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Potential distribution of the citrus Mal Secco disease in the Mediterranean basin under current and future climate conditions

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Abstract

Species distribution models are widely used to estimate the potential geographic distribution of species habitat. They are also used to predict the impact of climate change on species distributions. In this study, we examined the distribution of Mal Secco disease, an infective disease of citrus caused by the fungus *Plenodomus tracheiphilus*. To model the Mal Secco distribution under current and two future (2050 and 2070) climatic scenarios in the Mediterranean basin, eight climate variables were incorporated into the Maximum Entropy (MaxEnt) model. All three model distributions had high AUC values (0.97), indicating excellent performance. The precipitation during the wettest month and the minimum temperature during the coldest month contributed the most to the model. The suitable areas for the Mal Secco disease were predicted to decrease by up to 23% by the year 2070. For each of the three scenarios, the change in the proportion of suitable areas along the longitudinal (west–east) and latitudinal (south–north) geographical axes of the Mediterranean basin showed a similar trend. Our study highlights the supposition that while climate change is likely to reduce the extent of suitable areas, no range shift is expected to occur in the Mediterranean basin.

KEYWORDS

citrus, climatic scenarios, MaxEnt, pathogen, *Plenodomus tracheiphilus*, spatial distribution

1 | INTRODUCTION

In recent years, climate change has adversely impacted ecosystems and myriad biological species on a global scale (Smeraldo et al., 2021; Vermeiren et al., 2020). Continuously intensifying changes in climate may lead to different effects, including range contraction (Barbetti et al., 2012), range expansion (Blank & Blaustein, 2012) and in many cases shift in the distribution range (Bebber et al., 2013) of plant pathogens. In the context of agricultural systems, plant diseases are key factors affecting global agricultural productivity, and climate change is expected to further aggravate the situation (Gornall et al., 2010). Among other factors in this process, the effects of climate change on plants and pathogens that are influenced by the environment, directly or indirectly, are key. One expectation is that the range of pathogens will shift. Bebber et al. (2013) estimated that, since 1960, there has been a poleward shift among hundreds of pests and pathogens, but the shifts vary widely among taxonomic groups. Overall, over the past 30 years, more than 100 review articles have

been published, including opinion papers and book chapters, which focus on potential climate change effects on plant pathogens and future crop disease risks (Juroszek et al., 2020).

Species distribution models (SDMs) are widely used to estimate species' niches using specific algorithms based on species occurrence data and environmental variables (Elith & Leathwick, 2009; Raffini et al., 2020). These estimates can then be used to identify potentially suitable areas for certain species, thereby helping to simulate range shift due to climate change (Jeschke & Strayer, 2008). In addition, SDMs can contribute to identifying bioclimatic variables affecting pathogen distribution (Bosso et al., 2016; Shabani et al., 2014). Maximum Entropy (MaxEnt) model is a software for modelling species niches and distributions, based on environmental variables and species distribution records. The program integrates machine learning and maximum entropy principles to simulate the potential geographical distribution of species (Elith et al., 2011). Compared with other SDMs, MaxEnt uses presence-only data, and has been shown to remain effective even when occurrences are low (Blank & Blaustein, 2012; Costa et al., 2010; Hernández-Baz et al., 2016; Papeş & Gaubert, 2007); numerous studies have used it to model the distribution of various pathogens (Bebber, 2015; Bie et al., 2021; Shukla et al., 2020).

Plenodomus tracheiphilus (formerly *Phoma tracheiphila*) is a mitosporic fungus that causes Mal Secco disease, an infective disease of citrus (mostly lemons) that colonizes the host's vascular system (Nigro et al., 2011). It was originally discovered in the Chios and Poros islands (Greece) near the end of the 19th century, and based on the literature, its current geographical distribution encompasses the east coast of the Black Sea (Georgia) and citrus-growing countries of the Mediterranean (Migheli et al., 2009; Nigro et al., 2011). Surprisingly, despite the fact that no evidence exists of factors—climatic or cultural—that might limit the spread of this disease, it does not occur in the citrus-growing countries of the Americas, Asia or Oceania. Mal Secco is not even found in some citrus-growing countries of the Mediterranean basin, like Spain, Portugal and Morocco. A very recent limited outbreak of the disease in southern Spain was promptly eradicated.

Details on the epidemiology of Mal Secco have been described previously (Migheli et al., 2009; Nigro et al., 2011). The plant pathogen is disseminated by rain and wind. Infection is made possible by frost, hail, rain and wind, as well as other ways that create wounds, which *P. tracheiphilus* uses to penetrate the plant. Although infection can occur at moderate temperatures, between 14 and 28°C, the optimum temperature range for pathogen growth is 20–25°C. The economic losses linked to Mal Secco disease have been dramatic for the Mediterranean's citrus industry; nonetheless, its spatial distribution has not been studied extensively (Bebber et al., 2013; Migheli et al., 2009). A recent study assessing the incidence and spatial patterns of Mal Secco in lemon orchards in Israel implied that the rate of disease spread is primarily the result of orchard management practices (Ben-Hamo et al., 2020).

Predicting the potential distribution of this disease and suitable habitats for it under different climate change scenarios can help identify potential areas that are at risk for future exposure to the pathogen. With this in mind, the objective of this study was to model the potential distribution of *P. tracheiphilus* in the Mediterranean basin under current and different climate change scenarios.

2 | MATERIALS AND METHODS

2.1 | Study area and Mal Secco presence records

In this study, we included the entire Mediterranean basin between latitudes 50°N to 25°N and longitudes 10°E to 49°E (Figure 1). The Mal Secco distribution data, which included 53 independent presence records, were collected from various sources, including the professional literature and personal communications.

2.2 | Selection of ecogeographical variables

Global climate data were obtained from the WorldClim database (www.worldclim.org). A total of 19 bioclimatic variables and

FIGURE 1 Study area. Mal Secco occurrence data marked with red dots.

elevations were used for our analysis. All variable formats were raster files (grid) with a resolution of 5 arc-minutes.

To eliminate the highly correlated variables we used the 'corrplot' package in R (Wei & Simko, 2021) and retained predictors with a Pearson's $r < 0.80$ (Fotheringham & Oshan, 2016; Figure 2). From this set of variables, we considered only those most relevant to the biology of the species. This led to a final set of eight variables (Figure 3): (a) bio4—temperature seasonality, (b) bio5—max temperature of warmest month, (c) bio6—min temperature of coldest month, (d) bio8—mean temperature of wettest quarter, (e) bio13—precipitation of wettest month, (f) bio14—precipitation of driest month, (g) bio15—precipitation seasonality and (h) elevation. These variables were used to model the current and future potential distribution of *P. tracheiphilus* in the Mediterranean basin.

2.3 | Climate model

MaxEnt was used to create distribution models of Mal Secco in the Mediterranean basin. The MaxEnt ecological niche model integrates interactions among variables and can be applied to produce predictions even based on incomplete information, which yields higher accuracy predictions than other presence-only approaches (Rödder & Lötters, 2009). A set of 10,000 background points were randomly selected across the region studied to represent pseudo-absence points. The model was cross-validated by randomly selecting 75% of the records for training and the remaining 25% to test the model. This procedure was repeated 50 times. Variable contribution analysis, as well as variable response plots and expected distribution maps, were computed to create the current conditions model (1970–2000). The 10th percentile (the value above which the model correctly classifies 90% of the training locations) was selected as the threshold value for defining the presence of Mal Secco. The 10th percentile threshold is a conservative value commonly adopted in species distribution modelling studies (Bosso et al., 2013; Rebelo & Jones, 2010; Russo et al., 2015); it was used to reclassify our models into binary presence/absence maps. The average final map obtained had a logistic output format with suitability values from 0 (unsuitable habitat) to 1 (suitable habitat).

The percentage of suitable habitat was calculated to compare maps and evaluate the change in suitability over time. In addition, in order to evaluate potential spatial range shift, we calculated the mean suitability value along the west–east and north–south geographical axes of the studied area using the 'RasterVis' package in R (Lamigueiro et al., 2022).

2.4 | SDMs of *P. tracheiphilus* under future climate model

To predict the potential distribution of *P. tracheiphilus* under future climate conditions, we downloaded the projections of future bioclimatic variables from the WorldClim database. The sixth UN Intergovernmental Panel on Climate Change (IPCC) assessment
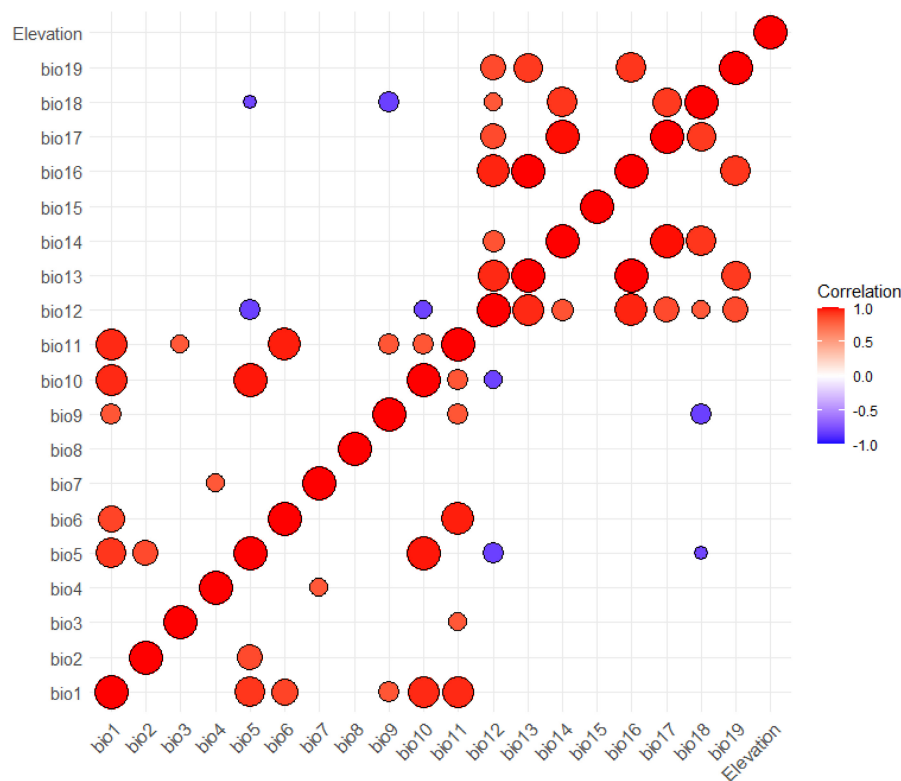

FIGURE 2 Correlation matrix of all the 20 bioclimatic variables tested. Negative and positive correlations are represented by red and blue dots respectively. Dot size and colour indicates correlation value, from −1 (blue) to +1 (red).
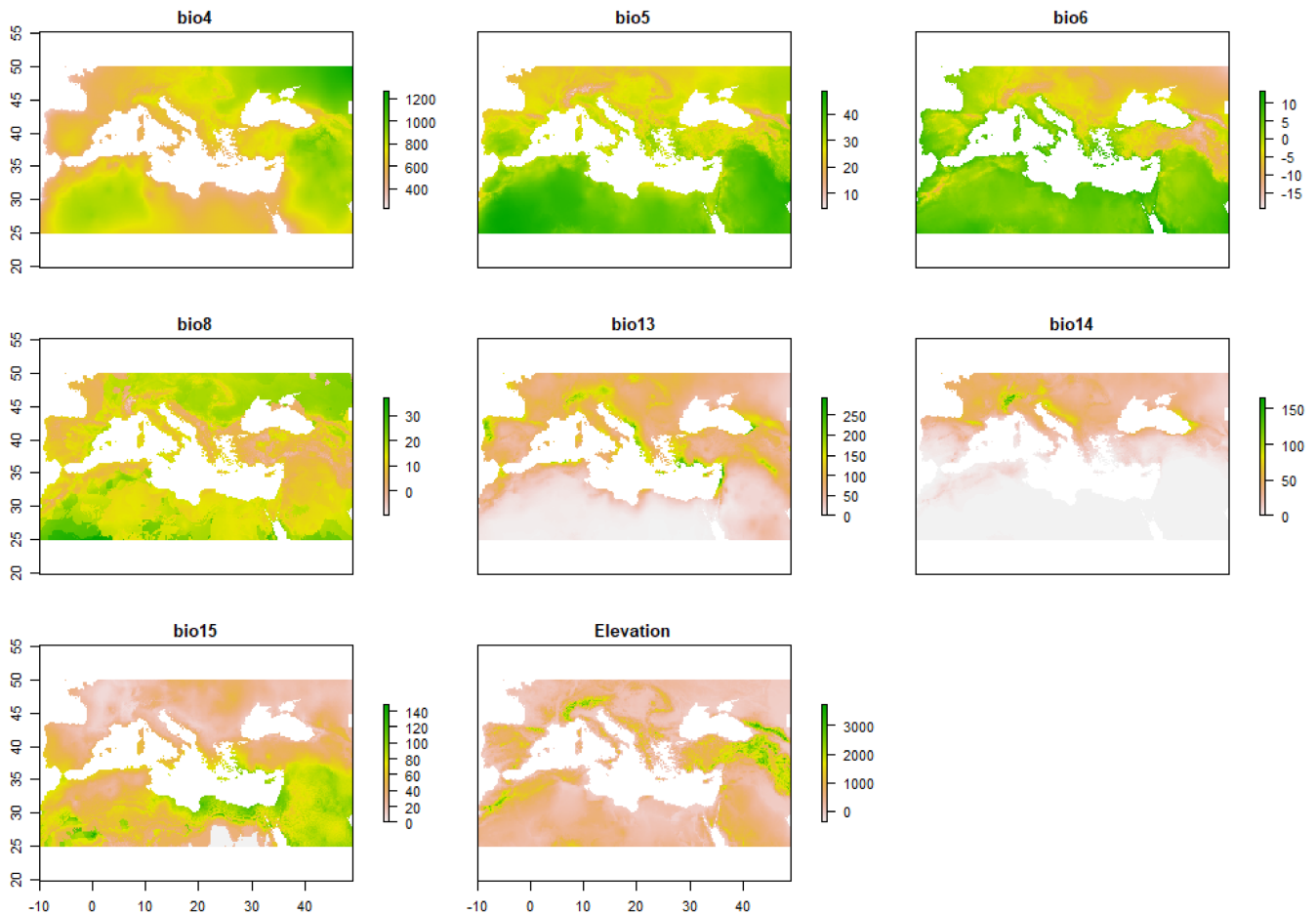
FIGURE 3 Maps of the eight selected bioclimatic variables and elevation.

report Coupled Model Intercomparison Project (CMIP6) published four climate change scenarios, namely, the Shared Socioeconomic Pathways (SSPs) SSP126, SSP245, SSP370 and SSP585. We chose the SSP245 scenario to generate the Mal Secco projection for 2041–2060 (Figure 4, map 2050) and 2061–2080 (Figure 4, map 2070). This scenario predicted greenhouse gas emissions would remain about the same as the current (1970–2000) level and the global average temperature would tend to decrease due to human intervention. Model evaluation and cross-validation were conducted using the same methods as those used to generate the current climate model: 75% of the records were randomly selected for training and the remaining 25% were used to test the model. The response curves for each bioclimatic variable were extracted for the model.

2.5 | Model validation

The area under curve (AUC) generated by the MaxEnt function was used to evaluate the model performance under each scenario. In general, model performance was measured using AUC, ranging from 0.5 (not better than random) to 1 (perfect discrimination) (Liu et al., 2005). The AUC was averaged across the 50 replicates running on the testing dataset, that is, 25% of the records. All data analysis

was conducted using R statistical software (v. 4.1.2). The MaxEnt model was configured by the packages 'Dismo' (Hijmans et al., 2017), 'zeallot' (Teetor, 2018) and 'SDMtune' (Vignali et al., 2020).

3 | RESULTS

3.1 | Model evaluations

The MaxEnt model for the current scenario had a mean AUC of 0.97 ± 0.012, indicating excellent predictive performance. The AUC was 0.97 ± 0.014 for both the 2050 and 2070 models. The expected distribution maps for the three scenarios are presented in Figure 4. The maps show that the areas with the highest disease suitability are around the Mediterranean Sea, in Spain, Italy, Greece, Turkey, Lebanon, Israel, Libya, Tunisia and Morocco.

3.2 | SDMs of *P. tracheiphilus*

The change in the proportion of suitable areas on longitudinal (west–east) and latitudinal (south–north) geographical axes is presented in Figure 5. The three scenarios showed a similar trend along both axes.
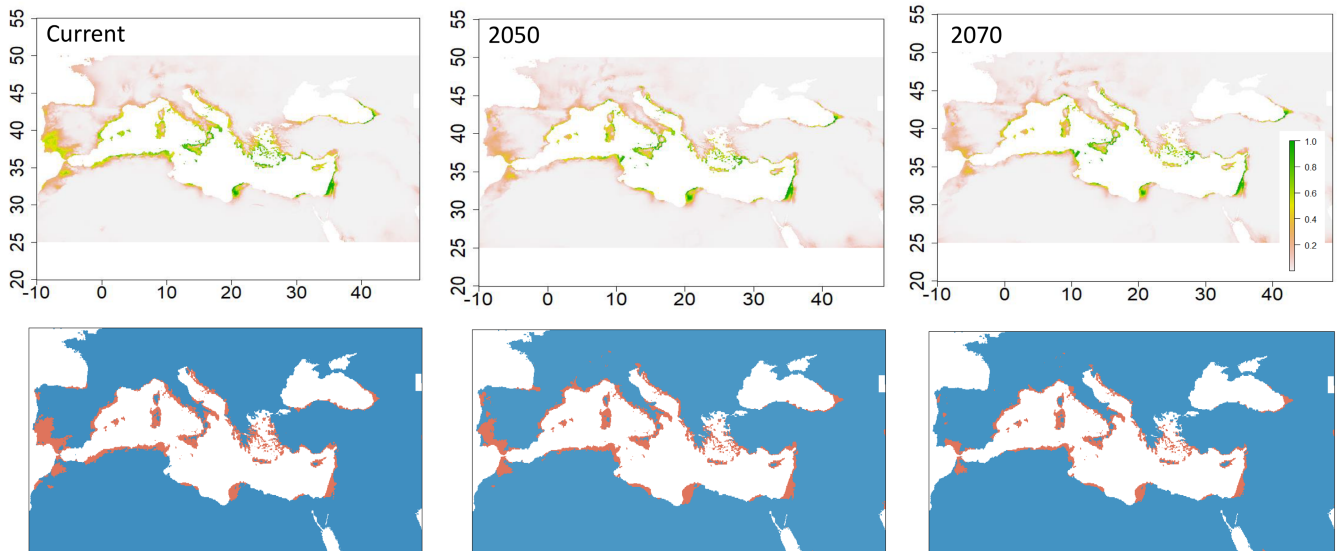
FIGURE 4 Distribution of the Mal Secco disease under current (maps on the left) and future SSP245 scenarios for 2050 (middle) and 2070 (right), according to MaxEnt modelling. Logistic maps (top row) show the probability of the disease presence ranging from 0 (red) to 1 (green) and binary maps (bottom row) show the extent of disease-suitable (red) and unsuitable (blue) areas.

The highest suitable value along the *x*-axis (longitude) is located in Spain and Morocco, with a mean suitability value of 0.14 under the current scenario. This value is considerably lower for 2050 (0.07) and 2070 (0.06). At longitude 10°E (Sardinia and northern Tunisia), the mean suitability values were also high (reaching 0.1) and peaked again (0.11) at both 15°E (mainland Italy and Sicily) and at 35°E (Lebanon and Israel). Generally, the current conditions model has the highest suitability values along most of the west–east axis, with the 2070 scenario showing the lowest values. The area of Israel is the only area where levels are high in all scenarios. Along the latitudinal axis, a similar trend was observed: the current scenario resulted in considerably higher suitability values compared to the values in the 2050 and 2070 scenarios. The disease suitability values under all three models increased from 30° N and peaked at 37° N (Sicily, southern Italy, southern Spain and Portugal). Compared to the current conditions model and based on the binary map, the percentage of suitable areas for Mal Secco disease is expected to decrease by 23% by 2070.

3.3 | Environmental variable contribution

The contributions to the Mal Secco distribution of two variables were considerable in all three models: precipitation during the wettest month (bio13) and the minimum temperature during the coldest month (bio6) (Table 1). Precipitation in the wettest month showed the highest average contribution (40%) in all three models. Minimum temperature in the coldest month was the next most important variable, with $34.66\% \pm 5.4$ under the current scenario, to $29.72\% \pm 6.29$ and $25.83\% \pm 6.17$ under the 2050 and the 2070 scenarios respectively. The species response curves showed that the probability of *P. tracheiphilus* presence increased with precipitation

in the wettest months and minimum temperature in the coldest month (Figure S1).

4 | DISCUSSION

The Mal Secco suitability models under all three scenarios had high AUC values, implying excellent performance of the MaxEnt modelling tool. The distribution of the suitable areas for Mal Secco disease showed a constriction in light of climate change. It is important to note that in this study we tried to predict the change in suitable areas for Mal Secco and not the actual distribution of the pathogen. Model predictions based on low numbers of occurrence sites should not be interpreted as predictions of a species' range, but rather as identifying regions with similar environmental conditions to those where the species is known to occur (Pearson et al., 2007). Caution in interpreting such models also derives from overlooking other potential factors in predicting disease spread, for example, host distribution, the pathogen's adaptation to the changing climate and dispersal patterns.

Previous studies demonstrated the possible changes in the location of suitable habitat that results from climate change (Hoveka et al., 2016). Kong et al. (2021) employed MaxEnt modelling to predict the likely distribution of *Osmanthus fragrans* and revealed that its central growth area would decrease and shift to south-west China by 2061–2080. Zhang et al. (2020) found that the suitable area of *Euscaphis japonica* would geographically expand further north in the 2050s and 2070s. Bebber et al. (2013) demonstrated an average poleward shift of 2.7 ±0.8 km per year since 1960 in observations of hundreds of pests and pathogens. In our study, we could not find a directional shift in the suitable areas, but we found an overall decrease of 23% in the extent of suitable habitat for *P. tracheiphilus*
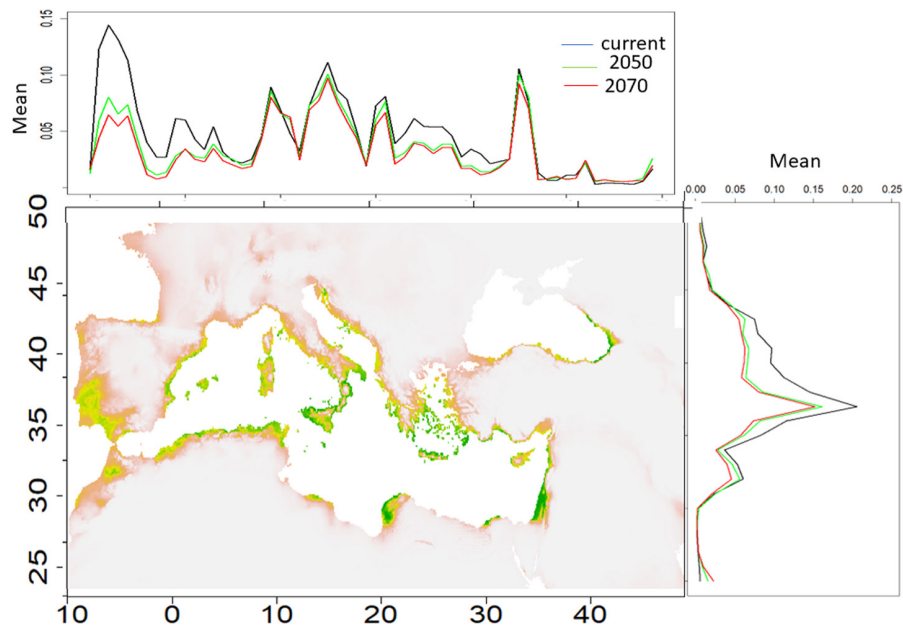
FIGURE 5 Suitability map of Mal Secco disease showing the mean suitability values of the three scenarios (current, 2050 and 2070). The change in the average suitability along each geographical axis (coordinate) is presented.

TABLE 1 Summary of variables contribution (%)

Variable	Current scenario contribution ± SD	Future map 2050 contribution ± SD	Future map 2070 contribution ± SD
Bio4—temperature seasonality	9.77 ± 2.8	11.14 ± 2.54	13.90 ± 2.32
Bio5—max temperature of warmest month	0.01 ± 0.02	2.34 ± 0.82	1.18 ± 0.94
Bio6—min temperature of coldest month	34.66 ± 5.4	29.72 ± 6.29	25.83 ± 6.17
Bio8—mean temperature of wettest quarter	1.47 ± 0.71	2.02 ± 0.93	7.01 ± 1.01
Bio13—precipitation of wettest month	40.38 ± 4.07	39.78 ± 4.11	37.42 ± 2.79
Bio14—precipitation of driest month	2.99 ± 0.73	1.75 ± 0.81	1.84 ± 0.81
Bio15—precipitation seasonality	6.30 ± 1.88	11.73 ± 5.31	10.14 ± 4.95
Elevation	4.38 ± 2.60	1.48 ± 1.95	2.62 ± 2.93
AUC	0.97 ± 0.012	0.97 ± 0.014	0.97 ± 0.015

Note: Values are averaged across 50 permutations ± SD.

by 2070. Nonetheless, a large area of the Mediterranean basin will still be suitable for *P. tracheiphilus* infection. Noteworthy is that in this study we selected scenario SSP245, which predicts a smaller increase in temperature compared to other, more extreme scenarios. Specifically, SSP245 predicts maximum temperature increases of 0.2–0.6°C per decade, while SSP3700 predicts a 0.4–1.0°C increase per decade and SSP585 predicts increases of 0.6–2.0°C per decade. Thus, the change we predicted in suitable areas might be conservative.

Based on the results and the current scenario, suitable areas for Mal Secco disease are the coastal areas of the Mediterranean Sea. The Mediterranean climate is characterized by relatively cool wet winters and hot dry summers. *P. tracheiphilus* appears to be less harmful where winter is not too cold; freezing events, that is, temperatures below 0°C, can decrease *P. tracheiphilus* viability (Migheli et al., 2009); moreover, they may be a limiting factor for the cultivation of lemon and limes, which are among the most susceptible citrus species. The southern Mediterranean region is characterized by lower levels of precipitation in both the wet and dry months, and higher temperatures. Such conditions are not well suited for growing citrus cultivars (Dutta et al., 2022), nor for the development of Mal Secco, and are probably the principal reason for the absence of *P. tracheiphilus* from most of the southern Mediterranean area. The actual distribution of Mal Secco in citrus-growing countries of the Mediterranean basin is also conditioned by the distribution of lemon (*Citrus × limon*), the primary host of *P. tracheiphilus* (Migheli et al., 2009).

Although changes in climatic patterns differ across regions around the world, evidence indicates that the Mediterranean region is one of the most vulnerable to climate change, with decreasing precipitation and rising temperatures (Korres et al., 2016). Temperature is the most discussed parameter involved in the potential climate change effects on plant pathogens (Juroszek et al., 2020). Presumably, that is because temperature is widely found to be related to pathogen

life cycles (Boland et al., 2004). For example, Boland et al. (2004) showed that the projected milder winters in Ontario, Canada, may promote increased survival of most pathogens due to a reduced number of frost days. We found the minimal temperature during the coldest month (bio6) to be the primary variable in terms of temperature related to the suitability model of *P. tracheiphilus*, constituting approximately 25%–35% of the contribution of temperature as a condition of suitability. Xu et al. (2020) found bio6 to be the most critical climate factor affecting the distribution of the apple canker (*Valsa mali*), which similarly to *P. tracheiphilus*, penetrates the tree and causes an infection in the branches. Because the optimum temperature for growth of *P. tracheiphilus* ranges between 20 and 25°C, the higher the minimum temperature in the winter, the higher the chances for the pathogen to survive until infection can occur as the temperature rises.

In order for *P. tracheiphilus* to infect citrus trees, in addition to a suitable temperature, winds, hail and heavy rains can contribute by damaging the plant tissue. During heavy rains, microscopical wounds are formed in the plant through which the pathogen can later penetrate (Ezra et al., 2007; Migheli et al., 2009; Nigro et al., 2011). Moreover, rain is regarded as the main natural dispersal agent of *P. tracheiphilus* (Migheli et al., 2009). Indeed, we found that the most important bioclimatic variable in our model is precipitation in the wettest month (bio13). Other studies also found that precipitation rates played an important role in pathogen infections. Previous observations indicated that mid-November to mid-April was the most conducive period for pathogen infection in Israel, coinciding exactly with the rainy season. Ajene et al. (2020) found that precipitation in the wettest month contributed 35% to the distribution of 'Candidatus Liberibacter asiaticus' (Las) and 'Candidatus Liberibacter africanus' (Laf) in citrus. Al Ruheili et al. (2021) found that precipitation contributed 20% to the spread of phytoplasma disease in lime and alfalfa. Blank et al. (2019) found winter precipitation to have a high and significant independent contribution to the spread of *Fusarium circinatum* in pine forests.

This is the first study modelling the distribution of *P. tracheiphilus* in the Mediterranean basin. We discuss the potential biological effects of the two climatic variables identified in this study on the development of Mal Secco disease. However, it is important to note that high minimum temperature in the coldest month and high precipitation in the wettest month might be associated with factors affecting the spatial distribution of the citrus hosts in the Mediterranean basin. Obviously, the distribution of the host has an impact on the occurrence and distribution of *P. tracheiphilus*. Regardless, a fundamental requirement for the establishment of any species outside its native range is that the climate in the recipient location is comparable to that of the invader's original range. This study highlighted the importance of investigating the geographic distribution of pathogens, even those with a relatively limited range, which constitute a major threat to an economy, in this case the lemon industry, and potentially to food security. As stated, based on the literature, the current geographical distribution of Mal Secco primarily covers all the citrus-growing countries of the Mediterranean basin, except for Morocco, Spain and Portugal, and runs east as far as the east coast of the Black Sea (Georgia). The study showed that Morocco, Spain and Portugal, while still free of Mal Secco disease, have suitable conditions for its development. Because *P. tracheiphilus* is difficult to control, and even more so to eliminate, management efforts should focus on preventing the fungus from spreading to new areas through the use of disease-free propagation material and use of resistant cultivars. The efficient control of the disease relies on a thorough comprehension of all factors involved in the epidemiological processes of a pathogen, including its survival, spread, pathogenicity and its interactions with the continually changing climate.

DATA AVAILABILITY STATEMENT
The data that support the findings of this study are available from the corresponding author upon reasonable request.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.