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Ecological niche modeling of *Schinus molle* reveals the risk of invasive species expansion into biodiversity hotspots

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Abstract: Invasive species need a closer look on the threats they may cause to the environment, mainly considering the scenario of climatic changes predicted for the next decades. *Schinus molle* is a pioneer tree native from South America, reported as an important invasive species in four continents. Using ecological niche modeling we show that a wide area over the world is propitious for *S. molle* establishment under current climatic conditions, including 14 of the 25 world's biodiversity hotspots. Current projections of climate changes suggest scenarios implying the rise of areas favorable for *S. molle* expansion. Therefore, particular attention should be taken in regions where it was introduced, while approaches for long-term intervention may be necessary for regions of *S. molle* natural occurrence if its expansion threatens other native species. However, the natural dynamic of the ecosystems should be studied and contemplated in such regions.

Key words: Peruvian peppertree, ecological niche modeling, invasiveness, ecosystem management.

INTRODUCTION

Invasive plant species may represent a threat for biodiversity hotspots, given their high dispersal capacity under different climatic and environmental conditions. Sometimes, these species may be even more adapted for surviving in an invaded environment than the native plants, resulting in the extinction of local species, followed by a drastic change in all trophic levels of this ecosystem (Weber 2017).

Schinus molle L. (Anacardiaceae) is a pioneer tree species well-known by its application in the popular medicine (Dikshit et al. 1986), by the pharmaceutical uses of its essential oils (Marongiu et al. 2004), by the production of the spicy pink pepper (Goldstein and Coleman 2004) and by its role in the ecological succession (Lemos et al. 2014). Native to South America, *S. molle* has been reported as an invasive species in Central and North America (Howard and Minnich 1989, Asner

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et al. 2008, Ramírez-Albores et al. 2016), South Africa (Iponga et al. 2009) and Europe (Stinca et al. 2017) where it was introduced for ornamental purposes. In some areas in these regions, the self-establishment has been documented and *S. molle* is considered a naturalized species (Iponga et al. 2009, Richardson et al. 2010).

Within its natural range of occurrence in southern Brazil, the genetic analysis of nine natural populations of *S. molle* revealed low genetic diversity and estimations of gene dispersion distances larger than the current populations' area (Lemos et al. 2015). So, it is likely that the long-distance gene flow compensates the low genetic diversity of *S. molle*, and together with factors as high reproductive output and high resilience, allows the occupation of new geographic areas without further difficulties.

Modeling the ecological niche of *Schinus molle* within the Pampa biome in South America, a wide geographical area was identified as potential habitat for this species, with population expansion limited mainly by anthropic intervention (Lemos et al. 2014). Given the aptitude of this species for harboring forest expansion, these authors further pondered the importance of *S. molle* in the maintenance of the natural ecological dynamic of the Brazilian Pampa.

Considering the invasive ability of *S. mole* and the predicted scenarios of climatic changes for the next decades, the present study intended to expand the ecological niche modeling of this species over the world, in order to evaluate the potential risk of invasion for different biodiversity hotspots by *S. molle*, based on current climate data.

MATERIALS AND METHODS

For this study, geographical data on *S. molle* occurrence over the world was recovered from the SpeciesLink (http://splink.cria.org.br/) and the Global Biodiversity Information Facility (GBIF; https://www.gbif.org/) databases. The ecological niche modeling (ENM; see Soberón et al. 2017) was achieved with the maximum entropy distribution model algorithm, as performed in the software MaxEnt 3.4.1 (Phillips et al. 2005), using the software's standard parameters and the minimum of 1000 interactions with cumulative output.

Nineteen bioclimatic variables were extracted from the WorldClim database (http://www.worldclim.org; Hijmans et al. 2005) and used for the niche characterization in the modeling analysis. A first run was performed with all 19 variables, using a Jackknife test to determine the prediction power of each variable and its percentage of contribution to the model (Supplementary Material - Table SI). With the Jackknife results, a correlation test was done on the ENMtools software (Warren et al. 2008) and the strongly correlated (from $r = -0.8$ to $r = 0.8$) environmental variables were removed from the analysis. The MaxEnt algorithm was re-run twice keeping only the non-correlated variables presenting more than 1% of contribution to the model, as suggested by Peterson (2011). Finally, the modeling was run using five bioclimatic variables (Table I). For correcting AUC parameter, we used the partial ROC analysis (pROC; Peterson et al. 2008) from Niche Analyst (NicheA) program (Qiao et al. 2016). Employed parameters were setting as follow: convergence threshold = 10^{-5}; maximum iterations = 1000; regularization multiplier = 1; duplicate presence records removal. The model training was performed using 80% of species records and 20% was used to test the model. The Geographic Information System Quantum-GIS version 2.18 was used to compile MaxEnt results and generate the probability distribution maps. Climatic surfaces for global land areas were interpolated in 2.5 arc minutes maps (about 4.5 km² resolution).

RESULTS AND DISCUSSION

A total of 7329 collection points of *S. molle* were compiled from SpeciesLink and GBIF databases

(549 and 6780 respectively). Removing duplicate records, 1864 points remained for training. The distribution model revealed excellent quality (pROC = 0.983). The map for the predicted distribution of *S. molle* is the consensus for both databases (Figure 1).

The most important climatic variables determining the distribution of *S. molle* are related directly to temperature (Table I). Minimum temperature of coldest month and isothermality respond to 77.4% of the contribution to the model. Annual mean temperature, mean temperature of coldest quarter, and mean temperature of warmest quarter have a contribution of 22.6% to the model (Table I). The order of importance of the climatic variables in the present study slightly differs from the regional modeling performed for *S. molle* by Lemos et al. (2014) based in occurrence data of the species in the Brazilian Pampa. Differing from our global study, the modeling of Lemos et al. (2014) revealed precipitation seasonality and precipitation of the driest month as the two main variables contributing to the model (37.7% and 13.4% respectively), followed by four variables related to temperature. *Schinus molle* occurs in arid environments and the overall factors generating this dryness can marginally diverge among regions and are responsible by these differences (Iponga et al. 2009, Lemos et al. 2015). The much higher number of occurrence points with wider distribution employed in our global modeling covers a more complete representation of such overall factors, making the present study a better representation of the potential ecological niches of *S. molle*. The maximum entropy model performs confident analyses with information about presence-only point occurrences (Phillips et al. 2005) and can be improved by over-sizing the collection area (Ramírez-Albores et al. 2016).

TABLE I
Most influential current climatic variables determining the occurrence areas of *Schinus molle* in the globe, after exclusion of correlated* and less influential (< 1%) variables.

Variable	Percent of Contribution
Min Temperature of Coldest Month	50.8
Isothermality	26.6
Annual Mean Temperature	10.4
Mean Temperature of Coldest Quarter	8.9
Mean Temperature of Warmest Quarter	3.3

*The correlated variables excluded from the analysis were: mean diurnal range, temperature seasonality, temperature annual range, mean temperature of wettest quarter, mean temperature of driest quarter, annual precipitation, precipitation of wettest month, precipitation of wettest quarter, precipitation of driest quarter, precipitation of warmest quarter and precipitation of coldest quarter.

The predicted occurrence areas with very high probability (near 100%) for *S. molle* occurrence in South America are the Brazilian Atlantic coast, the Chilean mountains, and the Pampean regions of Brazil, Argentina and Uruguay. The Central American islands and Mexico are predicted areas of occurrence, as are the Southernmost and the west coast regions of the United States of America (Figure 1). Further regions predicted for occurrence of *S. molle* are the West and Mediterranean regions of Europe, the South Balkans in Asia, the Madagascar Island, the Mediterranean coast, the Southernmost and the Northeast regions of the African continent, the Middle East region, and the southernmost Australia and surrounding islands (Figure 1).

According to the model, *S. molle* has the capacity of establishment (probability > 75%) in 14 out of 25 biodiversity hotspots (Figure 1) proposed by Myers et al. (2000): Atlantic Forest, Chocó/Darlén/Western Ecuador, Central Chile, Mesoamerica, Caribbean Islands, California Floristic Province, Madagascar, Mediterranean Basin, South-Central China, Cape Floristic Province, Succulent Karoo, Sundaland, Southwest Australia and New Zealand.

Confident niche modeling is dependent not only on the bioclimatic factors, but also on biotic elements (ecological interactions) and on the

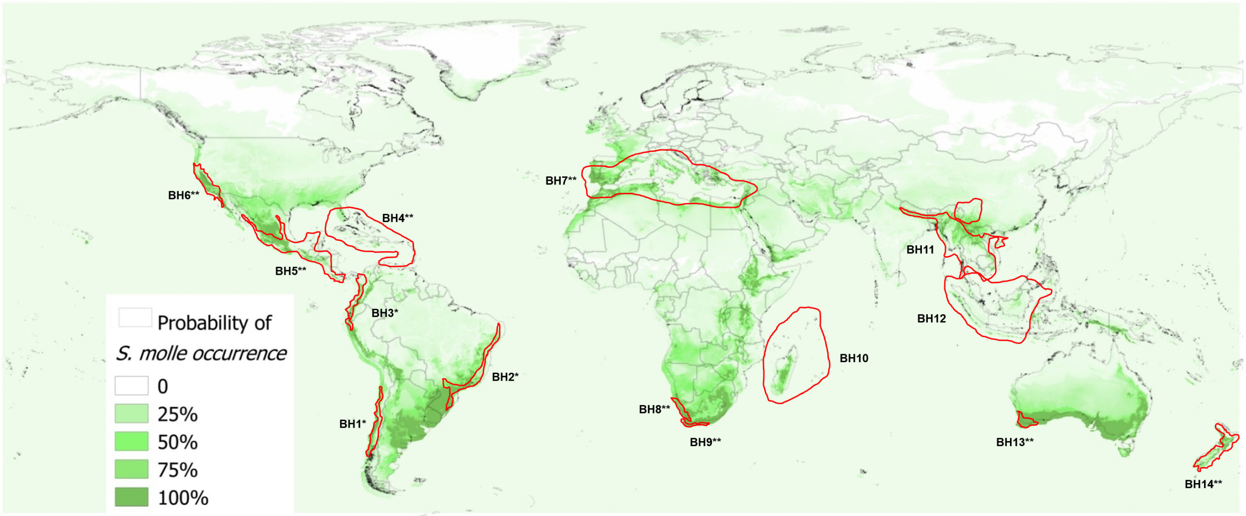

Figure 1 - Current ecological niche modeling map for *Schinus molle*. Highlighted areas are the 14 biodiversity hotspots (BH; Myers et al. 2000) that are susceptible to *S. molle* expansion. *Biodiversity Hotspots where *S. molle* is native. **Biodiversity Hotspots where S. molle invasion is already reported. BH1: Central Chile; BH2: Atlantic Forest; BH3: Chocó/Darlén/Western Ecuador; BH4: Caribbean Islands; BH5: Mesoamerica; BH6: California Floristic Province; BH7: Mediterranean Basin; BH8: Succulent Karoo; BH9: Cape Floristic Province; BH10: Madagascar; BH11: South-Central China; BH12: Sundaland; BH13: Southwest Australia; BH14: New Zealand.

species accessibility to environments, without barriers to movement and colonization (the M-area; Soberón and Peterson 2005, Barve et al. 2011). Even though the natural occurrence area of S. molle in South America presents geographic barriers to its dispersion throughout Europe, Africa, Asia and Oceania, the human-mediated introduction of the species in most of these regions (Figure 1) turns the invasion of such biodiversity hotspots a real threat.

The high dispersal and survival capacities of *S. molle* enable this species to invade about 56% of the world's biodiversity hotspots, with higher risk of prompt invasion in regions where this species is already established, near such hotspots. The introduction of *S. molle* was already reported in California, where it is viewed as a pest in orange groves and other sites of irrigation (Howard and Minnich 1989); Israel, found along roadsides and in wastelands (Danin 2000); Hawaii, where it poses a threat to the rare endemic flora (Asner et al. 2008); South Africa, where a high density of young plants of *S. molle* is reported expanding over non-forested biomes as the savanna (Iponga et al. 2009, Richardson et al. 2010); Mexico, where it is widely naturalized (Ramírez-Albores et al. 2016); and Italy, where it escaped from cultivation and now is naturalized (Stinca et al. 2017).

This scenario may be even worse, because the area under consideration has become substantially drier since the 1980s, mainly as effect of the global warming induced by greenhouse gases (Dai and Zhao 2017). Projections of climate changes for 21th century suggest scenarios in which the warming increases over all latitudes and precipitation decreases over subtropical lands, while a continued intensification in global agricultural drought frequency and area is expected even under low-moderate gas emissions scenarios (Zhao and Dai 2017). Such forecasted scenario implies in increasing areas favorable for *S. molle* expansion, mainly in regions already predicted in our model (Figure 1) in South and Central Americas, Mexico, Southern USA, Mediterranean Europe, Africa and Australia (See Figure 4 in Zhao and Dai 2017).

As a general conclusion, we suggest that the risk of invasion over biodiversity hotspots should consider the map of predicted occurrence areas for *S. molle* presented in this study. This map was constructed based on current bioclimatic data, but climate change models have demonstrated increased variance of precipitation and seasonal changes worldwide, with wet zones becoming wetter, and dry zones becoming drier (Dore 2005, Miranda et al. 2011, Zhao and Dai 2017). In addition, an increase in temperature variability in tropical countries over the next decades have being consistently projected. Temperature variability escalations by about 15% per degree of global warming in Amazonia and Southern Africa are expected (Bathiany et al. 2018). *Schinus molle* commonly occurs in arid regions and so, the climatic oscillations tend to maintain or even increase the areas suitable for the expansion of this species. Therefore, special management strategies should be planned for the biodiversity hotspots in order to avoid negative impacts of *S. molle* dispersion, mainly over non-forested areas, where the species may reveal a particularly high dispersion capacity (Lemos et al. 2014). Such management strategies include: (1) prevention of expansion through educational initiatives, avoiding new introductions of *S. molle* near or within areas with risk of invasion; (2) early detection of the expansion and coordinated containment and eradication response, preventing large dissemination of the species; and (3) rehabilitation and restoration of degraded areas with fast-growing native species, diminishing potential areas for invasive species dispersion. In South America, where *S. molle* is a native species, three biodiversity hotspots are predicted areas for the species expansion (Atlantic Forest, Chocó/Darlén/Western Ecuador, and Central Chile) and the natural dynamic of the ecosystems should be studied and contemplated, as proposed for the Brazilian Pampa (Lemos et al. 2014).

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AUTHOR CONTRIBUTIONS

RPM Lemos and CBD'O Matielo, performed the MaxEnt simulations; AS Marques Jr., MG Santos, VG Rosa, DS Sarzi, and JVS Rosa performed the data collection; VM Stefenon was responsible for the obtention of funds and the administration of project. RPM Lemos and VM Stefenon elaborated the conceptualization, methodology, formal analysis and discussed the results. All authors contributed to the manuscript elaboration.

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SUPPLEMENTARY MATERIAL

Table SI - Percent of contribution of the nineteen current climatic variables determining the occurrence areas of ***Schinus molle*** in the globe in the first MaxEnt run.