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New records and potential distribution by Ecological Niche Modeling of *Monoxia obesula* in the Mediterranean area

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Abstract

New records for the adventive species *Monoxia obesula* Blake (Coleoptera Chrysomelidae Galerucinae) in the Mediterranean region are reported. An Ecological Niche Modeling (ENM) analysis to estimate the potential distribution of this leaf beetle in the secondary range, through the assessment of the habitat suitability, was performed. The expected distribution, as predicted by the ENM analysis, is rather limited in the Mediterranean region, with high suitability areas only in southern Spain, Sardinia, Sicily, southern peninsular Italy, Tunisia and Egypt. Nevertheless, the Ensemble Models for future climatic conditions predict an expansion from all the currently suitable territories of the Mediterranean region, especially in coastal areas.

Key words: Amaranthaceae, Galerucini, introduced species, future range shifts, climate change.

Introduction

Alien and adventive species are major threats to many natural and human-managed ecosystems, in terms of biodiversity conservation (Crowl *et al.*, 2008; Bellard *et al.*, 2016; Gilioli *et al.*, 2017), socio-economic costs and management efforts (Williams *et al.*, 2010; Oreska and Aldridge, 2011; Early *et al.*, 2016). The successful establishment of an invasive alien species depends on many environmental variables, which can be summarized in the BAM diagram (Soberon and Peterson, 2005); the research in this field is very active, and many analytical approaches are used.

In this context, Ecological Niche Models (ENMs) gained more and more popularity during last years, because of their capability of predicting suitable areas outside the known distribution range of the target species (Ficetola *et al.*, 2009; Mainali *et al.*, 2015; Taucare-Ríos *et al.*, 2016; da Silva *et al.*, 2017). Once calibrated on the native range of the adventive species, the ENMs can map the areas considered suitable, usually with a continuous distribution of predicted suitability; this can be obtained through presence-only records (GPS points from the field, museum records, online databases), which can be also integrated with the more difficult-to-collect absence data (Urbani *et al.*, 2015; 2017). The variables commonly used to model species' distribution are the climatic (temperature and precipitation) (D'Alessandro *et al.*, 2018; Iannella *et al.*, 2018a; 2018b), topographic (altitude, aspect and slope) (Cerasoli *et al.*, 2017; Iannella *et al.*, 2017; Di Musciano *et al.*, 2018) and many others, such as edaphic maps, land use, etc. (Pérez-García *et al.*, 2017; Midzi *et al.*, 2018). In particular, the so-called "bioclimatic" variables are commonly used because of the primary influence that climate exerts over species, especially for ectotherms; these variables are freely available on online repositories (Hijmans *et al.*, 2005; Kriticos *et al.*, 2012; Karger *et al.*, 2017) and describe climate for the current and possibly infer past and future scenarios.

In this work, the possible distribution of *Monoxia obesula* Blake (Coleoptera Chrysomelidae Galerucinae) (figure 1), a leaf beetle belonging to the tribe Galerucini, was investigated. It was first recorded as adventive to the Mediterranean area (Sardinia, Italy) in 2014 (Clark *et al.*, 2014) and in 2016 a second find was reported from Malta (Mifsud, 2016). The most recent records are from Balearic Islands (Petitpierre *et al.*, 2017) and eastern Spain (Valencia Province) (Montagud Alario and Rodrigo Coll, 2017). In this contribution, we supply new data records for the secondary range of *M. obesula* and perform an Ecological Niche Modeling (ENM) analysis for predicting the potential extension of this species in the Mediterranean area, through the assessment of the habitat suitability.

Materials and methods

Material examined

Specimens were examined and dissected using a Leica M205C binocular microscope. Photomicrographs were taken using a Leica DFC500 camera and the Zerene Stacker software version 1.04. Scanning electron micrographs were taken using a Hitachi TM-1000. Geographical coordinates of the localities were reported in degrees, minutes and seconds (DMS-WGS84 format); coordinates and geographical information that are included in square brackets were added by the authors using information from the web site of Google Earth.

Dataset and study area

M. obesula localities are summarized in table 1; all these occurrences were used to generate the ENMs, as described below. The whole study area for our analyses can be defined as the sum of primary (North America) and secondary range (Mediterranean region).

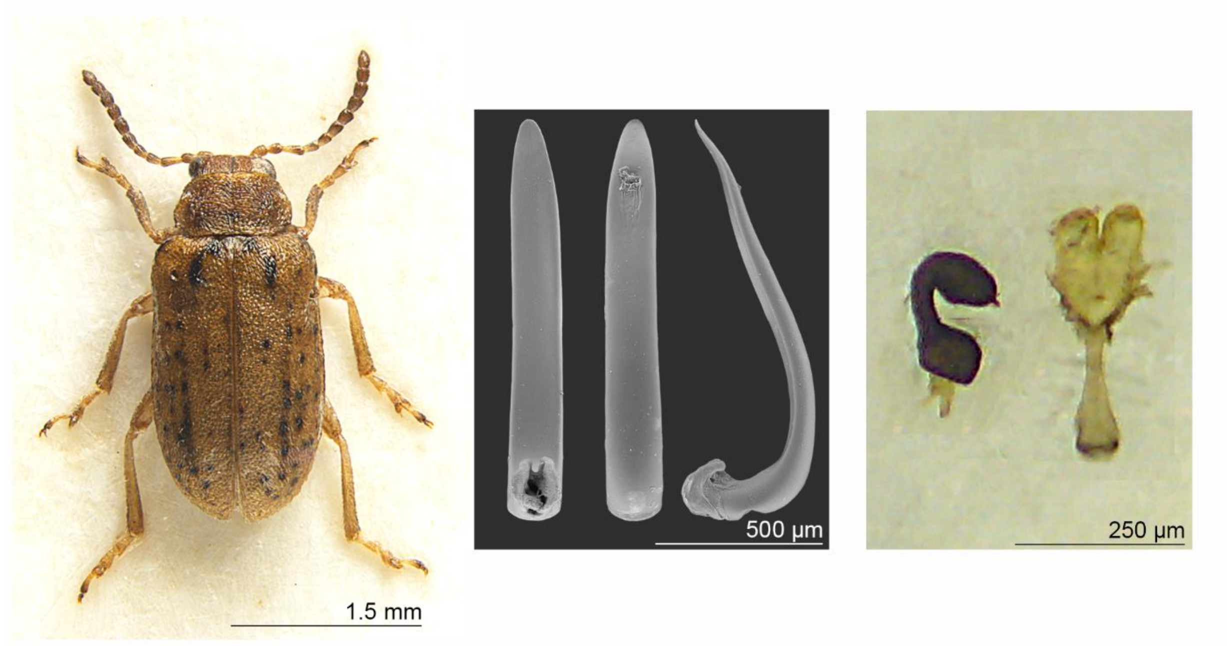

Figure 1. *M. obesula*: habitus; aedeagus in ventral, dorsal and lateral view; spermatheca and vaginal palps.

Ecological Niche Modeling (ENM)

Nineteen bioclimatic variables were downloaded from the Worldclim.org online repository, at a spatial resolution of 30 arc-seconds, for ‘current’ climatic conditions (Hijmans *et al.*, 2005); codes and names for each variable are reported at the end of this paper (appendix). Considering that some differences exist among the projections of the future in available Global Climate Models (GCMs), we chose the CCSM4 (Gent *et al.*, 2011), IPSL (Marti *et al.*, 2010) and MIROC-CHEM (Watanabe *et al.*, 2011) GCMs to perform the future projections, and then merged each resulting model into a single one (see below).

To avoid any multicollinearity-related bias in the models, a correlation matrix among all these candidate predictors was built through the ‘Band Collection Statistics’ tool in ArcMap 10.0 (ESRI, 2010); when a pair of variables exceeded a Pearson’s value of $|r| > 0.85$ (Elith *et al.*, 2006), the less ecologically-influenced variable was discarded from the modeling process, based on available information on the target species or considering an expert-based procedure, for all the reasons reported in Brandt *et al.* (2017).

Models for the target species were built through the ‘biomod2’ package (Thuiller *et al.*, 2016) in R environment (R Core Team, 2016). This modeling technique is considered particularly powerful because it can combine different modeling approaches (ranging from linear models to machine-learning techniques) into one single Ensemble Model (EM). The modeling techniques used in our analyses were Generalized Linear Models (GLMs), Multiple Adaptive Regression Splines (MARS), Gradient Boosted Models (GMB, also known as Boosted Regression Trees, BRTs) and Maxent. Models built for *M. obesula* were parametrized as follows: General Linear Models (GLM): type = 'quadratic', interaction level = 3; Multiple Adaptive Regression Splines (MARS): type = 'quadratic', interaction level = 3; Generalized Boosting Model (GBM): number of trees = 10000, interaction depth = 3, cross-validation folds = 10; maxent (MAXENT.Phillips): maximum iterations = 5000. Pseudo-absences were selected through a Surface Range Envelope (‘sre’), with a quantile set to = 0.05.

Five sets of 500 pseudo-absences each were generated for each modeling technique, for a total of 100 single models, and model calibration was performed by using the “BIOMOD_Modelling” function for the whole study area.

To obtain reliable EMs, the discrimination performances of each model were assessed through the True Skill Statistics (TSS) (Allouche *et al.*, 2006) and the Area Under the Curve of the receiver operator characteristics curve (Phillips *et al.*, 2006), choosing only models with TSS > 0.85 and AUC > 0.75, for all the reasons reported in Iannella *et al.* (2018b).

The best performing models were then combined to obtain the EMs through the “BIOMOD_EnsembleModeling” function (using the ‘wmean’ algorithm, a function which proportionally combines single models based on their respective discrimination scores), and the “BIOMOD_EnsembleForecasting” function was used to obtain predictions on the target species’ secondary range. A further analysis was performed through this function to model possible future scenarios: two 2050 future projections were performed, for the 6.0 and the 8.5 Relative Concentration Pathways (RCPs) scenarios. The differences between these two RCPs are linked to the radiative forcing increase forecast taking into account the end of greenhouse gas emissions, with the first peaking in 2080 and the second not ending at least until 2100 (Meinshausen *et al.*, 2011; Riahi *et al.*, 2011). Models obtained from the three different GCMs used were combined using the Multivariate Environmental Dissimilarity Index (MEDI) (Iannella *et al.*, 2017), an algorithm which can proportionally combine projections from different

Table 1. Records of *M. obesula* in primary and secondary range.

Locality Latitude Longitude	Host plant	Date	Source
Primary Range			
USA, Nebraska, Arbor Lake 40°54'0.1"N 96°40'52.9"W	*Atriplex dioica* *Chenopodium* sp.	2-7.xi.2013	Clark *et al.*, 2014
USA, Nebraska, Waverly [40°55'10.33"N 96°31'39.20"W]	*Chenopodium* sp.	13.xi.1923	Clark *et al.*, 2014
USA, Texas, Kingsville [27°30'57.13"N 97°51'21.99"W]	*Chenopodium* sp.	12.v.1909	Clark *et al.*, 2014
Dubitative Primary Range			
USA, Maryland, Dundalk [39°15'17.47"N 76°31'11.98"W]	*Chenopodium* sp.	21.viii.1991	Clark *et al.*, 2014
Secondary Range			
*Italy, Latium (RM), Ostia [41°43'41.77"N 12°17'23.41"E]	Unknown	18.xi.2018	G. Pace leg.
*Italy, Sardinia (CA), Poetto Beach [39°12'29.48"N 9°10'1.68"E]	Unknown	29.vii.2012	D. Sechi leg.
Italy, Sardinia (CA), Stagno di Molentargius [39°12'24.94"N 9°8'55.03"E]	*Atriplex halimus* *A. portulacoides*	2.viii.2013	Clark *et al.*, 2014
*Italy, Sardinia (CA), Villanova [39°12'42.75"N 9°7'0.63"E]	Unknown	23.vii.2016	G. Ruzzante leg.
*Italy, Sardinia (OG), Marina di Tertenia [39°41'35.51"N 9°39'24.14"E]	Unknown	22.viii.2014	A. Carlin leg.
*Italy, Sicily, Catania 37°31'18.08"N 15°5'38.26"E	*Chenopodium album*	20.xi.2018	S. Longo leg.
Malta, St. Thomas Bay [35°50'59.01"N 14°33'54.98"E]	*Chenopodium album*	30.xi.2015	Mifsud, 2016
Spain, Balearic Islands, Mallorca, Es Carnatge [39°32'34.41"N 2°42'14.52"E]	*Atriplex halimus*	x.2015	Petitpierre *et al.*, 2017
*Spain, Balearic Islands, Mallorca, near Cala Ratjada [39°42'27.58"N 3°27'33.57"E]	Unknown	24.v.2018	M. Becker leg.
Spain, Castellón, Grau de Castelló 39°58'44.15"N 0°1'20.64"E	*Atriplex halimus*	20.vii.2017	Montagud Alario and Rodrigo Coll, 2017
Spain, Valencia, Campus de Burjassot 39°30'34.31"N 0°25'29.46"W	*Atriplex halimus*	25.vii.2017	Montagud Alario and Rodrigo Coll, 2017
Spain, Valencia, El Arenal 39°37'48.65"N 0°18'0.94"W	*Atriplex halimus*	28.vii.2017	Montagud Alario and Rodrigo Coll, 2017
Spain, Valencia, Jardin del Túria (1) 39°28'40.84"N 0°23'21.01"W	*Atriplex halimus*	12.vii.2017	Montagud Alario and Rodrigo Coll, 2017
Spain, Valencia, Jardin del Túria (2) 39°27'18.90"N 0°20'50.82"W	*Atriplex halimus*	12.vii.2017	Montagud Alario and Rodrigo Coll, 2017
Spain, Valencia, Polideportiva 39°30'22.93"N 0°25'3.86"W	*Atriplex halimus*	28.vii.2017	Montagud Alario and Rodrigo Coll, 2017
Spain, Valencia, Saplaya 39°31'34.86"N 0°18'50.98"W	*Atriplex halimus*	28.vii.2017	Montagud Alario and Rodrigo Coll, 2017

(*) New records.

GCMs depending on the MESS scores (Elith *et al.*, 2010) they reached, thus reducing the models' extrapolation. The MEDI-processed models were further binarized (presence/absence) using a threshold, obtained by averaging a TSS-max for all Ensemble Models through the 'ecospat' package (Di Cola *et al.*, 2017). This technique is particularly reliable when dealing with presence-only models, as it permits obtaining of results comparable with the presence/absence models (Liu *et al.*, 2013). The current and future binarized models were compared through the "BIOMOD_RangeSize" function, which calculates the possible areas of gain, stability and loss between certain climatic scenarios; in our case, 'current' versus '2050_RCP 6.0' and 'current' versus '2050_RCP 8.5' predictions were assessed.

Results

M. obesula is associated with the plant family Amaranthaceae s.l. (including the former family Chenopodiaceae) (The Angiosperm Phylogeny Group, 2016) both in its primary (North America) (figure 2a) and secondary (southern Europe) (figure 2b) range. In particular, this leaf beetle species completes its entire life cycle on *Atriplex* spp., mainly *Atriplex halimus* L., and, to a lesser extent, on *Chenopodium* spp., mainly *Chenopodium album* L. (table 1). The introduction of *M. obesula* in the Mediterranean area could prove alarming because it causes serious damages to its host plants, sufficient to cause death, through heavy defoliations (Clark *et al.*, 2014; Mifsud, 2016; Montagud Alario and Rodrigo Coll, 2017). *M. obesula* seems to be spread by

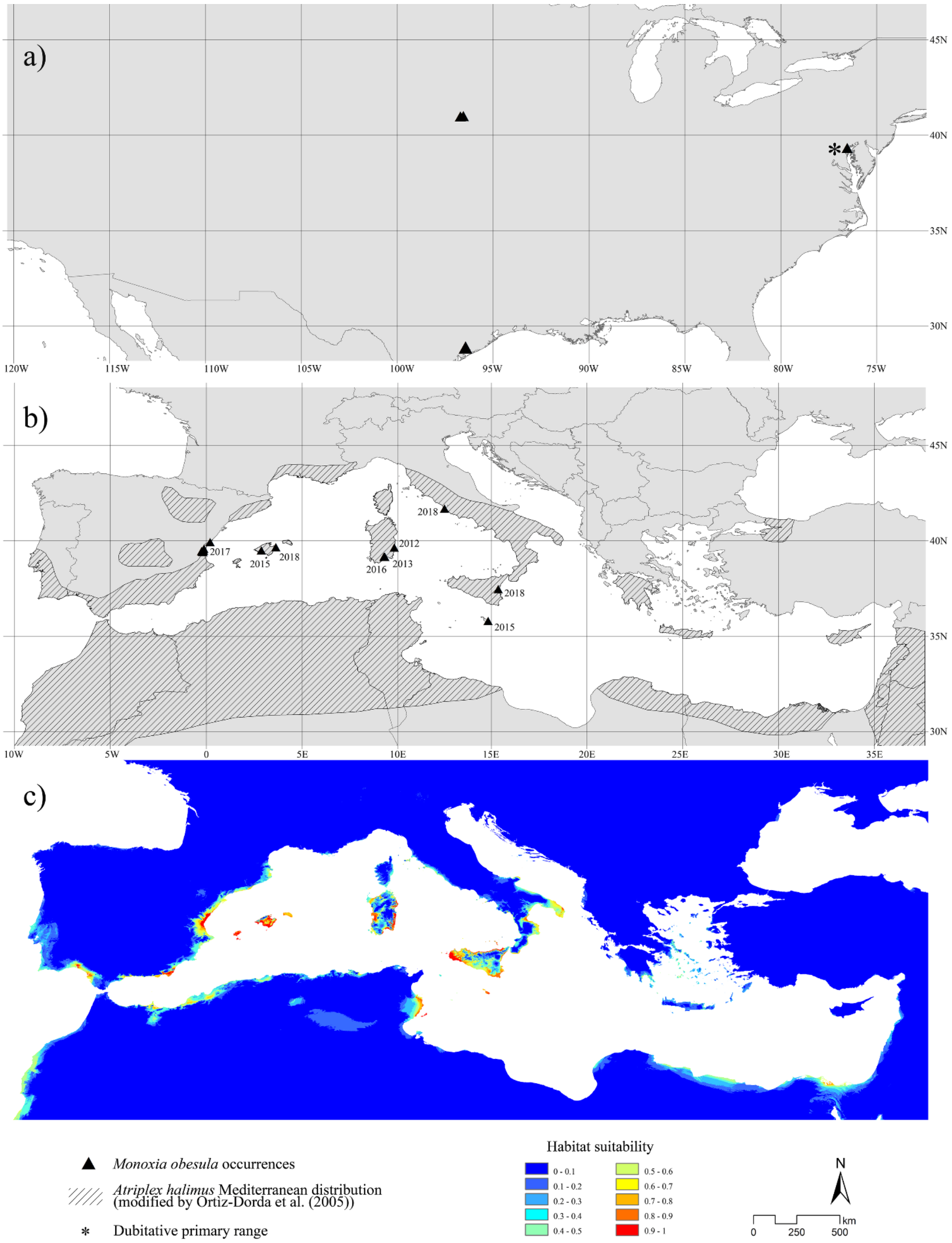

Figure 2. a) *M. obesula* primary range; **b)** *M. obesula* secondary range (with the corresponding occurrence year) and its host plant *A. halimus* Mediterranean range; **c)** *M. obesula* predicted habitat suitability for current climatic conditions.

ornamental plants. In this regard, an important role in its propagation is probably also played by the other host plant, *C. album*, which is common and widespread in the Mediterranean area.

The new data records of *M. obesula* in the Mediterranean region involve five areas of Italy and one in Spain (table 1, figure 2b). Particularly relevant are two records from Italy: Sicily, Catania (via Sassari), 37°31'18"N 15°5'38"E, 38 m a.s.l., 20.xi.2018, S. Longo leg., on *Chenopodium album* (Amaranthaceae); Latium, Ostia (Rome), 41°43'41.77"N 12°17'23.41"E, 1 m a.s.l., 18.xi.2018, 1 specimen, G. Pace leg.. These extend the secondary range of this species to Sicily and peninsular Italy.

The Ensemble Models reached high scores of both TSS (= 0.933) and AUC (= 0.986) and describe an interesting potential distribution for *M. obesula* in the Mediterranean area (figure 2c). We can observe that the potential distribution estimated by the ENM analysis for this adventive species is rather limited in the Mediterranean region, with the most contributive variables BIO8 (Mean Temperature of Wettest Quarter, 34% of the total contribution) and BIO12 (Annual Precipitation, 18%) respectively. For many of the expected suitability areas, *M. obesula* has been already reported (table 1), while new records could still come from some areas of Spain, such as the Cabo de Gata area and Almeria Gulf on the eastern coast, or from the Atlantic coast facing the Cadiz Gulf. Within Italy, we expect a wider spread in Sardinia, especially on the eastern coast, and in Sicily, in particular in the north-western area and on the northern coast. With regard to peninsular Italy, the ENM returns some areas with elevated habitat suitability in the coastal area of the southern Calabria (Capo Spartivento area) and further North in the Sibari Plain, while in Apulia, several areas are “turned on” by the EM in the Salentinian Peninsula. It is interesting also to highlight that, notwithstanding the record of the Latium coast (Ostia), this area represents no particularly high suitability habitats for the presence of this leaf beetle species. Also, we have to underline other two potentially suitable areas for *M. obesula* in North Africa, namely the eastern coast of Tunisia (Sfax and Sharqui Island) and the Mediterranean coast of Egypt, approximately between Port Said and Alexandria. The suitable distribution of *M. obesula*, as predicted by the models, is strictly limited to areas with Mediterranean conditions; that could seem strange considering that this species is occurring also in Nebraska. However, in the two sites from Nebraska considered for the analysis, the most contributive variables, BIO8 and BIO12 respectively, show values falling perfectly in the range of the Mediterranean sites [BIO8 (°C) = 21.6 (site 1) and 21.8 (site 2), "Mediterranean" range 13.3-26.7; BIO12 (mm) = 748 (site 1) and 766 (site 2), "Mediterranean" range = 374-1101].

More importantly, the future potential distributions resulted in two scenarios of increased suitability, as reported in the range-shift maps of figure 3 (obtained after the binarization, with a TSS-max threshold = 0.16). Comparing the distributions, the range shift for 2050_RCP 6.0 from current scenario (figure 3a) shows a great increase of suitable areas in many territories already predicted for current climatic conditions; a similar result, but with a greater increase with respect to the RCP 6.0, is also forecast for the 2050_RCP 8.5 (figure 3b). In both range shift maps, the gain of suitable area is observed in spatial continuity with respect to the current predictions (the “stable” areas), and many “coastal” corridors could be available in the future for the target species.

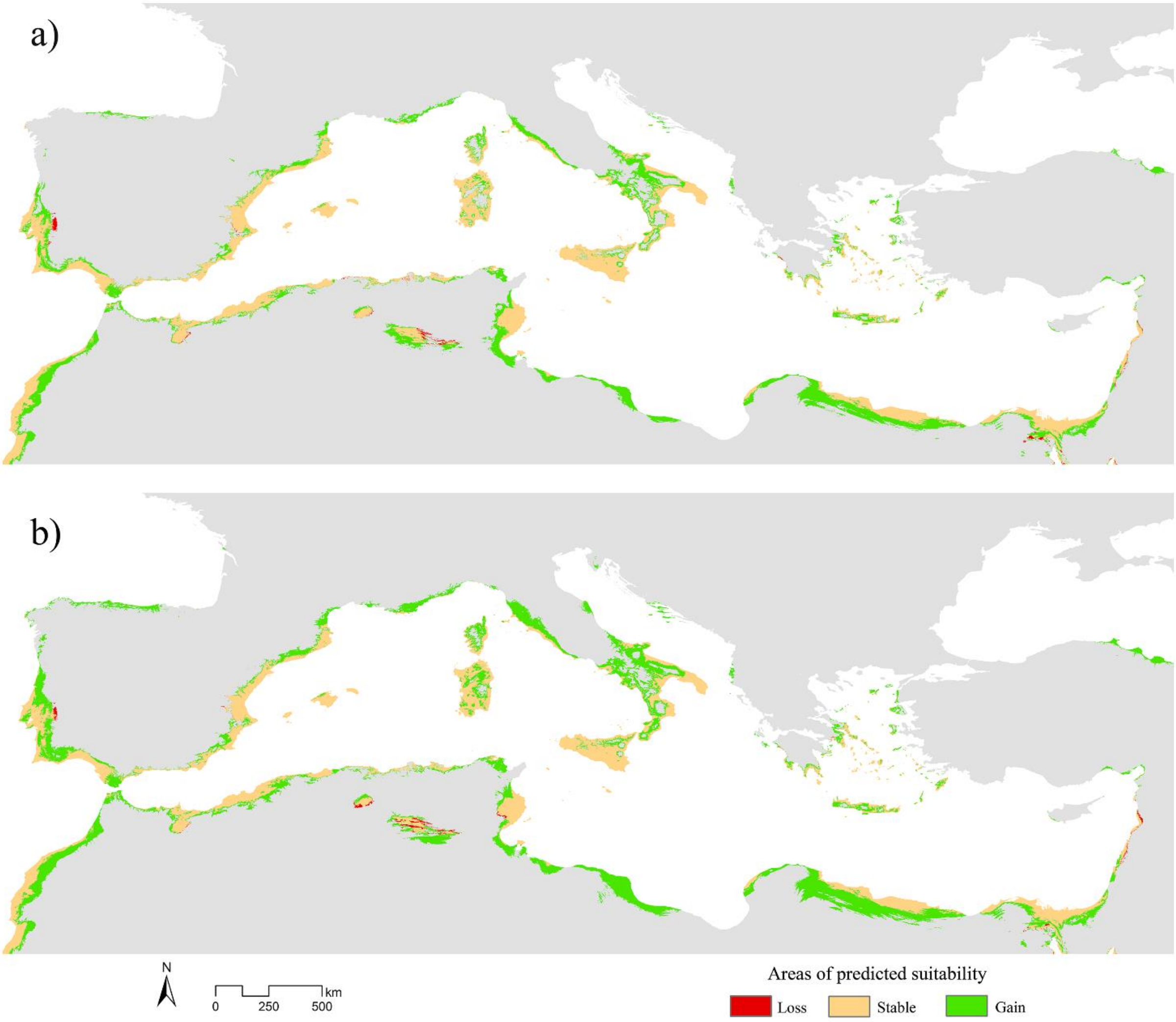

Figure 3. Range shifts of predicted areas of suitability for **a)** current climatic conditions versus 2050_RCP 6.0 and **b)** current climatic conditions versus 2050_RCP 8.5 for *M. obesula* secondary range.

Discussion and conclusions

The Ensemble Model for current climatic conditions matches the occurrences' distribution found for *M. obesula* across its secondary range, thus some considerations about its current potential invasiveness can be made. Considering that many coastal Mediterranean areas outside the target species' current range are predicted with high suitability, it is likely that its future introduction could favour the establishment in some Spanish and north African areas. This scenario is also favoured by the presence of the primary, *A. halimus*, and secondary, *C. album*, host plants, which occur throughout the areas predicted by the current EM. Further, the range shifts observed for both the RCPs of 2050 EMs are consistent with a hypothesis *M. obesula* spread in the Mediterranean area, considering that *A. halimus* covers (figure 2b) the entire range of predicted gain and stable areas for future climatic conditions.

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(www.facebook.com/groups/floraspontaneasiciliana)

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Appendix

The set of the nineteen bioclimatic variables considered as candidate predictors (from Worldclim.org), with their codes and explication. In bold, the variables selected as predictors for the Ecological Niche Modeling.

BIO1 = Annual Mean Temperature
BIO2 = Mean Diurnal Range [Mean of monthly (max temp – min temp)]
BIO3 = Isothermality (BIO2/BIO7)*100
BIO4 = Temperature Seasonality (standard deviation*100)
BIO5 = Max Temperature of Warmest Month
BIO6 = Min Temperature of Coldest Month
BIO7 = Temperature Annual Range (BIO5-BIO6)
BIO8 = Mean Temperature of Wettest Quarter
BIO9 = 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)
BIO16 = Precipitation of Wettest Quarter
BIO17 = Precipitation of Driest Quarter
BIO18 = Precipitation of Warmest Quarter
BIO19 = Precipitation of Coldest Quarter