. Entomol.* **1994**, *118*, 347–353. [CrossRef]
70. Ruf, C.; Fiedler, K. Colony survivorship of social caterpillars in the field: A case study of the small eggar moth (Lepidoptera: Lasiocampidae). *J. Res. Lepid.* **1999**, *38*, 15–25. [CrossRef]
71. Beirne, B.P. Effects of precipitation on crop insects. *Can. Entomol.* **1970**, *102*, 1360–1373. [CrossRef]
72. Vendramin, G.G.; Fady, B.; González-Martínez, S.C.; Hu, F.S.; Scotti, I.; Sebastiani, F.; Soto, Á.; Petit, R.J. Genetically depauperate but widespread: The case of an emblematic mediterranean pine. *Evolution* **2008**, *62*, 680–688. [CrossRef]
73. Sofia, C.; Dos Santos, S.; Wilton De Vasconcelos, M. Identification of genes differentially expressed in *Pinus pinaster* and *Pinus pinea* after infection with the pine wood nematode. *Eur. J. Plant Pathol.* **2012**, *132*, 407–418. [CrossRef]
74. Mutke, S.; Vendramin, G.G.; Fady, B.; Bagnoli, F.; González-Martínez, S.C. Molecular and quantitative genetics of stone pine (*Pinus pinea*). In *Genetic Diversity in Horticultural Plants*; Springer: Cham, Switzerland, 2019; pp. 61–84. [CrossRef]
75. Altieri, M.A. Green desert: Monocultures and their impacts on biodiversity. In *Red Sugar, Green Deserts: Latin American Report on Monocultures and Violations of the Human Rights to Adequate Food and Housing, to Water, to Land and to Territory*; FIAN International, FIAN Sweden, HIC-AL, and SAL: Stockholm, Sweden, 2009; pp. 67–76.
76. Straub, C.S.; Simasek, N.P.; Dohm, R.; Gapinski, M.R.; Aikens, E.O.; Nagy, C. Plant diversity increases herbivore movement and vulnerability to predation. *Basic Appl. Ecol.* **2014**, *15*, 50–58. [CrossRef]
77. Wright, A.J.; Mommer, L.; Barry, K.; van Ruijven, J. Stress gradients and biodiversity: Monoculture vulnerability drives stronger biodiversity effects during drought years. *Ecology* **2021**, *102*, e03193. [CrossRef]
78. Stefani, A. Le pinete litoranee e il nuovo testo unico forestale. In *I Georgofili, Quaderni: I. Le Pinete Litoranee Come Patrimonio Culturale*; Polistampa: Firenze, Italy, 2019; pp. 53–57.
79. Caudullo, G.; Welk, E.; Jesús, S.-M.-A. Chorological maps for the main European woody species. *Data Br.* **2017**, *12*, 662–666. [CrossRef]
80. Tagarelli, N.; Avosani, S.; Tucci, M.; Verrastro, V. First report of *Toumeyella parvicornis* (Hemiptera: Coccidae) in Puglia (South-Eastern Italy). *EPPO Bull.* **2022**, *52*, 487–492. [CrossRef]
81. Boselli, M.; Vai, N.; Mirotti, A.; Mazzini, F.; Mazzoni, F.; Mosti, M.; Foschi, S.; Scapini, C. *Crisococcus pini* (Homoptera, Pseudococcidae) in Emilia Romagna: Delimitazione dell'area infestata e piano di controllo. In *Proceedings of the Giornate Fitopatologiche; Giornate Fitopatologiche*: Chianciano Terme, Italy, 2018; p. 8.
82. Bragard, C.; Di Serio, F.; Gonthier, P.; Jaques Miret, J.A.; Justesen, A.F.; Magnusson, C.S.; Milonas, P.; Navas-Cortes, J.A.; Parnell, S.; Potting, R.; et al. Pest categorisation of *Crisococcus pini*. *EFSA J.* **2021**, *19*, e06928. [CrossRef]
83. EPPO. Available online: <https://gd.eppo.int/reporting/article-7314> (accessed on 1 December 2022).
84. Cutini, A.; Chianucci, F.; Manetti, M.C. Allometric relationships for volume and biomass for stone pine (*Pinus pinea* L.) in Italian coastal stands. *Iforest—Biogeosci. For.* **2013**, *6*, 331. [CrossRef]
85. Camarda, I.; Laureti, P.; Angelini, P.; Capogrossi, R.; Carta, L.; Brunu, A. *Il Sistema Carta della Natura della Sardegna*; Serie Rapp.; ISPRA: Rome, Italy, 2015.

86. Gallego, D.; Riba, J.M.; Molina, N.; González, E.; Di Sora, N.; Núñez, L.; Closa, A.M.; Comparini, C.; Leza, M. Las invasiones silenciosas de escoltíidos: El caso del género *Xylosandrus* (Coleoptera, Curculionidae, Scolytinae). *Foresta* **2020**, *78*, 78–83.
87. Rabkin, F.B.; Lejeune, R.R. Some aspects of the biology and dispersal of the pine tortoise scale, *Toumeyella numismaticum* (Pettit and McDaniel) (Homoptera: Coccidae). *Can. Entomol.* **1954**, *86*, 570–575. [[CrossRef](#)]
88. Devy-Vareta, N. Investigación sobre la historia forestal portuguesa en los siglos xix y xx: Orientaciones y lagunas. *Hist. Agrar.* **1999**, *18*, 57–94.
89. Barranco Reyes, J.; Ortuño Pérez, S.F. Aproximación al sector del piñón en España. *Rev. Española Estud. Agrosoc. Y Pesq.* **2004**, *201*, 165–189. [[CrossRef](#)]
90. Proença, V.M.; Pereira, H.M.; Guilherme, J.; Vicente, L. Plant and bird diversity in natural forests and in native and exotic plantations in NW Portugal. *Acta Oecol.* **2010**, *36*, 219–226. [[CrossRef](#)]
91. Lloret, F.; Calvo, E.; Pons, X.; Díaz-Delgado, R. Wildfires and landscape patterns in the eastern iberian peninsula. *Landscape Ecol.* **2002**, *17*, 745–759. [[CrossRef](#)]
92. Pausas, J.G.; Bladé, C.; Valdecantos, A.; Seva, J.P.; Fuentes, D.; Alloza, J.A.; Vilagrosa, A.; Bautista, S.; Cortina, J.; Vallejo, R. Pines and oaks in the restoration of mediterranean landscapes of Spain: New perspectives for an old practice—a review. *Plant Ecol.* **2004**, *171*, 209–220. [[CrossRef](#)]
93. Álvarez, G.; Etxebeste, I.; Gallego, D.; David, G.; Bonifacio, L.; Jactel, H.; Sousa, E.; Pajares, J.A. Optimization of traps for live trapping of pine wood nematode vector *Monochamus galloprovincialis*. *J. Appl. Entomol.* **2015**, *139*, 618–626. [[CrossRef](#)]
94. De la Fuente, B.; Beck, P.S.A. Invasive species may disrupt protected area networks: Insights from the pine wood nematode spread in Portugal. *Forests* **2018**, *9*, 282. [[CrossRef](#)]
95. Gallego, D.; Cánovas, F.; Esteve, M.A.; Galián, J. Descriptive biogeography of *Tomicus* (Coleoptera: Scolytidae) species in Spain. *J. Biogeogr.* **2004**, *31*, 2011–2024. [[CrossRef](#)]
96. Gallego, D.; Galián, J.; Diez, J.J.; Pajares, J.A. Kairomonal responses of *Tomicus destruens* (Col., Scolytidae) to host volatiles α -pinene and ethanol. *J. Appl. Entomol.* **2008**, *132*, 654–662. [[CrossRef](#)]
97. Choudhary, J.S.; Kumari, M.; Mali, S.S.; Dhakar, M.K.; Das, B.; Singh, A.K. Predicting impact of climate change on habitat suitability of guava fruit fly, *Bactrocera correcta* (Bezzi) using MaxEnt modeling in India. *J. Agrometeorol.* **2019**, *21*, 24–30. [[CrossRef](#)]
98. Ji, W.; Han, K.; Lu, Y.; Wei, J. Predicting the potential distribution of the vine mealybug, *Planococcus ficus* under climate change by MaxEnt. *Crop Prot.* **2020**, *137*, 105268. [[CrossRef](#)]

Disclaimer/Publisher’s Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.