

Article

The Spread of the Invasive Locust Digitate Leafminer *Parectopa robiniella* Clemens, 1863 (Lepidoptera: Gracillariidae) in Europe, with Special Reference to Ukraine

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Abstract: The spread and outbreaks of phytophagous pests are often associated with global warming. In addition to economic interest, these species may be of interest in terms of biological indication of climate changes. In this context, we considered the locust digitate leafminer *Parectopa robiniella* Clemens, 1863 (Lepidoptera: Gracillariidae). This phytophage was first discovered in Europe in 1970 near Milano in Italy. Since then, it has been spreading across the continent. In Ukraine, it was recorded for the first time in 2003. In 2020–2021, we found areas of massive leaf damage caused by the black locust (*Robinia pseudoacacia*) in locations on Trukhaniv Island in Kyiv and some places in the Kyiv administrative region. Using 1041 georeferenced records of *P. robiniella* across Europe and a Bayesian additive regression trees algorithm (BART), we modeled the distribution of the moth. Predictors of current climate (WorldClim v.2, CliMond v.1.2 and ENVIREM) and a black locust habitat suitability raster were employed. Sets of SDMs built for *P. robiniella* with and without the habitat suitability raster for the host tree performed equally well. Amongst the factors that determine the niche of the locust digitate leafminer, most important are temperature-related conditions assumed to facilitate the spread and naturalization of the pest. In Ukraine, the appearance of the moth has coincided with increasing mean annual temperatures. Particularly favorable for the species are areas in the west and south-west of the country, and Transcarpathia. In the near future, the moth could reach locations in Nordic countries, Estonia, the British Isles, Black Sea coastal areas in Turkey, further into Russia, etc.

Keywords: locust digitate leafminer; *Parectopa robiniella*; invasive species; species distribution model; Europe; Ukraine



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1. Introduction

Earth's temperature has risen by 0.08 °C per decade since 1880, and the rate of warming over the past 40 years has been more than twice that: 0.18 °C per decade since 1981 [1]. Numerous studies provide evidence for biological responses to recent climate change [2], and in particular, focused on changes in the distribution and range shifts of species [3–5]. For pest insects, it is expected that climate warming will affect both incidence and the geographical extent and intensity of population outbreaks, with potentially severe economic and ecological consequences [6]. In this context, we considered the locust digitate leafminer *Parectopa robiniella* Clemens, 1863 (Lepidoptera: Gracillariidae), which has been suggested as a model species indicating climate change. It is native to North America, but was accidentally introduced to Italy, where it was first found in Milano in 1970 [7]. The moth has now been recorded in a number of European countries, ranging from Spain to Latvia [8–21].

On average, the spread of the pest occurs at a speed of about 100 km per year [22]. The moth is associated with the black locust (*Robinia pseudoacacia* L.), a tree introduced to Europe from North America at the beginning of the XVII century for decorative reasons, and to Ukraine it was brought at the end of the XVIII century [19]. In some countries, such as Romania and Hungary, it has become an essential landscape element [23,24]. In Ukraine too, particularly in the south, the tree has been widely cultivated for variety of purposes. *R. pseudoacacia* is considered an excellent plant for growing in highly disturbed areas as an erosion control plant [25], and the black locust is also a major honey-producing plant [26].

In Ukraine, the species was recorded for the first time in Kyiv and Chernivtsi (a regional capital in the south-west of the country) in 2003 [27]. In 2020, we discovered an extensive outbreak of the pest on Trukhaniv Island, a floodplain island located within the city boundaries of Kyiv. In 2021 a second outbreak was found in Obukhiv District, some 50 km south of the capital city. *P. robiniella* larvae develop in chambers (“mines”) inside the leaves, causing “finger-like” excavations all around the margins of the central blotch of the mine [28] (Figure 1). Strong damage to the leaves leads to reduction of the black locust’s flowering period and a decrease in nectar production, which adversely affects the honey harvest [29].



Figure 1. Locust digitate leafminer’s (*P. robiniella*) mines on black locust’s (*R. pseudoacacia*) leaves, Trukhaniv Island, June 2020.

Although *P. robiniella* is now widely prevalent in Europe, there are heterogeneities in the pest’s distribution that are likely linked to environmental parameters. In this respect, species distribution models (SDMs) have proven to be useful tools for predicting pest distribution and elucidating the importance of a wide range of environmental covariates that are considered to affect pest species occurrence [30]. Using SDMs, our objective was to: (1) identify areas of habitat suitability for the moth; (2) identify conditions that constrain the geographic distribution of *P. robiniella* in Europe, particularly in Ukraine; (3) against the background of the appearance of *P. robiniella* in Kyiv, verify the assumption that positive dynamics of the average annual temperature in the city could act as one of the possible factors promoting the invasion of this species.

2. Materials and Methods

2.1. Occurrence Records and Environmental Variables

As input, SDMs require georeferenced biodiversity observations. Localities for *P. robiniella* were gathered from GBIF [31,32], records found in the literature (see <https://>

dabasdati.lv/en/ [13–21]), and our personal field surveys. As many uncertainties are associated with SDM projections, particularly when it comes to building a SDM for a species expanding its home range in a new area [33], we used for the analysis only records of European localities. In its introduced range, black locust grows successfully in climatic conditions that are quite different from those of its native range [34]. This was for us an additional reason to focus on the invasive range of the pest, which is tightly associated with the tree host. SDMs commonly utilize associations between environmental variables and known species occurrence records to identify environmental conditions within which populations can be maintained. SDMs extrapolate in situ habitats in both space and time to obtain spatially explicit and continuous surfaces indicating the probability of species occurrence [35]. SDMs are primarily climate-driven, meaning that the variables used to develop them typically portray climatic factors [36]. This makes sense because climate is a chief driver of environmental suitability [30,36,37].

Information on the bioclimatic parameters was collected as raster layers from three climatic data bases and used separately for building the anticipated SDMs and checking their performances for both the moth and host tree.

From the WorldClim website (<http://www.worldclim.com/version2> (accessed on 21 January 2022)), 19 bioclimatic variables, indicating general trends in precipitation and temperature, including extremes and the seasonality of temperature [38], were downloaded at 2.5' resolution; however, we excluded four variables (Bio 8, Bio 9, Bio 18, and Bio 19) owing to their known spatial artifacts, following the protocol implemented in previous similar studies [39,40]. Other “Quarter” variables were removed too, because they are correlated a lot with monthly values and carry large amounts of redundant information.

CliMond v.1.2 datasets were downloaded from <https://www.climond.org/> at 10' resolution. These included the core set of 19 bioclimatic variables (temperature and precipitation) and an extended set of 16 additional variables (solar radiation and soil moisture) [41]. As in the previous case, quarterly variables were discarded.

In this study, we used for modelling purposes a set of 16 climatic and 2 topographic variables (the ENVIREM dataset, downloaded from <http://envirem.github.io> (accessed on 21 January 2022) in a 2.5' resolution), which were found by recently reconsidering biological significance; many of them are likely to have direct relevance to ecological or physiological processes determining species distributions [42,43]. These variables are worth consideration in species distribution modeling applications, especially as many of the variables (in particular, potential evapotranspiration) have direct links to processes that are important for species ecology. The included topographic variables are potentially important too, because they can modify the effects of the climate descriptors.

Although environmental conditions may predict a species' potential geographic distribution broadly, climatic factors typically used to represent those conditions are questionable surrogates for factors such as host availability [30]. Therefore, we included in each set of the used environmental predictors a raster reflecting the habitat suitability of the black locust in Europe. For this purpose, occurrences were extracted from the GBIF database [44].

Following M. A. Nuñez and K. A. Medley [45], we measured the spatial autocorrelation of occurrences by calculating Moran's I for multiple distance classes using the SAM v4.0 software [46]; values < 0.3 were considered acceptable for building meaningful SDMs [47]. The extent used during the niche modeling process has a profound influence on the outcome of the model [36]. In other words, if the extent under consideration is too limited to be accessible to the species area via dispersal, the importance of coarse-resolution factors such as climate in delimiting species' distributions may be underestimated [47].

2.2. Modelling Procedure

The extent used during the niche modeling process has a profound influence on the outcome of the model [35]. In other words, if the extent under consideration is too limited to represent accessible to the species area via dispersal, the importance of coarse-resolution factors such as climate in delimiting species' distributions may be underestimated [48].

To represent this area, in SAGA GIS [49] a bounding box was drawn around European point records of the leafminer and buffered to accommodate areas where the black locust is found in Europe. In this way, areas accessible to the species could stretch from Spain and Britain in the west and portions of Nordic countries, to the Caucasus–Caspian region in the east and south to the Mediterranean area and Turkey. Subsequently, environmental raster layers were clipped to this extent.

Climate variables often show high collinearity, and most SDM approaches require the selection of one among strongly correlated variables [50]. In order to carry out such selection, the “removeCollinearity” function in the “virtualspecies” R package was employed [51]. This function analyses the correlation among variables of the provided stack of environmental variables and returns a vector containing names of variables that are not collinear, and also groups variables according to their degrees of collinearity. As climate variables are commonly skewed or have outliers (e.g., when working with precipitation variables), the Spearman correlation method has been used.

SDMs were generated by employing Bayesian additive regression trees (BART), a powerful machine learning approach. Running SDMs with BARTs has recently been substantially facilitated by the development of an R package, “embarcadero” [52], which is highly effective at identifying informative subsets of predictors. Additionally, the package includes methods for generating and plotting partial dependence curves, illustrating the effects of selected variables on habitat suitability. The algorithm computes habitat suitability values ranging from 0, for fully non-suitable habitat, to 1, for fully suitable habitat.

Model performance was assessed using a measure based on the threshold-independent receiver operating characteristic (ROC) approach, where the calculated area under the ROC curve (AUC) is considered as a measure of prediction success [53]. The ROC curve is a graphical method that represents the relationship between the false-positive fraction (one minus the specificity) and the sensitivity for a range of thresholds. It has a range of 0–1: a value greater than 0.5 indicates a better-than-random performance event. A rough classification guide is the traditional academic point system: poor (0.5–0.6), fair (0.6–0.7), good (0.7–0.8), very good (0.8–0.9), and excellent (0.9–1.0).

Maps of habitat suitability in the GeoTIFF format were processed and visualized in SAGA GIS.

Against the background of the appearance of *P. robiniella* in Kyiv, positive dynamics of the average annual temperature in the city were hypothesized to act as one of the possible factors promoting the invasion of this species; data from the E-OBS (European Observations) website [54] were used for this purpose. Time series data were processed in R [55,56].

3. Results

In total, 1041 records of *P. robiniella* were collected from European localities. The GBIF database gave above 137,000 records for *R. pseudacacia* in Europe. For computational reasons, this number of records was reduced to 2447 using the “point thinning” module in SAGA GIS.

Figures 2–4 show groups of variables from the three considered databases of environmental predictors according to their degrees of collinearity; names of selected variables that are not collinear are presented in the captions, together with those that have been discarded (Figures 2–4).

Ecological niche models are sensitive to sample bias and spatial autocorrelation, which would produce models of lower rather than higher quality [57]; therefore, initial sets or records, for both the moth and black locust, were filtered out using the corresponding module in the “embarcadero” package. Due to the grid resolution issue, the total numbers of records for the moth and tree species were reduced to 832 and 2444, respectively, when predictors were used from the WorldClim v.2 and ENVIREM datasets, and to corresponding 318 and 1940 records, when employing the CliMond v.1.2 set of predictors. In all cases, Moran’s I is <0.3 ($p < 0.05$).

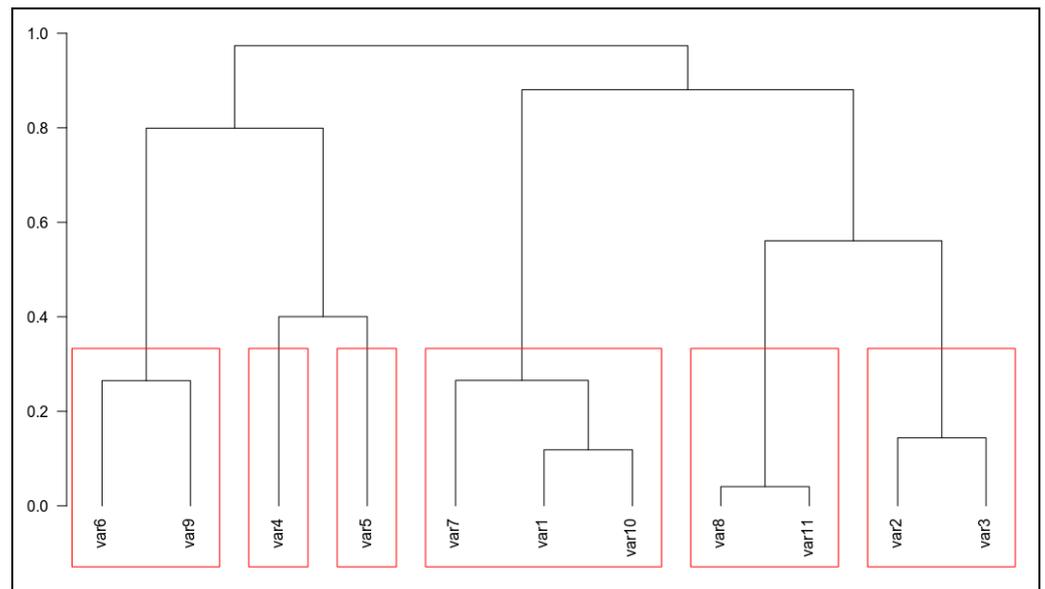


Figure 2. Groups of intercorrelated variables from the WorldClim v.2 dataset at cutoff 0.7; the y-axis represents distances between groups (1-Spearman's r). Variables (var): var1—annual mean temperature, var2—annual precipitation, var4—precipitation driest month, var5—precipitation seasonality, var9—max. temperature of the warmest month, var11—temperature annual range. Discarded variables: var3—precipitation of wettest month, var6—mean diurnal range, var7—isothermality, var8—temperature seasonality, var10—min. temperature of the coldest month.

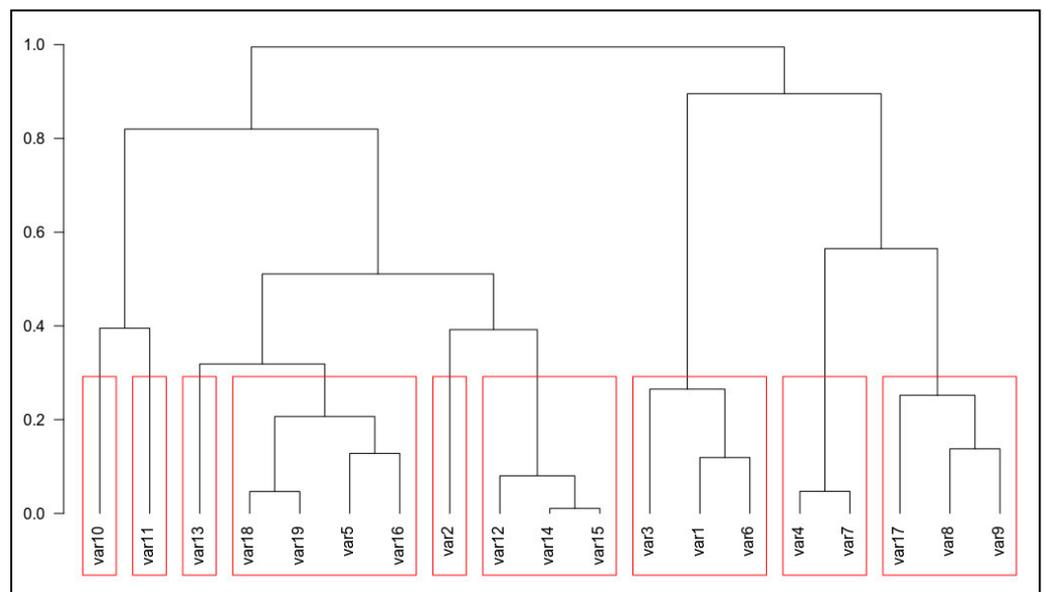


Figure 3. Groups of intercorrelated variables from the CliMond v.1.2 dataset at cutoff 0.7; y-axis as in Figure 1. Variables (var): var1—annual mean temperature, var2—mean diurnal temperature range, var4—temperature seasonality, var10—precipitation of driest week, var11—precipitation seasonality, var13—highest weekly radiation, var15—radiation seasonality, var16—annual mean moisture index, var17—highest weekly moisture index. Discarded variables: var3—isothermality, var5—max. temperature of warmest week, var6—min. temperature of coldest week, var7—temperature annual range, var8—annual precipitation, var9—precipitation of wettest week, var12—annual mean radiation, var14—lowest weekly radiation, var18—lowest weekly moisture index, var19—moisture index seasonality.

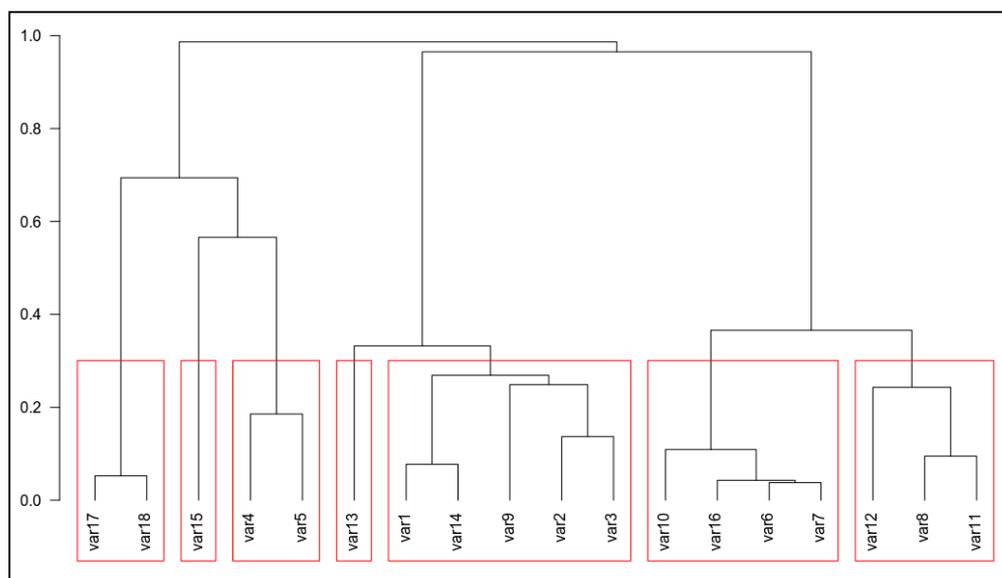


Figure 4. Groups of intercorrelated variables from the ENVIREM dataset to cutoff 0.7; y-axis as in Figure 2. Variables (var): var2—Thornthwaite aridity index (I_{Th}), var4—continentality, var6—growing degree days with mean temperature greater than 0 °C (gdd0), var8—maximum temperature of the coldest month, var13—monthly variability in potential evapotranspiration (PET), var15—mean monthly PET of the warmest quarter, var18—topographic wetness index. Discarded variables: var1—annual PET, var3—climatic moisture index, var5—Emberger’s pluviothermic quotient, var7—growing degree days with mean temperature greater than 5 °C (gdd5), var9—minimum temp. of the warmest month, var10—count of the number of months with mean temp greater than 10 °C, var11—mean monthly PET of coldest quarter, var12—mean monthly PET of driest quarter, var14—mean monthly PET of warmest quarter, var16—thermicity index, var17—terrain roughness index.

In Table 1, measures of accuracy are shown for each of the built SDMs: for the moth and host tree using bioclimatic predictors alone; and the other also incorporated the habitat suitability raster for the black locust, assumed to account for biotic interactions.

Table 1. Measures of accuracy of produced SDMs. *—SDMs built for *P. robiniella* (P), *R. pseudoacacia* (R) and *P. robiniella* incorporating the habitat suitability raster for *R. pseudoacacia* (P+R).

SDMs *	WorldClim v.2			CliMond v1.2			ENVIREM		
	P	R	P+R	P	R	P+R	P	R	P+R
AUC	0.935	0.770	0.936	0.936	0.772	0.926	0.944	0.772	0.943
±SE	0.009	0.010	0.009	0.012	0.011	0.012	0.009	0.010	0.008

One of the most crucial in SDM operations is identifying the key environmental variables that determine the niche of the species in question. Usually, SDMs are calibrated only with abiotic variables as predictors, assuming that biotic interactions are indirectly represented by abiotic variables because they strongly correlate [58]. For instance, the presence of the host plant (stonecrop, *Sedum* L. species) for the caterpillars of the butterfly *Parnassius apollo* Linnaeus, 1758 is critical; separate SDMs built just upon the use of bioclimatic parameters for the phytophage and host plant strongly correlate ($R_2 = 0.725$, $p < 0.05$), meaning much of the biotic interaction has been captured [59]. Commonly, it is understood that the addition of biotic interactions usually improves the predictive performance of SDMs [60].

Despite the presumption that climatic factors typically used to represent habitat conditions are rarely adequate surrogates for factors such as host availability [30,61], the AUC measure of accuracy showed that in all three cases, each of the two SDMs built

for the moth (one using the corresponding bioclimatic predictors alone, and the other also incorporated the habitat suitability raster for the black locust) performed excellently (AUC values ranging from 0.935 to 0.944, and from 0.926 to 0.943, respectively). Differences between the corresponding AUC values are statistically insignificant ($p > 0.05$). Additionally, both models in all three cases are highly correlated ($p < 0.05$): $R_2 = 96.18\%$, using the WorldClim v.2 predictors, $R_2 = 94.21\%$, using the CliMond v1.2 set, and $R_2 = 94.06\%$, using the ENVIREM set of variables.

The variable selection procedure in R package “embarcadero” identified informative subsets of variables, explaining in sum $> 60\%$ of variance in the corresponding SDMs (Table 2).

Table 2. Variables explaining in sum $> 60\%$ of variance in the SDM (ranked in order of variable importance).

WorldClim v.2	CliMond v.1.2	ENVIREM
1. Annual mean temperature	1. Temperature seasonality	1. Host habitat suitability
2. Host habitat suitability	2. Annual mean temperature	2. Thornthwaite aridity index (I_{TH})
3. Temperature annual range	3. Host habitat suitability	3. gdd0
4. Annual mean precipitation		

Of these seven predictors ranked in order of their importance, host habitat suitability is represented in each case (Table 2). Perhaps most sharply, this relationship is exemplified in the ENVIREM case, where habitat suitability for the moth rapidly increases with rising habitat suitability for the host tree (Figure 5A). In other words, “better for the host—better for the pest”—said, of course, in terms of the bioclimate. Most likely, the cause of the poorer performance of the SDM being obtained for the black locust itself was that other features essential for the tree (for example, soil) were not considered in the modelling, as the emphasis in this study was on the bioclimate. Nonetheless, at least in terms of the AUC, the SDM performed acceptably (0.740), and showed strong dependence on temperature variables, such as the annual temperature range and the minimum temperature of the coldest month. Similarly, strong dependence on temperature variables has been shown for the black locust in another study employing a maximum entropy model [62].

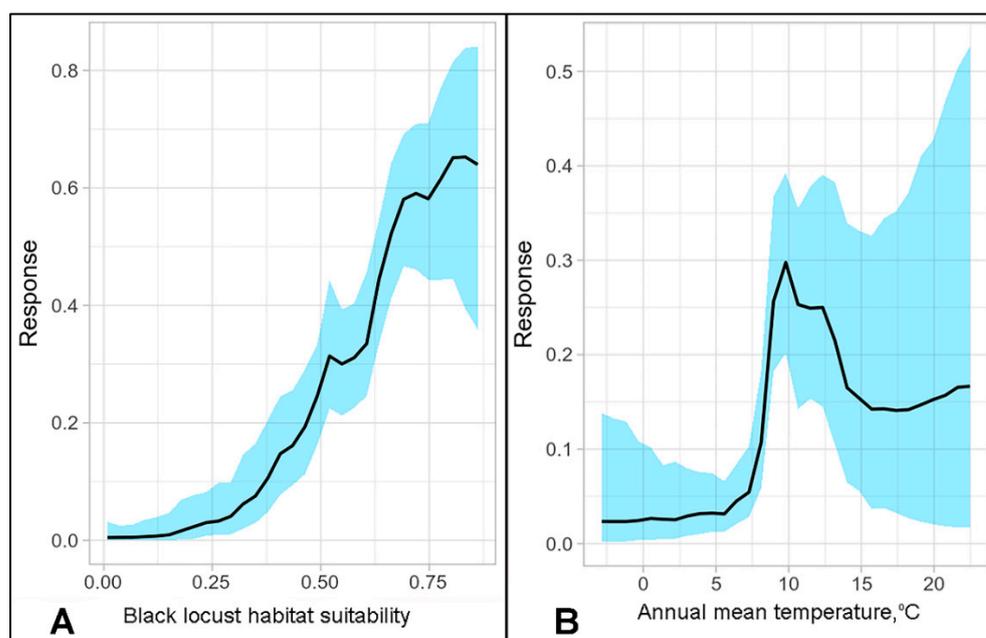


Figure 5. (A) Partial dependence plot for predictor: black locust habitat suitability. Response = predicted moth habitat suitability; blue area = 95% confidence interval; (B) partial dependence plot for predictor: annual mean temperature, °C.

Interestingly, cold season conditions turned out to be less influential for establishing the moth niche. Such parameters as the maximum temperature of the coldest month (ENVIREM set) and precipitation of driest month (WorldClim v.2 set) have been selected by the BART algorithm; however, they are low ranking in terms of variable importance. Probably, this is because the moths successfully pass the winter at the pupal stage under the reliable protection of leaf litter [19,27].

4. Discussion

Plots of partial dependence curves of identified informative bioclimatic predictors manifesting the model for *P. robiniella* are presented in Figures 5B and 6A. In Figure 5B, the curve demonstrates the dependence of the well-being of the moth on annual mean temperature (exemplified by the CliMond v.1.2 set). From below the level of 5%, habitat suitability reaches a maximum (approximately 30%) at around an annual mean temperature of 10 °C, and further gradually drops to a more or less stabilized level close to 15% (Figure 5B). Figure 6 represents the response curve for the Thornthwaite aridity index (from the ENVIREM set), based on the relationship between precipitation and potential evapotranspiration, and describes the interplay among rainfall, temperature, and evaporation [63]. On a global scale, the index has been used to categorize the world into nine moisture zones ranging from arid to perhumid [64,65]. From the graph, it can be seen that the highest habitat suitability values for the moth are in the range of $0 < I_{Th} < 20$, which relate to a moist subhumid climate (type C2) (Figure 6A).

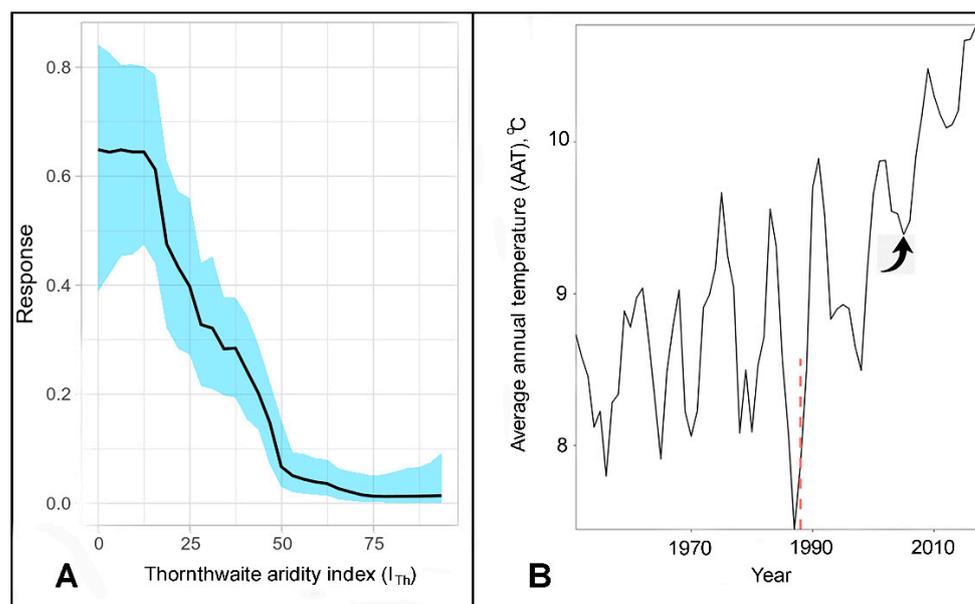


Figure 6. (A) Partial dependence plot for predictor: Thornthwaite aridity index (I_{Th}); dimensionless. (B) Dynamics of the average annual temperature (AAT) in Kyiv for 1950–2017; x-axis—years, y-axis—AAT (°C); the red dotted line indicates 1988 ('breakpoint'), after which there is a steady tendency to rising AAT; the arrow marks the time of the first appearance of *P. robiniella* in Kyiv (2003).

For building a summarizing model of the potential distribution of *P. robiniella* in Europe under the current climate, we employed variables explaining in sum > 60% of variance in each of the SDMs built for a separate environmental dataset (Table 2). These are raster images representing black locust habitat suitability, annual mean temperature, annual temperature range, temperature seasonality, growing degree days with mean temperature greater than 0 °C, Thornthwaite aridity index (I_{Th}), and annual precipitation.

Using the SDM and the 10th percentile threshold [65], locations can be found in Europe that are assumed under current climatic conditions to support the spread and naturalization of the moth. In Figure 7, these areas are colored in green and cover a vast

range in Western and Central Europe, much of Italy, and the Balkans, reaching as far as the eastern Black Sea region and the Caucasus (Figures 7 and 8). In Ukraine, which is particularly favorable for the pest, there are areas in the west and south-west of the country, and Transcarpathia, bordering the Pannonian Plain. Favorable areas for the moth are predicted in the United Kingdom; however, there have been no records of the moth. As *P. robiniella* is obviously expanding its home range and is not yet in equilibrium with its environment, we used the 1st percentile threshold as a less conservative threshold to discern between suitable and unsuitable environments. Perhaps in the near future, these areas (colored in blue in Figure 7) will be more widely invaded by the moth, reaching locations in Nordic countries and Estonia, the British Isles, Black Sea coastal areas in Turkey, more of Russia, etc. (Figure 7).

For linking the appearance of *P. robiniella* in Kyiv with climatic dynamics, average annual temperature records in the city for 1950–2017 were downloaded from the E-OBS database. According to the E-OBS, the average annual temperature in Milano in the 1970s, where *P. robiniella* was first detected, was 12.99 °C, which assumes that local conditions were favorable for its naturalization, which in fact happened. At that time, the average annual temperature in Kyiv was 8.73 °C, and the difference from Milano was then 4.26 °C. Since 1988, there has been a significant ($p < 0.05$, 1000 bootstrap) trend of increasing average annual temperature in Kyiv (Figure 6B), and now the difference in temperature between itself and Milano is 64% less than what it was in the 1970s: precisely 2.73 °C. In the 2000s, when *P. robiniella* was already detected in Kyiv, the average annual temperature was increasingly favorable for the species, -9.70 °C, and in the past decade it has risen to 10.26 °C. In light of our modelling exercises, we consider steeply rising average annual temperatures (perhaps more exactly, temperatures rising on average in the summer, when the moths are active in their development) are involved in setting the scene for the spread and naturalization of the pest, although in a recent study [66] a negative correlation was found between temperature and spread.

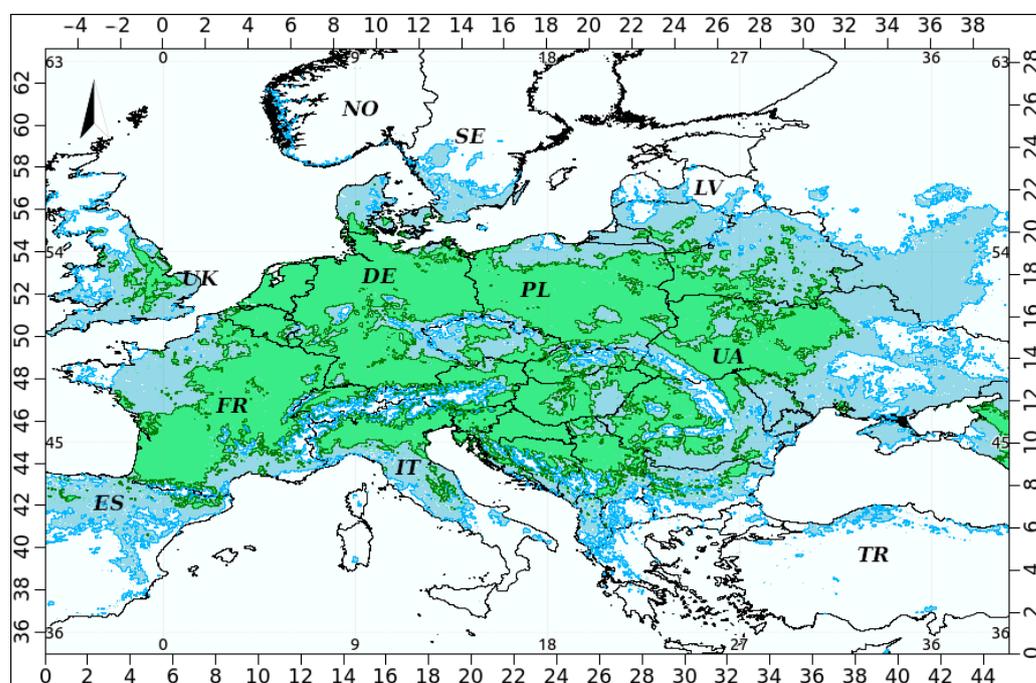


Figure 7. Map of the potential distribution *P. robiniella* in Europe. Areas within the 10th percentile threshold are colored in green; areas within the 1st percentile threshold are colored in blue; country codes: France (FR), Germany (DE), Italy (IT), Latvia (LV), Norway (NO), Poland (PL), Spain (ES), Sweden (SE), Turkey (TR), United Kingdom (UK), Ukraine (UA).

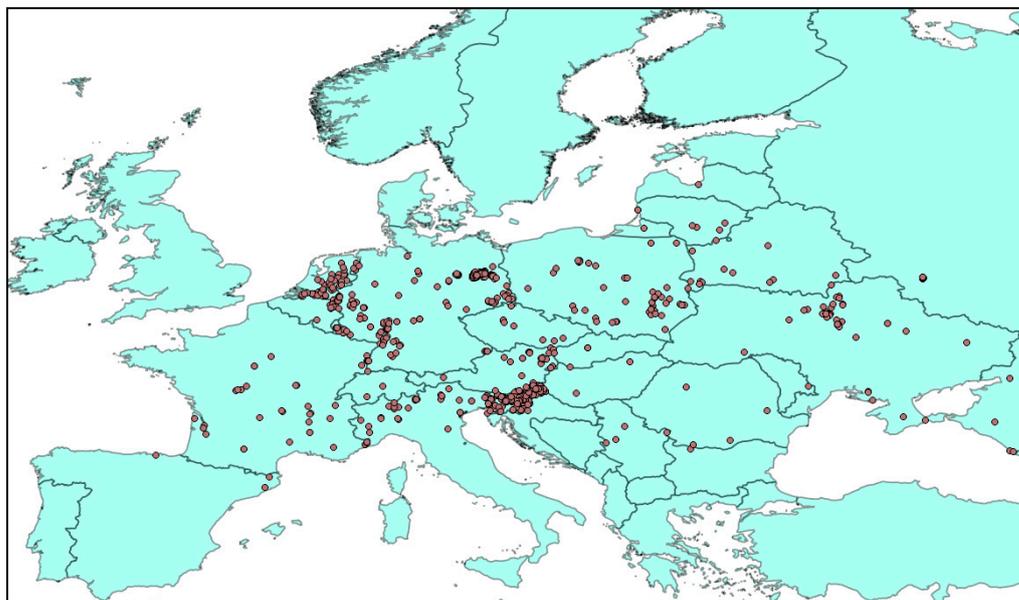


Figure 8. Map of the actual records (non-duplicable) of *P. robiniella* in Europe [13–21,31,32].

5. Conclusions

SDMs seeking to identify features that characterize a species' known distribution are likely to provide basic quantitative information about the species' apparent habitat preferences [67,68] and potential distribution. In our study, the extraction of such information was accomplished by the use of the SDM response curves for a number of environmental covariates identified as an informative subset of predictors. Emphasis was put on warmth conditions facilitating the spread and naturalization of the considered pest.

Contrary to the common understanding that the addition of biotic interactions usually improves the predictive performance of SDMs, in our study both sets of SDMs built for *P. robiniella* (with and without the habitat suitability raster for the host tree) performed equally well.

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Data Availability Statement: The data presented in this study are openly available in [*Paractopa robiniella*. GBIF.org. GBIF Occurrence Download. Available online: <https://doi.org/10.15468/dl.dp8wtr> (accessed on 19 October 2020) and *Robinia pseudoacacia*. GBIF.org. GBIF Occurrence Download. Available online: <https://doi.org/10.15468/dl.8f4mb4> (accessed on 5 February 2022)].

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Conflicts of Interest: The authors declare no conflict of interest. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

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