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Species distribution modelling of invasive alien species; Pterois miles for current distribution and future suitable habitats

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ABSTRACT

The present study aims to predict the potential geographic distribution and future expansion of invasive alien lionfish (*Pterois miles*) with ecological niche modelling along the Mediterranean Sea. The primary data consisted of occurrence points of *P. miles* in the Mediterranean and marine climatic data layers were collected from global databases. All the used models run 100% success predictions, and true skill statistics and area under the receiver operating characteristic curve values ranged from 0.42 and 0.71 to 0.86 and 0.95 for current distribution modelling; and 0.0 and 0.0 to 0.83 and 0.94 for the future distribution modelling, respectively. The mean sea surface temperature and maximum bathymetry played an important role in the prediction of the model and explained relatively higher biological importance to the extension and adaptation of *P. miles* with extreme environmental factors. The predicted suitable habitats of *P. miles* under the current climate dominantly occurred in the east parts of coastal areas of the Mediterranean. The predicted future suitable habitats of *P. miles* revealed that *P. miles* increase its range of distribution dominantly to the central and west part of the Mediterranean in a spatial extent, indicating high suitability of these areas for its future distribution.

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INTRODUCTION

Climate change has led to episodic fluctuations in sea-surface temperature, sea ice and sea-level that have given rise to radical species range-shifts. Consequently, the invasion and establishment of nonindigenous species are important drivers for biodiversity loss and disorders of ecosystem functioning and services. Besides the ecological impacts, invasive alien species (IAS) also have significant impacts on human livelihoods and health worldwide. The changing climates and increasing international trade (Otero *et al*., 2013; Chapman *et al*., 2016) accelerate the numbers of invasive species and their subsequent impacts worldwide (Young *et al*., 2017). The invasion of lionfish (*Pterois miles*) to the Mediterranean has created a new threat to fish communities, fisheries and human health. *P. miles* inhabit warm marine waters at depths from 1 to 100 m on hard bottom, caves, mangroves and reefs (Turan *et al*., 2017; Sabido-Itzá and García-Rivas, 2019). The high feeding capacity of *P. miles* give rise to a substantial threat to marine community in their invaded habitats (Higgs, 2013). The first occurrence of this species was on the Israel coast in the Mediterranean (Golani and Sonin, 1992), and there is a strong consensus on the introduction of *P. miles* into the Mediterranean Sea from the Red Sea via the Suez Canal. Afterward, *P. miles* were reported from Lebanon coast (Bariche *et al*., 2013), Cyprus coasts (Evripidou, 2013; Bariche *et al*., 2013), Turkish coasts (Turan *et al*., 2014), and it's the extension from the northeastern Mediterranean to the Aegean Sea and central Mediterranean were reported (Crocetta *et al*., 2015; Turan and Ozturk, 2015; Mytilineou *et al*., 2016; Giovos *et al*., 2018; Dailianis *et al*., 2016; Azzurro *et al*., 2017; Vavasis *et al*., 2019) that emphasize successful and rapid expansion of *P. miles* along the Mediterranean coasts. Vavasis et al. (2019) provided its distribution range to the northernmost limit of the Ionian Sea (close to the border with the Adriatic Sea), complementing the recent sighting of *P. miles* in southern Italian waters (Azzurro et al., 2017). The invasion and establishment of *P. miles* in the Mediterranean have brought out severe threats to marine biodiversity, structure and function, beside economic and human health implications (Turan, 2018). Marine spatial planning and management require spatial information on invasive alien species distribution, regions at risk for these invasions, species response to continued climate change and environmental characteristics (Allnutt *et al*., 2012; Guerry *et al*., 2012) since a better understanding of invasion processes is a precondition for a sound management of the expansion of potentially detrimental species. Species distribution modelling (SDM) is a method that uses the relationships between species occurrence and climate for prediction which is now one of the most widespread approaches used by modern ecologists to detect which environmental variables effect current species occurrence, and may also be successfully applied to infer past or future distribution pattern of a given species. SDM has a wide array of applications for ecological and conservation studies, making it possible to provide answers to many questions, the most basic of which is to identify areas where a given species is likely to occur (Briones *et al*., 2014; Zhang *et al*., 2019). The goals of this study were 1) to predict richness of geographic distribution of *P. miles* and 2) to define the potential risk of new invasions of *P. miles* within the non-native range in the Mediterranean 3) to assess the relative importance of environmental factors influencing the spatial distribution of *P. miles*. This study has been carried out in Hatay region of Turkey in 2019.

MATERIALS AND METHODS

Data collection

The primary data consisted of non-native occurrence points of invasive *P. miles* in the Mediterranean were obtained from the published literatures, grey literatures and personal communications (Golani and Sonin, 1992; Bariche *et al*., 2013; Evripidou, 2013; Turan *et al*., 2014; Turan and Ozturk, 2015; Kletou *et al*., 2016; Yaglioglu and Ayas, 2016; Azzurro *et al*., 2017; Turan *et al*., 2018). Geographic coordinates that represent the location of 83 occurrence records of *P. miles* across the Mediterranean Sea were obtained, detailing it's the invasive distribution. Google Earth was applied to gather coordinates of the records if there were only localities (Fig. 1). QGIS was used to check accuracy of all occurrence records prior to use. Records with obvious geocoding errors were eliminated, and very close and duplicate records from the same locality were removed manually.

Marine predictor variables

Marine climatic variables available in the Bio-

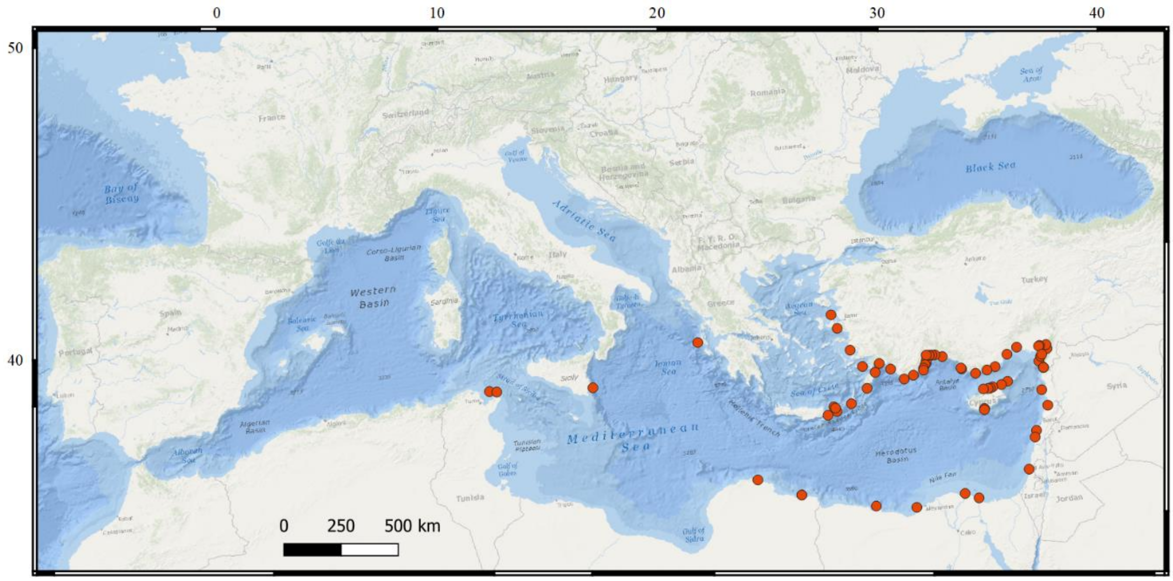

Fig. 1: The used non-native occurrence points of the lionfish *P. miles* in the Mediterranean (QGIS Esri Ocean, 2019)

ORACLE *v*2 published by Tyberghein *et al*. (2012) and Assis *et al*. (2018) and MARSPEC (Sbrocco and Barber, 2013) global databases, which provide an array of geophysical, biotic and climatic data at a spatial resolution of 9.2 km in the ESRI ASCII format, were used in the current analyses. The marine climatic variables were selected according to the availability in the Bio-ORACLE *v*2, its relevance to a species distribution with climatic conditions and previous relevant studies. The available predictor variables were tested for multicollinearity based on Spearman's rank correlation. For building models, a set of 15.000 randomly sampled pseudo-absence records along the Mediterranean Sea in the benchmark dataset were included. In order to quantify the potential range expansion of *P. miles*, the total suitable areas gained and lost under each climate change scenario were calculated that range shifts imply potential expansion/contraction of *P. miles* range of distribution. The center of each binary current and future spread were located, and latitudinal and longitudinal shifts between them were calculated (in km/decade). Intergovernmental Panel on Climate Change (IPCC) A1B emissions scenario (intermediate emission scenarios balanced across all sources), that is based on lower CO_2, N_2O, CH_4, and SO_2 emissions for 2100 (IPCC Fifth Report, 2013), was used for the future distribution projection. The future layers of only 5 candidate marine environmental variables (BO_salinity, BO_sstmax and BO_sstmin, BO_sstrange and BO_sstmean) were available for this scenario. Therefore, in order to use more predictive environmental variables in the current modellings, the current and future distribution modellings were run separately.

Modelling procedure

The correlative model with spatial habitat data map the probability of occurrence of a species across a landscape. Fifteen modelling techniques were tested to relate the distribution of *P. miles* in the Mediterranean environmental conditions: generalized additive model (gam), climate-envelope models (bioclim, bioclim.dismo), flexible discriminant analysis (fda), multiple adaptive regression splines (mars), generalized linear model (glm), fit a generalized linear model via penalized maximum likelihood (glmnet), Mahalanobis model in dismo (mahal.dismo), maximum entropy (maxent), recursive partitioning and regression trees (rpart), model occurrence probability using presence-only data (maxlike), mixture and flexible discriminant analysis (mda), create and train a multi-layer perceptron (mlp), support vector machines (svm), create and train a radial basis function (rbf), random forest (rf), as implemented in the sdm package (Naimi and Araujo, 2016). Pseudo-absence records (1.500) were randomly generated within the study area. True skill statistics (TSS) and the area under the receiver operating characteristic curve (AUC) were used to assess accuracy. The relative importance of each climatic variable in predicting the distribution of *P. miles* was also evaluated. All data processing were performed in R (Bosch *et al*., 2016; Naimi and Araujo, 2016) and all modelling algorithms were performed using the default settings.

RESULTS AND DISCUSSION

Model performance

Species distribution models for current distribution predicted regions of climatic suitability for *P. miles* with 100% run success for 15 models. TSS ranged from 0.42 for the mahal.dismo and to 0.86 for the Maxlike model. The lowest AUC value was 0.71 for bioclim model, and the Maxlike model revealed best predictive performance (AUC = 0.95) among the models and was used for current distribution of prediction and descriptive analyses. For future prediction of climatic suitability, all the models run 100% success predictions. TSS and AUC values were zero for the FDA and MDA models. The Maxlike model revealed the highest AUC (0.94) and TSS (0.83) values, indicating the best predictive performance and allowing corresponding usage with the current prediction modelling, was selected for further future modelling and descriptive analyses.

Variable contribution

For the current non-native distribution modeling of *P. miles*, 31 candidate marine environmental variables from Bio-Oracle and MARSPEC were tested, and 19 variables from the 31 input variables showed collinearity problem in the prediction analyses which were excluded for future analyses. Finally, spatial data referring to 12 marine environmental factors were retrieved: maximum, minimum, range and mean sea surface temperatures (BO_sstmax, BO_sstmin, BO_sstrange, BO_sstmean), salinity (BO_salinity), maximum sea water temperature at minimum depth (BO2_tempmax_bdmin), maximum sea water temperature at maximum depth (BO2_tempmax_bdmax), nitrate maximum bathymetry (BO_bathymax), mean primary production at max depth (BO2_ppmean_bdmax), primary production at min depth (BO2_ppmean_bdmin), min light at mean depth bottom (BO2_lightbotmin_bdmean), max light at mean depth bottom (BO2_lightbotmin_bdmax), East/West aspect derived from bathymetry (MS_biogeo01_aspect_EW_5m), North/South Aspect derived from bathymetry (MS_biogeo 02_aspect_NS_5m). The present layers of the used climatic data obtained from sdmpredictors are given in Fig. 2.

Different degree of contribution of predictor variables were observed for the current prediction that the mean sea surface temperature (BO_sstmean) and maximum bathymetry (BO_bathymax) contributed the most to the prediction of model (Fig. 3).

Table 1: The tested model performances of *P. miles* using the dataset for the current and fututre predictions

Model statistics	Current Distribution			Future Distribution		
Methods	AUC	TSS	Deviance	AUC	TSS	Deviance
bioclim	0.71	0.44	0.07	0.80	0.59	0.14
bioclim.dismo	0.87	0.70	0.05	0.83	0.63	0.15
fda	0.90	0.76	0.06	0	0	0
gam	0.91	0.73	0.04	0.76	0.60	0.06
glm	0.87	0.78	0.04	0.84	0.71	0.06
glmnet	0.78	0.67	0.09	0.81	0.69	0.11
mahal.dismo	0.73	0.42	0.04	0.82	0.70	0.20
mars	0.92	0.67	0.05	0.86	0.75	0.05
maxlike	0.95	0.86	0.02	0.94	0.83	0.01
mda	0.76	0.77	0.05	0	0	0
mlp	0.88	0.66	0.04	0.82	0.73	0.07
rbf	0.67	0.76	0.17	0.80	0.71	0.20
rf	0.90	0.81	0.03	0.88	0.80	0.04
rpart	0.81	0.59	0.05	0.77	0.64	0.05
svm	0.84	0.75	0.07	0.84	0.67	0.09

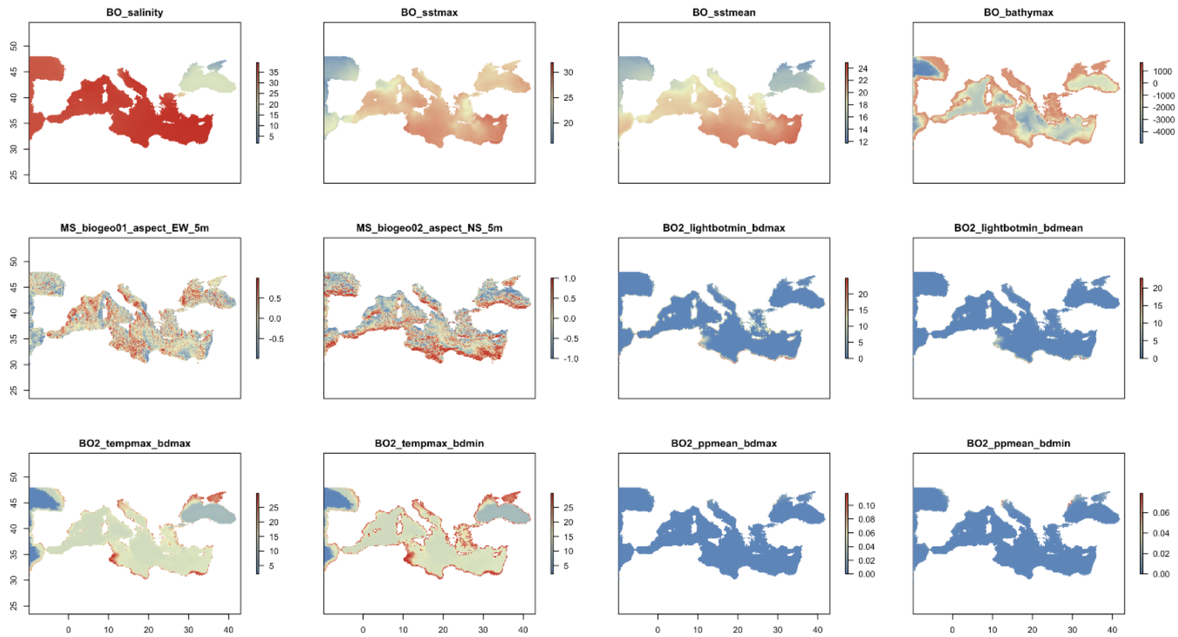

Fig. 2: The present raster layers of the climatic data from the Bio-ORACLE *v*2

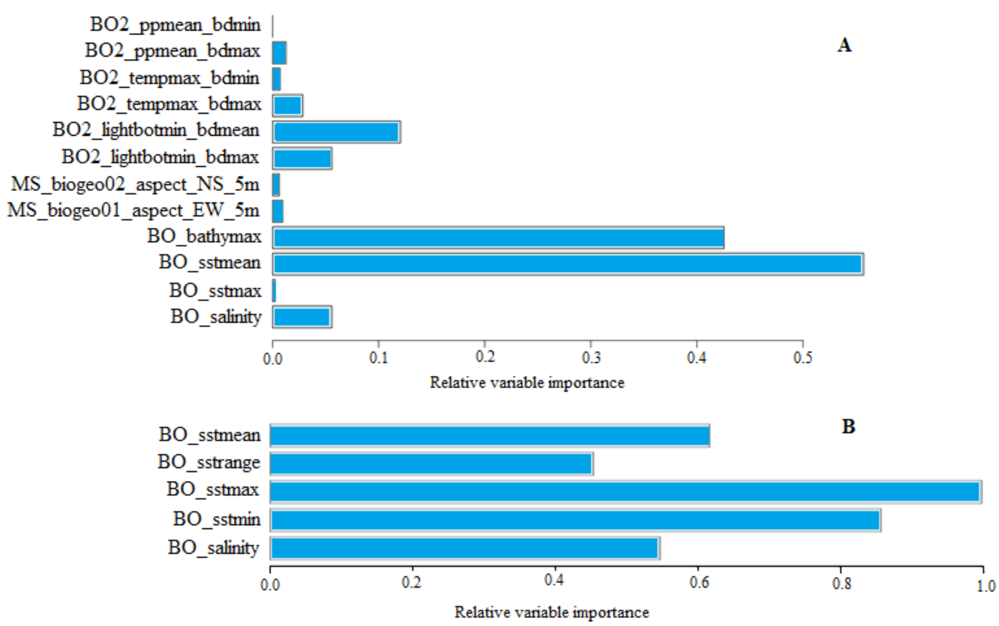

Fig. 3: The relative variable importance of each variable to the current (A) and future (B) distribution and adaptation of *P. miles* in the Mediterranean Sea

Therefore, mean temperature and bathymetry explained relatively higher biological importance to the extension and adaptation of *P. miles* with extreme environmental factors. Maximum sea surface temperature (BO_sstmax) and primary production at min depth (BO2_ppmean_bdmin) were not effective to the predictive performance of the model.

Response curves of *P. miles* to each variable indicated that high negative reaction was observed only to mean primary production at max depth (BO2_ppmean_bdmax) for current distribution (Fig. 4). No responses were observed from the other variables. For future distribution modeling of *P. miles*, 5 candidate marine environmental variables (BO_salinity, BO_sstmax and BO_sstmin, BO_sstrange and BO_sstmean) for prediction of future distribution revealed no collinearity problems in the prediction analyses which were used for future projections. The five predictor variables contributed in different degrees that the maximum, minimum and mean sea surface temperature contributed the most to predictions of the model, followed by salinity (Fig. 3). Thus, the sea surface temperature explained strong biological importance to the adaptation of *P. miles* with extreme environmental factors. Response curves of *P. miles* to each variable indicated strong reaction to the salinity, minimum and mean sea surface temperature and range of sea surface temperature (Fig. 4). There was no response of *P. miles* to maximum sea surface temperature.

Current predicted distributions

All of the collected non-native occurrence records in the Mediterranean were within the predicted suitable range at the Maxlike model. The predicted suitable habitats of *P. miles* under the current climate are presented in Fig. 5 that *P. miles* was dominantly occurred in the east parts of coastal areas of the Mediterranean and northeastern coasts of the Africa, indicating high suitability of these areas for *P. miles*. There was no any distribution pattern in the Marmara and Black Sea.

Future potential distributions

The predicted future suitable habitats and distribution of the invasive *P. miles* under future

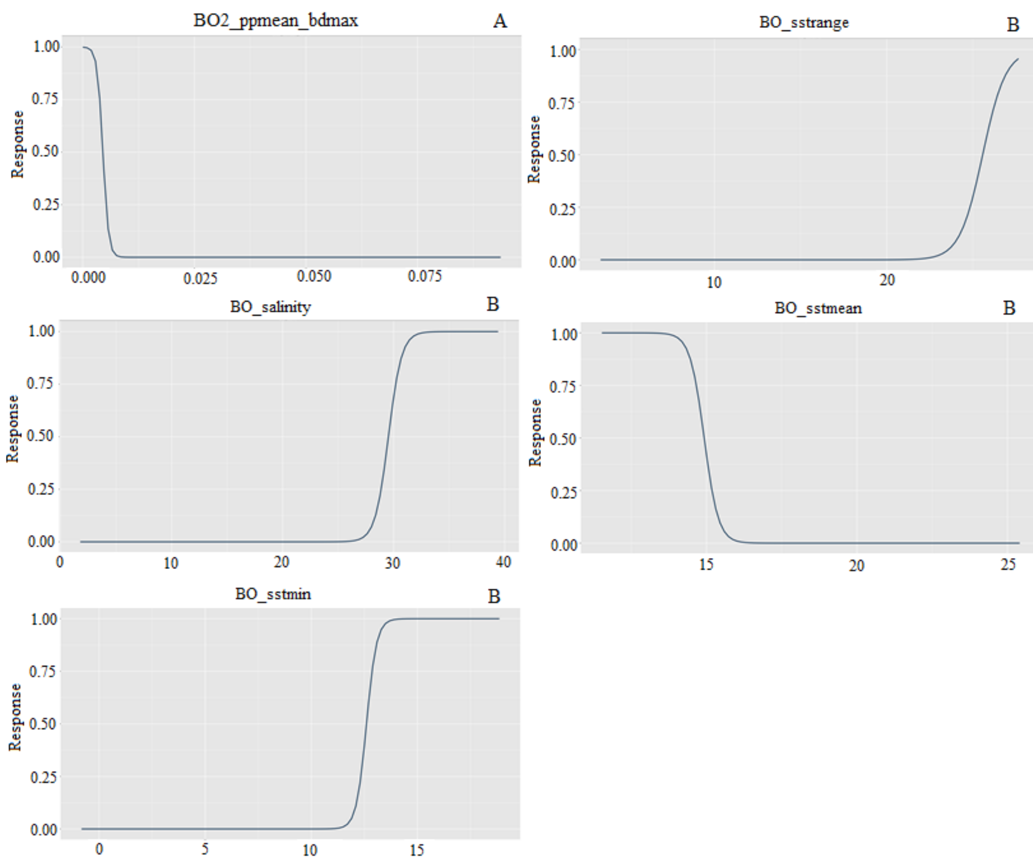

Fig. 4: Response curves of *P. miles* to the environmental variables for current (A) and future (B) predictions

climate scenario (A1B) according to the Maxlike model revealed that *P. miles* increase its range of distribution dominantly to the central and west part of the Mediterranean in a spatial extent, indicating high suitability of this areas for its future distribution (Fig. 6). There was no predicted future suitable habitats and distribution of *P. miles* in the northern Adriatic, Liguria, Marmara and Black Seas.

The Maxlike species distribution model with current and future climatic factors successfully predicted the magnitude of species distribution and range shift with changing climates between the periods. Thus, colonization, persistence and lose of habitats of *P. miles* by climate change in the Mediterranean were successfully forecasted by the Maxlike model. Suitable areas for *P. miles* are mainly concentrated along the east and south portion of the province of the Mediterranean. Suitable bioclimatic conditions and the most suitable coastal areas by the current invasion seem to be North-eastern part of African countries (Tunisia, Libya and Egypt) and eastern countries, Israel, Lebanon, Syria,

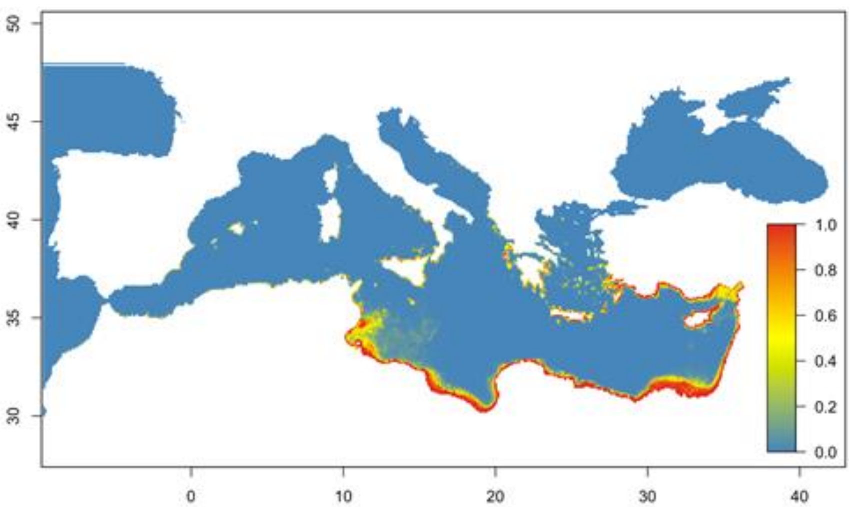

Fig. 5: Predicted current non-native distribution of *P. miles* in the Mediterranean based on Maxlike model. Scale bar show the probability of suitability

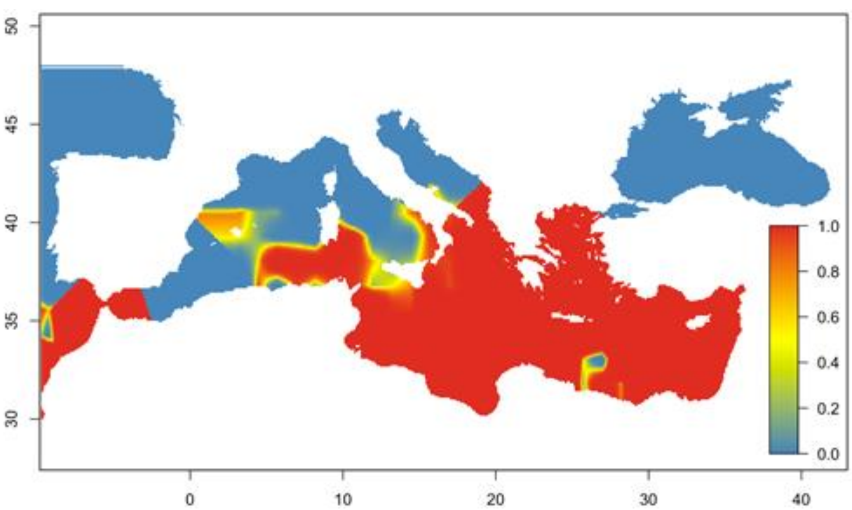

Fig. 6: Predicted future distribution of *P. miles* in the Mediterranean by 2100 under the IPCC climate change scenario A1B. Scale bar show the probability of suitability

Turkey, Cyprus) and central Mediterranean countries (Greece, Italy and Malta). On the other hand, there is low distribution pattern in the coastal areas of Italy. Azzurro *et al*. (2017) reported increasing number of lionfish in Sicily Island that support the current prediction analysis in Italian waters. Poursanidis (2015) predicted distribution of *P. miles* with MaxEnt model using only 5 occurrence record in the Mediterranean and reported similar distribution pattern of *P. miles* in coastal areas of east Mediterranean countries, but seem to be overestimated distribution, including the Marmara and Black Sea that any reports has not been given from these areas yet. Poursanidis et al. (2020) identified suitable areas for lionfish establishment in the Mediterranean, indicating a further geographical expansion in this basin and a likely spread of lionfish invasion in the Mediterranean. The A1B climate scenarios for future predictions, the Maxlike model forecasted a significant enlargement in suitable areas for *P. miles*. Because of climate change, the pattern of distribution of *P. miles* is projected to be changed that suitable environmental condition will shift westward and northward, surrounding coastal areas of the Adriatic, Tyrrhenian, Ionian, Balearic Seas. Considering the changes in its distribution, *P. miles* seems to have a high potential niche in these areas by 2100. Moreover, the richness of *P. miles* in the east coastal parts of the Mediterranean seems to be enlarged by the end of the century. Evangelista *et al*. (2016) used Generalized Linear Model (GLM) and the MaxEnt models to forecast suitable environments of red lionfish *Pterois volitans* in the western Atlantic and eastern Pacific Oceans and indicated that *P. volitans* could continue to occupy southern latitudes in the western Atlantic Ocean and might establish local populations in the eastern Pacific Ocean. When species distribution modellings are used to predict invasion risk, there is always some level of uncertainty with all models. Other ecological characteristics such as dispersal via ocean currents, bathymetry or regional biological interactions such as predators might also be an important driver for invasion which are not included in the present model. Only salinity and sea surface temperatures (sstmax, sstmin, sstmean, sstrange) future layers were available for the Bio-ORACLE for the climate scenarios. Although a number of ecological variables can effect distribution of marine species, a few predictor variables may also correctly predict distribution of marine species (Bosch *et al*., 2018; Goldsmit *et al*., 2018). Furthermore, the Marmara and Black Sea were predicted to be persisted to be still non-suitable for *P. miles* under this model. The variable contribution in Maxlike describes the importance of each climatic variable to the model. The mean sea surface temperature and bathymetry gained the strongest contribution among the environmental variables (Fig. 3). The low mean temperature (15) and high bathymetric features of the Black Sea may be the main barrier to the *P. miles* expansion for it' current and future distribution in the Black Sea. Likewise, Evangelista *et al*. (2016) modeled suitable habitats of invasive red lionfish *Pterois volitans* and reported that bathymetry was the strongest climatic predictor for Maxent model, and the other models also showed increasing suitability with bathymetry ranking. Moreover, the present model for *P. miles* showed low habitat suitability for salinities <28 that is lower than that given for *Pterois volitans* <30 (Evangelista *et al*., 2016), indicating low habitat suitability for lower salinities. Thus, *P. miles* seems to not tolerate low salinities and primarily prefer and persist in higher salinity habitats. *P. miles* responded to only mean primary production at maximum depth (BO2_ppmean_bdmax) for current distribution and did not respond to only maximum sea surface temperature for the future prediction. Response curve show how each environmental variable effect the prediction as each climatic variable is diverse, keeping the other climatic variables at their average sample value (Phillips and Dudik, 2008). If you have a strong-correlated variables, as the model may take advantage of groups of variables changing together, the curve can be hard to interpret. In the present study, the strong correlations in the environmental variables seems to cause the misleading of the marginal response curves for the predictions. The climate is an important driver of species distribution as govern by the variables that gain strong contribution. There have been numerous literatures, supporting the idea that climate is the key factor regulating species distribution (Occhipinti-Ambrogi, 2007; Turan *et al*., 2016; Paquit *et al*., 2017). However, the other factors besides climate should also be considered as scale in the modelled predictions (Pearson and Dawson, 2003). Ecological characteristics such as dispersal via ocean currents or regional biological interactions such as predators, dispersal barriers or specific facilitators might also be an important driver for *P. miles* invasion that are not accounted and not included in the models. Implications on alien invasive species management, *P. miles* is colonizing large tracts of the Mediterranean, and it seems to continue to spread to habitats which cover its bioclimatic range. Forecasting the current and future distribution of *P. miles* would be very crucial for its effective management strategies (Davies *et al*., 2009). *P. miles* has a potential to change the natural marine ecosystem of the region by distracting native species. Furthermore, this forecasted spread of *P. miles* give warning to the coastal managers to challenge in its range. Since, negative impacts of IAS are not seen directly, the environment departments and local government units should take heed of this challenge that would affect local livelihood. Invasion of marine alien species is one of the most important threat negatively affecting marine biodiversity worldwide with major economic and societal impacts. Forecasting which species are most estimated to become invaders and wherever they are likely to occupy even before their occupation outside their native distributional range has always been a primary goal of invasion biology. At present, *P. miles* is ongoing process to invade to habitats that are within its bioclimatic range. The predicting its current and future spread would be very crucial for its management plans. The present study indicate that its invasion would even increase because of climate change. The enlarged spread of *P. miles* could cause to the degradation of habitat quality, loss of biodiversity and impact local livelihood. In the present data, the current distribution and future invasions of *P. miles* are forecasted, and mean sea surface temperature, salinity and minimum sea surface temperature are identified as being important for the model predictions of the species' distributions.

CONCLUSION

Predictive habitat distribution modeling through Maxlike has demonstrated to be sufficient in assessing the potential impact of climate change to the current and future distribution of invasive *P. miles*. The suitable bioclimatic envelope of *P. miles* with the present investigation is forecasted to widen due to climate change. The present unsuitable areas might become suitable for *P. miles* if the temperature and salinity changes will drive as projected that would have terrific impact on local biodiversity and livelihood. Although climatic suitability is a prerequisite in a given habitat for a successful invasion of a species, the Maxlike model does not account fine-scale environmental features such as local biological interactions, dispersal barriers and predators for current and future prediction of geographic distribution. Therefore, the model reflect habitat suitability of lionfish given any means of introduction or transport and do not directly take into account for dispersal barriers or specific facilitators in the marine environment. The high climatic suitability of areas in the Mediterranean for super invasive *P. miles* were mapped by the Maxlike species distribution model that the suitable habitats under the current climate was dominantly occurred in the east parts of coastal areas of the Mediterranean with no distribution pattern in the Marmara and Black Sea. On the other hand, the projected future suitable environments of *P. miles* under future climate scenario was the central and west part of the Mediterranean, and there was no predicted future suitable habitats and distribution of *P. miles* in the northern Adriatic, Liguria, Marmara and Black Seas. The present climatic niche modeling propose a risk assessment of the areas, especially marine protected areas which are under high risk, and enlightens the relevant countries about the necessity to pay attention to the introduction of *P. miles* to prevent invasions. The prevention of invasive species invasions is commonly accepted to be more cost-effective and adequate than the eradication of an established species, long-term control, and restoring the damage posed by invasions. For that reason, this study provides a methodology to predict likely regions of invasion and the areas at risk for future potential invasion of *P. miles*. Thus, prompt effective actions from resource managers should be undertaken to mitigate impacts and spread of *P. miles*.

AUTHOR CONTRIBUTIONS

C. Turan contemplated the ideas, collected and analyzed the data, wrote and edited all the manuscript.

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CONFLICT OF INTEREST

The author declares that there is no conflict of interests regarding the publication of this manuscript. In addition, the ethical issues, including plagiarism, informed consent, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy have been completely observed by the authors.

ABBREVIATIONS (NOMENCLATURE)

AUC	Area Under The Receiver Operating Characteristic Curve
bathymax	nitrate maximum bathymetry
bioclim	Climate-Envelope Models
bioclim.dismo	Climate-Envelope Models
fda	Flexible Discriminant Analysis
gam	Generalized Additive Model
glm	Generalized Linear Model
GLM	Generalized Linear Model
glmnet	Generalized Linear Model Via Penalized Maximum Likelihood
IAS	Invasive alien species
IPCC	Intergovernmental Panel on Climate Change
lightbotmin	min light at mean depth bottom
mahal.dismo	Mahalanobis model in dismo
mars	Multiple Adaptive Regression Splines
maxent	Maximum Entropy
maxlike	Model Occurrence Probability Using Presence-Only Data
mda	Mixture And Flexible Discriminant Analysis
mlp	Multi-Layer Perceptron
ppmean	mean primary production
rbf	Radial Basis Function
rf	Random Forest
rpart	Recursive Partitioning and Regression Trees
SDM	Species distribution modelling
sstmax	Maximum sea surface temperatures
sstmean	Mean sea surface temperatures
sstmin	Minimum sea surface temperatures
svm	Support Vector Machines
tempmax	maximum sea water temperature
TSS	True Skill Statistics

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