



Global invasibility potential of the shrub *Baccharis dracunculifolia*

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Abstract

The genus *Baccharis* (Asteraceae) comprises over 440 species distributed along North and South America. Some species of this genus have remarkable invasiveness, and one of these species is the South American shrub *Baccharis dracunculifolia* DC. Most of the introductions of non-indigenous species are held indirectly through trade, so it is believed that this species could become invasive worldwide with a particular interest in the North American continent because of the increasing sale of products derived from honey to this continent. The resin extracted from *B. dracunculifolia* is the leading source for preparing the green propolis produced in Southeastern Brazil. Thus, the main objective of this work is to apply an approach based on distribution modeling to investigate possible areas of high environmental suitability for *B. dracunculifolia* in the North American continent and the potential to the entire globe using current and two future scenarios. Our results show many areas of environmental suitability for *B. dracunculifolia*. This species can invade over 33 countries distributed into five continents, including North America, some of the most critical parts of the southern USA, and large areas in Mexico. Since the best way of countering biological invasions is prevention, we propose that the introduction of this species should be monitored.

Keywords Biological invasion · Climate matching · Maximum entropy · Model selection · Niche · Projection scenarios

1 Introduction

The genus *Baccharis* L. (Asteraceae) (Linnaeus 1753) comprises more than 440 species and is distributed from Southern North America to Southern South America (Abad and Bermejo 2007; Fernandes et al. 2021; Heiden 2021). Some species of this genus have remarkable invasiveness potential traits, such as generalist behavior, effective dispersal mechanism, adaptation to pioneer stages of succession, high competitive ability, and seeds germinate under a wide range of environmental conditions (Fernandes et al. 2021;

Lázaro-Lobo et al. 2021). *Baccharis halimifolia* L. (Linnaeus 1753) and *Baccharis pilularis* DC. (Candolle 1836), both native to North America, and *Baccharis dracunculifolia* DC. (Candolle 1836), native to South America, are known for their invasive potential.

B. halimifolia L. is native to North America, and it is found at high density in disturbed sites in North American prairies (Allain and Grace 2001; Valéry et al. 2009). It is a successful invader of estuarine communities in Southern Europe (Caño et al. 2012; Fried et al. 2016; Calleja et al. 2019a, b). *Baccharis halimifolia* is sensitive to changes in environmental conditions such as light and temperature (15–20 °C) for optimum yield (Westman et al. 1975). Also, *B. halimifolia* is sensitive to soil conditions, e.g., water-logged conditions, high soil slit, and high conductivity, which seem to reduce its presence (Fried et al. 2016). Additionally, *B. halimifolia* has shown higher germination rates at low salinities and soils farther from the immersion influence of estuaries (Paudel et al. 2013). Some of the extreme effects when *B. halimifolia* is exposed to salinity are drastic biomass reduction, short plant height, and lower leaf production (Caño et al. 2013, 2016; Calleja et al. 2019a, b). Previous reports of *B. halimifolia* exposure to salinity showed intolerance at ranges > 30 g/l (Caño et al. 2014; Fried et al. 2016).

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Baccharis pilularis DC., also originated in North America, has been responsible for the shrub encroachment of prairie regions, driven primarily by the change in land use and other human impacts (Davis and Mooney 1985; Hobbs and Mooney 1986; Williams and Hobbs 1987). Moreover, *B. pilularis* can become more invasive due to its large seed production, long-distance dispersion, wide adaptability to soil nutrient conditions, and salinity compared to noninvasive species (Fernandes et al. 2021). Also, *B. pilularis* has proliferated in large regions in response to increased temperature and atmospheric CO₂ concentrations due to a drastic reduction of herbivory by snails and slugs (Gastropoda: Pulmonata), the most frequently observed herbivores on *B. pilularis* seedlings (Zavaleta 2005).

Baccharis dracunculifolia DC. is native to South America and considered a weed in disturbed, degraded areas (Lorenzi 1991; Gomes et al. 2002) and has a quick life cycle that increases its distribution properties (Fagundes et al. 2001, 2005; Gomes 2002; Espírito-Santo et al. 2003). This species is distributed throughout the Brazilian Cerrado (Gomes 2002), sea coast (Fagundes and Fernandes 2011), tropical rainforest (Fagundes and Fernandes 2011), and pampas of Brazil, Uruguay, Paraguay, Argentina (e.g., Altesor et al. 2005; Minteguiaga et al. 2021), Peru (Grant 2020), and Bolivia (Loayza et al. 1995); for reviews, see Fernandes et al. (2021).

Although there are no reports of *B. dracunculifolia* introduction in North America, the growing trade of honey-derived products between Brazil and the USA (Oliveira et al. 2021), which encompassed almost 27,360 tons of natural honey alone in 2020, can facilitate the invasive potential of *B. dracunculifolia* into North America (Abemel 2015). It is known that the resin extracted from *B. dracunculifolia* is the primary source for the preparation of green propolis, a resinous derived product produced in Southeastern Brazil (Alencar et al. 2005; Fernandes et al. 2018). Much of the introductions of non-indigenous species are held unintended by transporting seeds/seedlings by humans, from one region to another through trade and tourism (e.g., Lockwood et al. 2005; Reichard et al. 2009); these introductions occur mainly in urban areas (Von der Lippe et al. 2008). The achenes of *B. dracunculifolia* are tiny (between 1 and 2 mm) and resistant, facilitating their transport by crates or other materials originating from honey-producing regions in Brazil to the USA (Oliveira et al. 2021). Furthermore, given its high value in the North American market, there is a high chance for this species to be introduced into North America to be used for the production of green propolis (Amancio et al. 2021; Oliveira et al. 2021). *B. dracunculifolia* is a species whose distribution is growing in South America, mainly due to climate change and increasing human impacts (Gomes and Fernandes 2002). Thus, a potential invader if introduced into

North America, mainly because it can adapt to different habitats (highlands, wet or dry, hot, or cold, see Fagundes and Fernandes 2011), makes this species an attractive model to study biological invasion.

The ability to predict the entry of an invasive species into a new environment is a much-discussed “biological invasion” topic in conservation biology (Nyari et al. 2006; Giovanelli et al. 2008b; Jiménez-Valverde et al. 2011; Elith 2017). Biological invasions had been a significant cause of loss of biodiversity on the planet, synergistically acting with other components of global change like climate change, habitat destruction, and pollution (Dukes and Mooney 1999; Ludsins and Wolfe 2001; Bacher et al. 2018; Malacrinò et al. 2020; Pyšek et al. 2020; Faria et al. 2022). Moreover, it has caused considerable losses to the global economic system, currently being configured as one of the biggest problems of global agribusiness (Crystal-Ornelas et al., 2021; Zenni et al. 2021). Fantle-Lepczyk et al. (2022) estimated expenditures of about \$47 billion annually in the USA alone to control non-indigenous invasive species. These losses may reach 105 billion dollars a year for Brazil, including agriculture and human health (Adelino et al. 2021). Due to all these factors, in 1999, President Bill Clinton signed an executive order to create rules to prevent the entry of non-indigenous invasive species into the USA and also implemented guidelines for the management of these species to reduce the damages caused by them (Peterson and Vieglais 2001).

Species distribution models (SDM) have been used to predict areas of high invasibility for non-indigenous species into a new environment (Nyari et al. 2006; Giovanelli et al. 2008b; Pacifici et al. 2015; Bazzichetto et al. 2018). SDM is based on climatic matching between areas of origin and regions supposedly invaded; it is also recognized as an important tool for building environmental policies to control invasive non-indigenous species spread (Rodda et al. 2011). The SDM is developed by combining environmental data and species distribution, generating information on their potential distribution in areas (e.g., maps) with reasonable environmental suitability for this species (Zimmermann et al. 2010; Duarte et al. 2018). The SDM has been widely used in ecology to predict the effects of global warming on species and select priority areas for conservation (e.g., Elith et al. 2006; Peterson 2006; Barbosa et al. 2010; Pacifici et al. 2015; Zhang et al. 2021). In addition, it has been often used to describe potential areas of distribution where rare species could occupy (e.g., Raxworthy 2003; Giovanelli et al. 2008a; Barbosa et al. 2015). Furthermore, this approach has also been used to predict the potential entry areas/invasion routes of non-indigenous species (e.g., Vieglais and Peterson 2001; Papes and Peterson 2003; Peterson et al. 2003; Ficetola et al. 2007; Thapa et al. 2018).

The synergy provided by the broad spatial distribution, biological characteristics, and extensive use by humans of

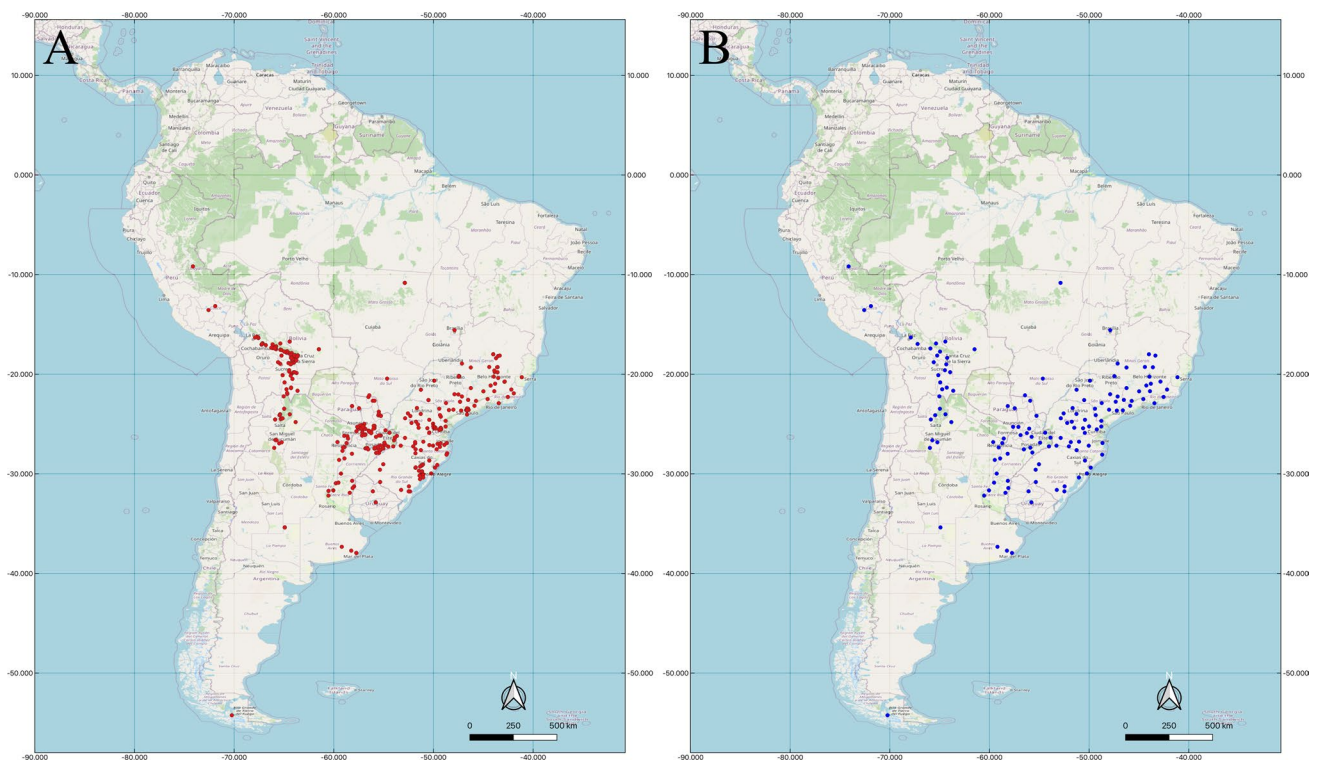


Fig. 1 Distribution of South American occurrences for *Baccharis dracunculifolia*, used in this study to develop the distribution model within the calibration area. (A) Original occurrences distribution from GBIF. (B) Curated occurrences distribution

the products supplied by *B. dracunculifolia* in line with the globalization and climate change scenarios provided the impetus for this study. This project sought an approach based on SDM to investigate possible entry areas with high environmental suitability for *B. dracunculifolia* on the North American continent and projection scenarios to find suitable conditions in which *B. dracunculifolia* can establish worldwide (Levine et al. 2003). Some possible impacts from the introduction of *B. dracunculifolia* worldwide could be: (i) change in the native plant community structure (Vivrette and Muller 1977; Pysek and Pysek 1995), (ii) impacts on higher trophic levels (Carroll et al. 1998; Schmidt and Whelan 1999), and (iii) impacts on hydrology and fire regimes (Van Wilgen and Richardson 1985; Gerlach 2000).

2 Materials and methods

Species and environmental data – We built the SDM using 1862 georeferenced occurrences of *B. dracunculifolia*, following the checklist provided in Feng et al. (2019) to ensure the reproducibility of methods. These occurrences were downloaded from the GBIF platform, all located in South America (GBIF 2021) (Fig. 1A). However, 1,304 occurrences were discarded because they overlapped in the same pixel, thereby reducing autocorrelation effects (Hernandez

et al. 2006; Phillips et al. 2006; Pearson et al. 2007; Thorn et al. 2009). The overlapped points were discarded using the *duplicated* function of the base R package (R Core Team 2021); remaining 558 occurrences and effects of spatial autocorrelation were avoided by thinning observations with a distance of 50 km using the *poThin* function of the RSpacial library (OShea 2021). From those 1862, a total of 209 occurrences were used for this study (Fig. 1B; Table S1), which were partitioned into two subsets being 75% for model calibration and 25% for testing; the random method of the ENMeval package was used to partition data (Muscarella et al. 2014).

Bioclimatic variables are good predictors for the distribution of biodiversity due to their strong associations with climate and biota (Mooney et al. 1995; Pearson and Dawson 2003; Schrag et al. 2008). Thus, the bioclimatic variables were obtained from the project Worldclim (2021) using a spatial resolution of 30" (~1km²) (Fick and Hijmans 2017). However, the BIO8, BIO9, BIO18, BIO19 bioclimatic variables that combine temperature and precipitation were discarded for knowing odd discontinuities between neighboring pixels (see Escobar et al. 2014) (Table 1). The altitude variable has demonstrated to be also a good predictor for the distribution of biodiversity (Parolo et al. 2008), it was used in conjunction with all other groups of variables, and it was also

Table 1 List of environmental variables (included and excluded) used in this study for the distribution model for *Baccharis dracunculifolia*

Included Variables	Excluded Variables	Spatial resolution	Reference
Altitude		30" (~ 1 km)	<i>WorldClim</i> (Fick and Hijmans 2017)
Aspect		30" (~ 1 km)	
Slope		30" (~ 1 km)	
BIO 1 = Annual Mean Temperature*		30" (~ 1 km)	
BIO 2 = Mean Diurnal Range		30" (~ 1 km)	
BIO 3 = Isothermality		30" (~ 1 km)	
BIO 4 = Temperature Seasonality*		30" (~ 1 km)	
BIO 5 = Max Temperature of Warmest Month		30" (~ 1 km)	
BIO 6 = Min Temperature of Coldest Month*		30" (~ 1 km)	
BIO 7 = Temperature Annual Range*		30" (~ 1 km)	
	BIO 8 = Mean Temperature of Wettest Quarter	30" (~ 1 km)	
	BIO 9 = Mean Temperature of Driest Quarter	30" (~ 1 km)	
BIO 10 = Mean Temperature of Warmest Quarter*		30" (~ 1 km)	
BIO 11 = Mean Temperature of Coldest Quarter*		30" (~ 1 km)	
BIO 12 = Annual Precipitation*		30" (~ 1 km)	
BIO 13 = Precipitation of Wettest Month		30" (~ 1 km)	
BIO 14 = Precipitation of Driest Month		30" (~ 1 km)	
BIO 15 = Precipitation Seasonality (Coefficient of Variation)		30" (~ 1 km)	
BIO 16 = Precipitation of Wettest Quarter*		30" (~ 1 km)	
BIO 17 = Precipitation of Driest Quarter*		30" (~ 1 km)	
	BIO 18 = Precipitation of Warmest Quarter	30" (~ 1 km)	
	BIO 19 = Precipitation of Coldest Quarter	30" (~ 1 km)	

*Variables used in the model

obtained from the Worldclim project at a spatial resolution of 30" (~ 1km²) (Fick and Hijmans 2017) (Table 1). The variables derived from the altitude, aspect, and slope were created using the *terrain* function of the *raster* R package (Hijmans 2021).

All bioclimatic variables were cropped to cover the calibration area (M) in South America, covering all occurrences of the species (Fig. 1B). For this purpose, the *convex_area* function with a *buffer_distance* of 75 km was used and was performed in the *ellipsenm* v0.3.4 R package. Also, a Pearson correlation test was performed to avoid the presence of multicollinearity between variables (Zar 1996). Those highly correlated ($r \geq 0.8$) were kept in the model as qualitative variables (Werneck et al. 2010). Furthermore, a jackknife process in Maxent (Phillips et al. 2018) was used to select distinct sets of variables that most contributed to models (Table 1). The *findCorrelation* function of the *caret* R package (Kuhn et al. 2020) was applied to select resulting bioclimatic variables. Further, a principal component analysis (PCA) was carried out to visualize the niche of *B. dracunculifolia* using the Niche Analyst tool (Qiao et al. 2016).

The resulting nine bioclimatic variables were grouped into 10 sets of eight/nine variables (Tables 2 and 3) using the

Table 2 Performance statistics for the four best SDM models based on independent 10 occurrence data of *Baccharis dracunculifolia*

Model Number	Set of variables	Mean AUC ratio	Partial ROC	Omission rate
1	Set 10	1.5073	0	0.111 0
2	Set 2	1.5689	0	
3	Set 4	1.5782	0	0
4	Set 6	1.5872	0	0

kuenm_varcomb function of *kuenm* R package (Cobos et al. 2019). In addition, two projection scenarios (2030 and 2050) and two representative concentration pathways (RCP) (RCP 4.5 and RCP 8.5) were evaluated, and the NCAR-CCSM4 general circulation model (GCM) for 2030 and 2050 time projections. Data were downloaded from the CGIAR spatial downscaling database (Navarro-Racines et al. 2020; CGIAR 2021).

Model calibration – For the SDM calibration process, 5,270 models were evaluated by combining ten sets of

Table 3 Sets of bioclimatic variables used to evaluate the SDM models

Set of bioclimatic Variables	Variables
Set 2	BIO1, BIO4, BIO7, BIO10, BIO11, BIO12, BIO16, BIO17
Set 4	BIO1, BIO4, BIO6, BIO7, BIO10, BIO11, BIO12, BIO16
Set 6	BIO1, BIO4, BIO6, BIO7, BIO10, BIO11, BIO16, BIO17
Set 10	BIO1, BIO4, BIO6, BIO7, BIO10, BIO11, BIO12, BIO16, BIO17

environmental predictors, considering the contribution of each predictor's regularized training gain. In addition, 17 values of regularization multiplier were used: [0.1, 1] using intervals of 0.1, [1.0, 6.0] using intervals of 1.0, and [8.0, 10] with intervals of 2.0. Also, 29 combinations of all feature classes were used: linear, quadratic, product, threshold, and hinge. Candidate model performance was evaluated using the statistical significance metric partial ROC (pROC), with 500 iterations, 50% of bootstrapping, and omission rates of 5%. Finally, omission rate (OR) and Akaike information criterion corrected (AICc) were used as model selection criteria. With this combination of parameters, the best models were selected according to the following criteria: (1) significant models, (2) OR (≤ 0.5), and (3) AICc values (≤ 2) (Table 2) (Cobos et al. 2019). The creation and selection of models were performed using the *kuenm_cal* and *kuenm_ceval* functions of the *kuenm* R package.

The construction of each SDM was executed by an algorithm that uses the maximum entropy approach, which has shown the best performance among several other modeling methods (Elith et al. 2006; Hernandez et al. 2006), and can perform practical analysis even with small samples (Hernandez et al. 2006; Pearson et al. 2007; Thorn et al. 2009) using only present data (Phillips et al. 2006). The SDM was performed in MaxEnt software 3.4.4v (Phillips et al. 2006; Steven et al. 2021).

Model evaluation and extrapolation risk – The final SDM models were selected based on the best combination of parameters, with 500 replicates as bootstrap and logistic outputs. Then, they were evaluated with calculations of partial ROC and omission rates of 5% using 58 independent occurrence data points of *B. dracunculifolia* (Table 4) and performed with the *kuenm_mod* and *kuenm_feval* functions of the *kuenm* R package (Cobos et al. 2019). These resulting SDM models were later projected to the entire world to find potential climate matching in areas where *B. dracunculifolia* could potentially establish, with a particular interest in North America.

Also, two pathways were evaluated using the NCAR-CCSM4 general circulation model (GCM). Extrapolation risk was calculated using the mobility-oriented parity (MOP) analysis (Owens et al. 2013) included in the *kuenm_mmop* function of the *kuenm* R package. This function compares the environmental variables between the calibration area

and the extrapolated areas. As a result, areas where strict extrapolation risk exists and similarity levels between the projection regions and the calibration area are obtained. Also, descriptive statistics were calculated to get the amount of variation across multiple parameter settings and see variance among models transferred to the projection areas, using the *kuenm_modstats* function of the *kuenm* R package.

Lastly, to ensure reproducibility of methods, the authors created a GitHub repository in which source code and data are available for the following tasks: (1) cleaning and preparing occurrence data, (2) selecting bioclimatic variables, and (3) calibrating models, select best models, extrapolation, and risk evaluation. This repository can be found in the Data and Source Code Availability section.

3 Results

After applying a correlation analysis, only nine highly correlated variables ($r \geq 0.8$) were kept in the model (Fig. 2, Table 1). According to the jackknife results, the bioclimatic variables that most contributed to the training gain of the final SDM models were: annual mean temperature (BIO 1), temperature seasonality (BIO 4), min temperature of coldest month (BIO 6), temperature annual range (BIO 7), mean temperature of warmest quarter (BIO 10), mean temperature of coldest quarter (BIO 11), annual precipitation (BIO 12), precipitation of wettest quarter (BIO 16), and precipitation of driest quarter (BIO 17) (Fig. 3). The importance of these variables for *B. dracunculifolia* had been previously reported (Gomes and Fernandes 2002; Fagundes and Fernandes 2011). The SDM evaluation using variables cited above resulted in four selected models (Fig. 4). Three-dimensional environmental space convex hull denotes the environmental distribution of *B. dracunculifolia* in South America (Fig. 5).

The SDM models resulted in two types of maps, being the first a habitat suitability (invasibility) map projection with higher environmental suitability denoting a potential distribution for *B. dracunculifolia* (Fig. 6), which depicts the invasive potential of *B. dracunculifolia* for the current scenario (Hirzel and Le Lay 2008; Estay et al. 2014; Avendaño et al. 2021). Also, two future projections were evaluated for 2030 and 2050 using the CCSM4 GCM and the pathways RCP 4.5 intermediate scenario emissions

Table 4 Performance statistics for the best four SDM candidate models during calibration for *Baccharis dracunculifolia*

SDM Model Number	Mean AUC ratio	Partial ROC (pROC)	Omission rate (OR) at 5%	OR_AICc	Delta AICc	W AICc	Number of parameters
1	1.381	0	0.034 0.034	6128.689	0.000	1.000	15
2	1.389	0		6128.689	0.000 0.001	0.250	15
3	1.384	0	0.034	6128.689	0.0001	0.334	15
4	1.388	0	0.034	6128.696	0.0007	0.499	15

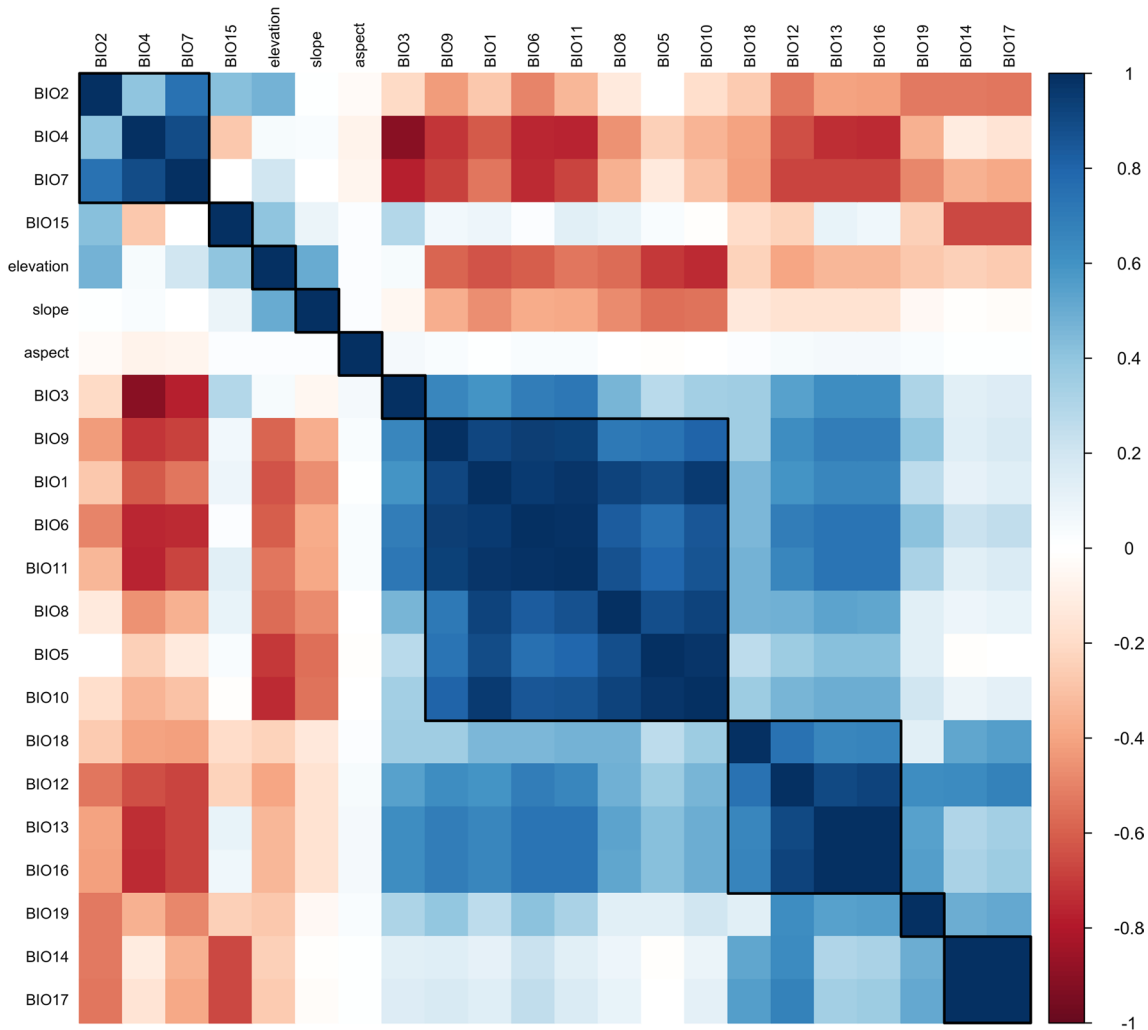


Fig. 2 Correlation matrix of environmental variables of calibration area in South America. Legend depicts the correlation between variables, ranging from -1 to 1. Squares denote highly positively correlated variables

peak around 2040 then declined, and RCP 8.5 emissions continue to rise throughout the twenty-first century. These two pathways represent variations in climatic conditions and allow us to simulate the response of *B. dracunculifolia* under these climatic conditions.

The invasiveness potential of *B. dracunculifolia* increases over time and is slightly positively accentuated

with the increase in greenhouse gas emissions in RCP 8.5 (Fig. 7). Each map in Fig. 7 represents the average values of four sets of environmental variables using logistic outputs for the final selected models. Additionally, logistic outputs were binarized into two classes that denote suitability or unsuitability for *B. dracunculifolia* for a given area (Saunders et al. 2020). The second type map denotes

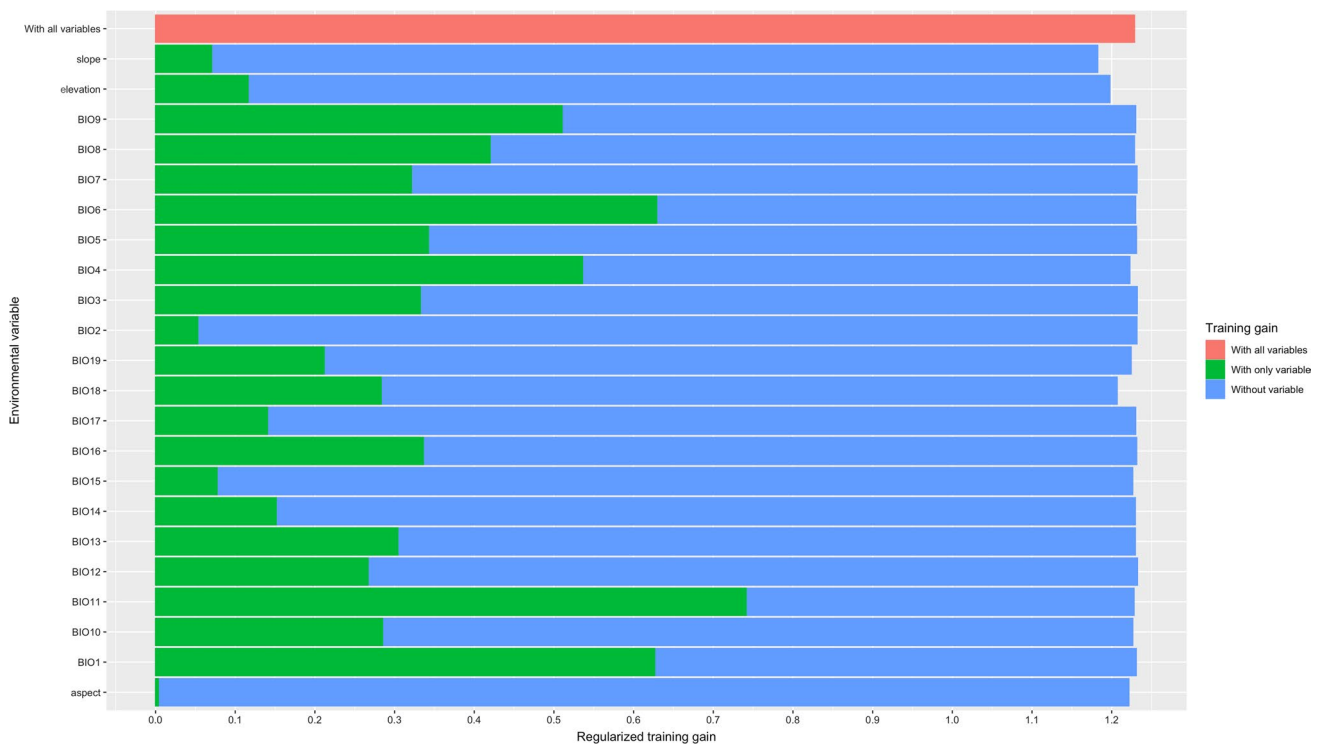


Fig. 3 Model contribution of environmental variables evaluated using the jackknife process. Legend denotes training gain using all variables (red bar), individual variables (green bars), and training gain using all variables except the indicated one (blue bars)

the extrapolation risk map projection, in which higher environmental similarity indicate broad areas of strict extrapolation for *B. dracunculifolia* (Owens et al. 2013; Cobos et al. 2019; Obiakara et al. 2020; Raghavan et al. 2020) (Fig. 8).

Accordingly, potential impacts of the introduction of *B. dracunculifolia* were evaluated using model transfer for two future scenarios (see Figs. 7 and 8). The CCSM4 GCM was used, and two representative concentration pathways are as follows: RCP 4.5 and RCP 8.5. The SDM results suggest that variables related to temperature per se, in general, have greater importance than those related to precipitation. The distribution areas of native *B. dracunculifolia* in Southeastern South America have high precipitation levels during the summer.

Furthermore, there is a high risk of invasion into the African continent in South Africa, Zimbabwe, Namibia, Angola,

Zambia, Mozambique, Tanzania, Kenya, Etiopia, Angola, Madagascar, Morocco, and some parts of the Congo Republic. Also, in Europe, there is a high risk of invasion in Portugal, Spain, France, Ireland, the UK, and some regions of Italy, Libano, and Israel. Similarly, other *Baccharis* spp. are also established in Europe and classified as invasive, indicating a high probability of proliferation for *B. dracunculifolia* if introduced (Fried et al. 2016). Additionally, there is a high risk of invasion in Asia in China, Taiwan, Vietnam, Laos, Cambodia, Thailand, Burma, Bangladesh, India, and Nepal. This high risk is also persistent in Australia, Tasmania, New Zealand, and New Caledonia.

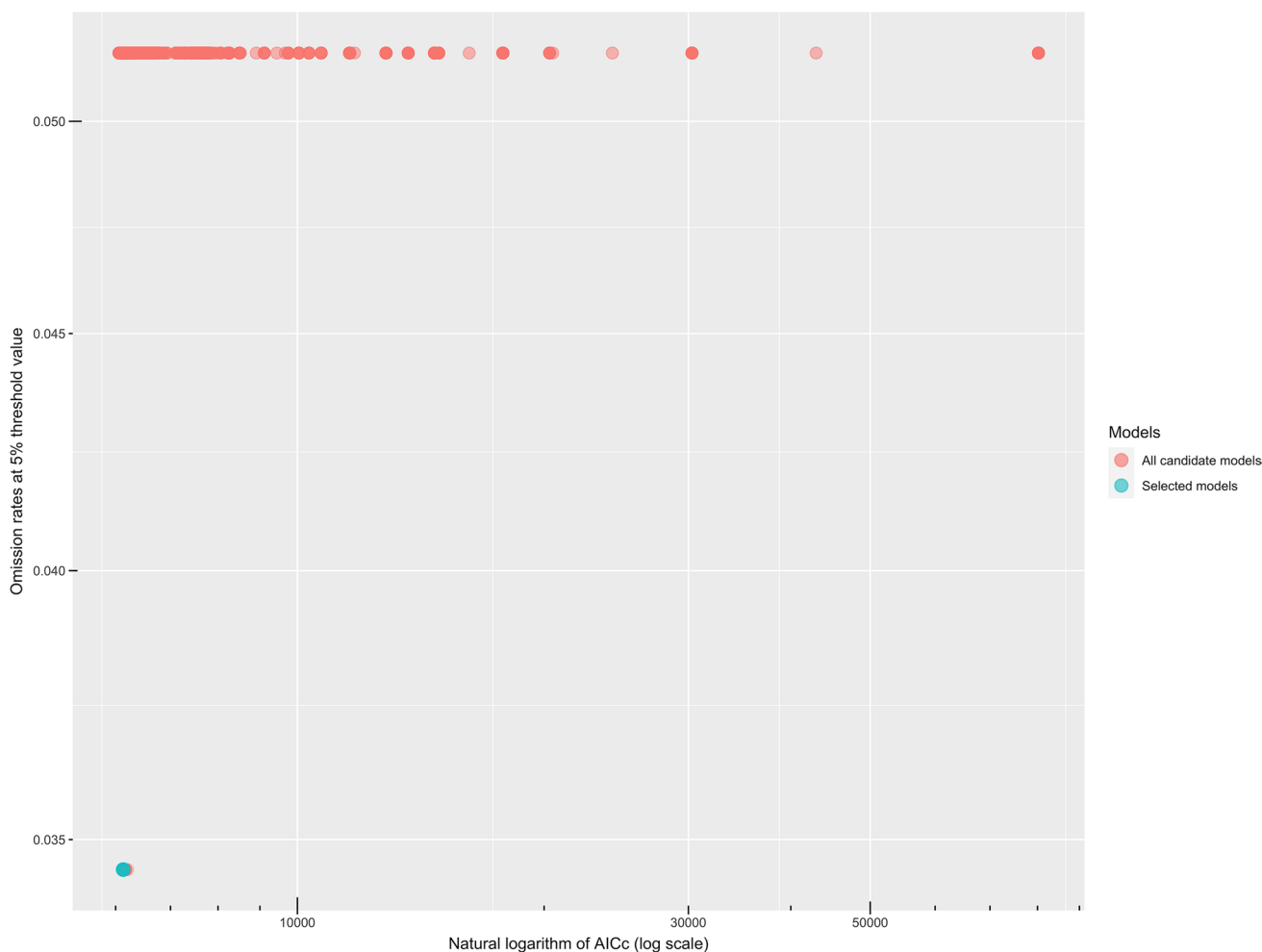


Fig. 4 Selected models that met the omission rate (OR) or Akaike information criterion corrected (AICc) criteria. The four selected models overlapped on the same point

4 Discussion

The area of introduction of an invasive non-indigenous species often reflects a more significant extension of suitability than that found in the native field (Fitzpatrick et al. 2007; Kearney et al. 2008). Nonetheless, our projection results of *B. dracunculifolia* suggest that this affirmation has to be reconsidered for this species. In all the cases except Africa, the highest suitability is located in South America, South China, and Eastern Australia. Darwin (1859) postulated that most species seem to have a limited distribution in nature, and these limitations are more a result of biotic rather than

by climatic factors. However, the model presented here encompasses probably a significant portion of the fundamental niche for *B. dracunculifolia*, given the wide range of habitats colonized by this species in South America (Gomes and Fernandes 2002; Marques et al. 2002; Altesor et al. 2005; Loayza et al. 1995; Fagundes and Fernandes 2011). Thus, the future projections probably reflect much of the species' fundamental niche worldwide. Likewise, the climatic similarity of areas where a species can proliferate is only one aspect to consider. In addition, other aspects to consider are nutrient availability, light availability, and salinity (Lázaro-Lobo et al. 2021).

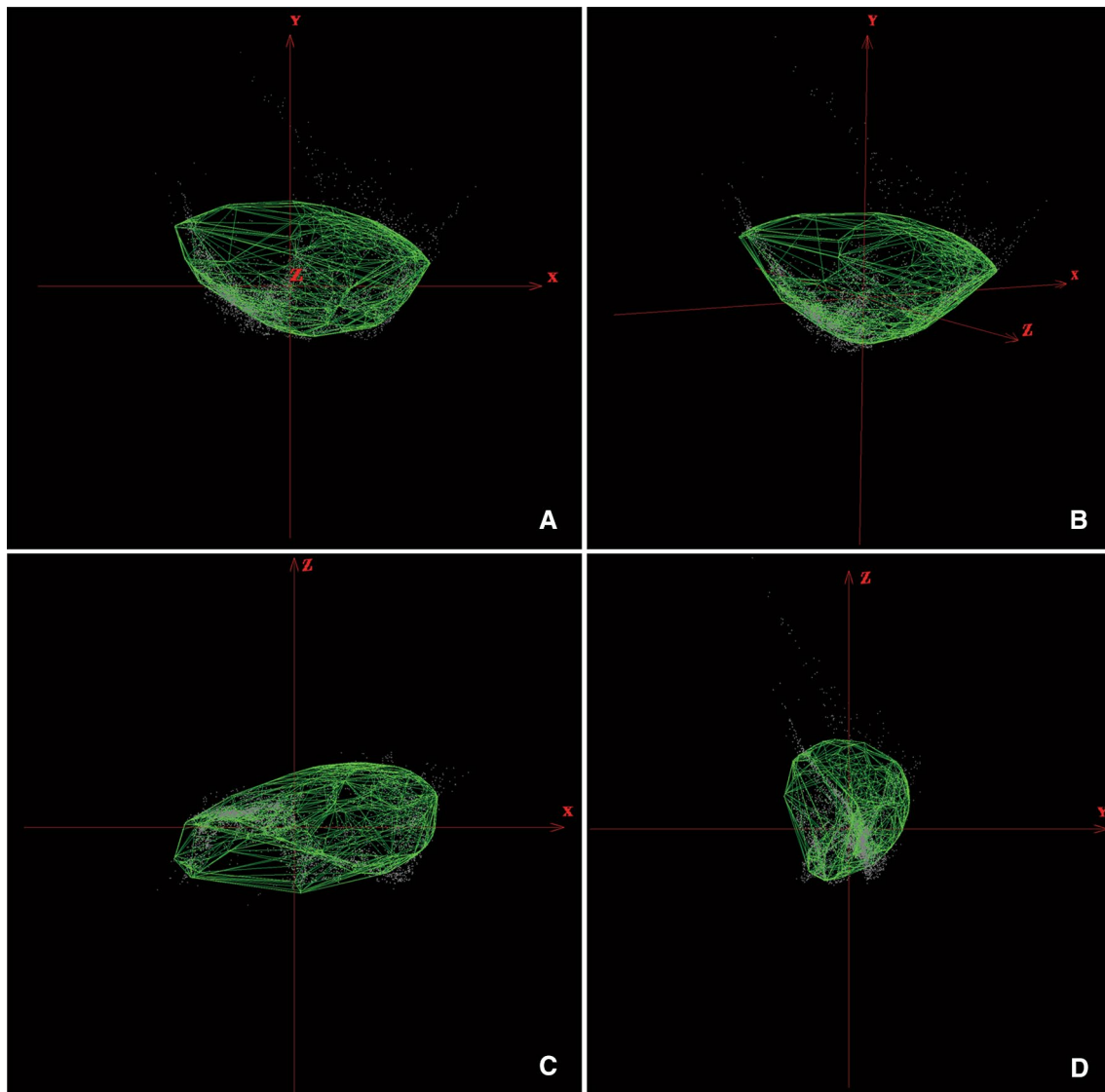


Fig. 5 Distribution of *Baccharis dracunculifolia* using a representation of three-dimensional environmental space using PC1 (proportion of variance 0.7392, X-axis), PC2 (proportion of variance 0.1677, Y-axis), and PC3 (proportion of variance 0.0691, Z-axis). (A) View of the niche based on PC1 and 2, (B) view of the niche based on PC 1, PC2, and PC3, (C) view of the niche based on PC 1 and 3, and (D) view of the niche based on PC2 and 3

Realized climatic space for *B. dracunculifolia* is denoted by a convex hull. The background cloud of points denotes all the possible climates in the calibration area (Qiao et al. 2016). Besides, the convex hull represents the environmental conditions in which *B. dracunculifolia* DC. can proliferate in a certain period (Qiao et al. 2017). However, the climate is dynamic, and currently, it is constantly changing due to the anthropogenic activities that produce greenhouse

gas emissions (Kaufmann et al. 2011; Zwiener et al. 2018). Formerly, new scenarios must be evaluated assuming different emission pathways to assess whether this species can proliferate under different climate conditions in future periods and other geographic regions (Gong et al. 2020). Additionally, other aspects related to biotic, abiotic, and accessibility conditions of a species to a given area should be considered. This last aspect is of great relevance in species

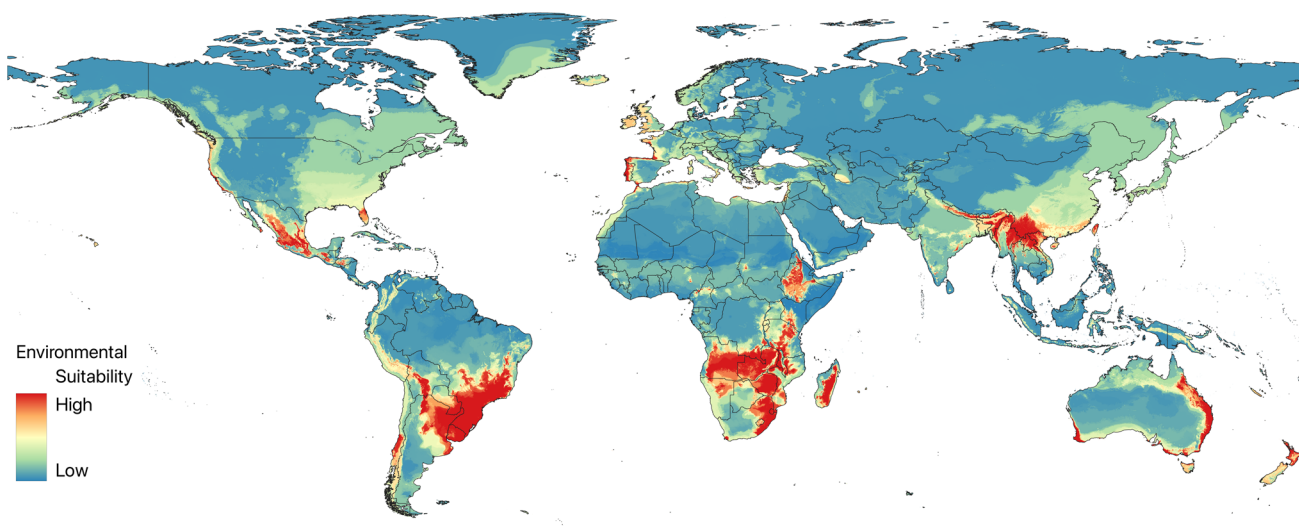


Fig. 6 Environmental suitability map in current pathway with a logistic projection of the final 4 SDM models meeting the selection criteria OR and AICc to the entire world, allowing extrapolation and clamping. Legend denotes environmental suitability, higher environmental suitability denoting a potential distribution for *B. dracunculifolia*

whose exploitation represents an economic benefit or trading products. This interest facilitates the introduction of species in areas in which species are not naturally distributed. That is the case with the increased demand for honey-derived products obtained from *B. dracunculifolia* (Lázaro-Lobo et al. 2021).

The environmental suitability of the current scenario for *B. dracunculifolia* in North America encompasses some of the most critical ports of the west coast of the USA, in states such as California, Oregon, and Washington. Thus, the results based on climate matching between the natural habitat of *B. dracunculifolia* and North America show us that much of the west coast and Florida have a high risk of invasion by this species. In addition, a half territory of the USA is a mid-risk of invasion, at least 29 states. Part of the central region of the USA, in areas of significant incidence of livestock activities, agriculture, and grasslands, also presents favorable conditions for establishing this species if it is introduced. Furthermore, there are large areas of high environmental suitability for *B. dracunculifolia* in Mexico. At least 20 states are at high risk. Also, there are broad areas at high risk in Guatemala, Dominican Republic, and Honduras. Mid-risk of invasion is also present in Cuba, Haiti, Jamaica,

and Puerto Rico. The fact that other species of *Baccharis* are present in these areas and are recognized as pests of agriculture indicates that *B. dracunculifolia* can become invasive in these regions since the realized niche tends to be retained over time (Peterson et al. 1999).

The rest of the North American continent presents a cold and drier climate that is unsuitable for establishing *B. Dracunculifolia*. Several studies have correlated climate correspondence to success in establishing some non-indigenous invasive species, indicating the importance of this approach in preventing and identifying invasions (e.g., Blackburn and Duncan 2001; Duncan et al. 2001; Forsyth et al. 2004). In addition, several plant species failed to settle in certain regions predicted as unsuitable for them (Grace 1987; Kornas 1990; Williamson and Fitter 1996; Pyšek 2003).

The transfer for future scenarios is a common practice in current studies that evaluate the invasiveness potential of species (Sequeira et al. 2018). Nonetheless, these transfers can lead to incorrect extrapolations (Elith et al. 2011). The mobility oriented parity (MOP) metric was conceived to lead with incorrect extrapolations by improving identifications of extrapolative areas (Owens et al. 2013). According to the extrapolation risk map, *B. dracunculifolia* could invade over

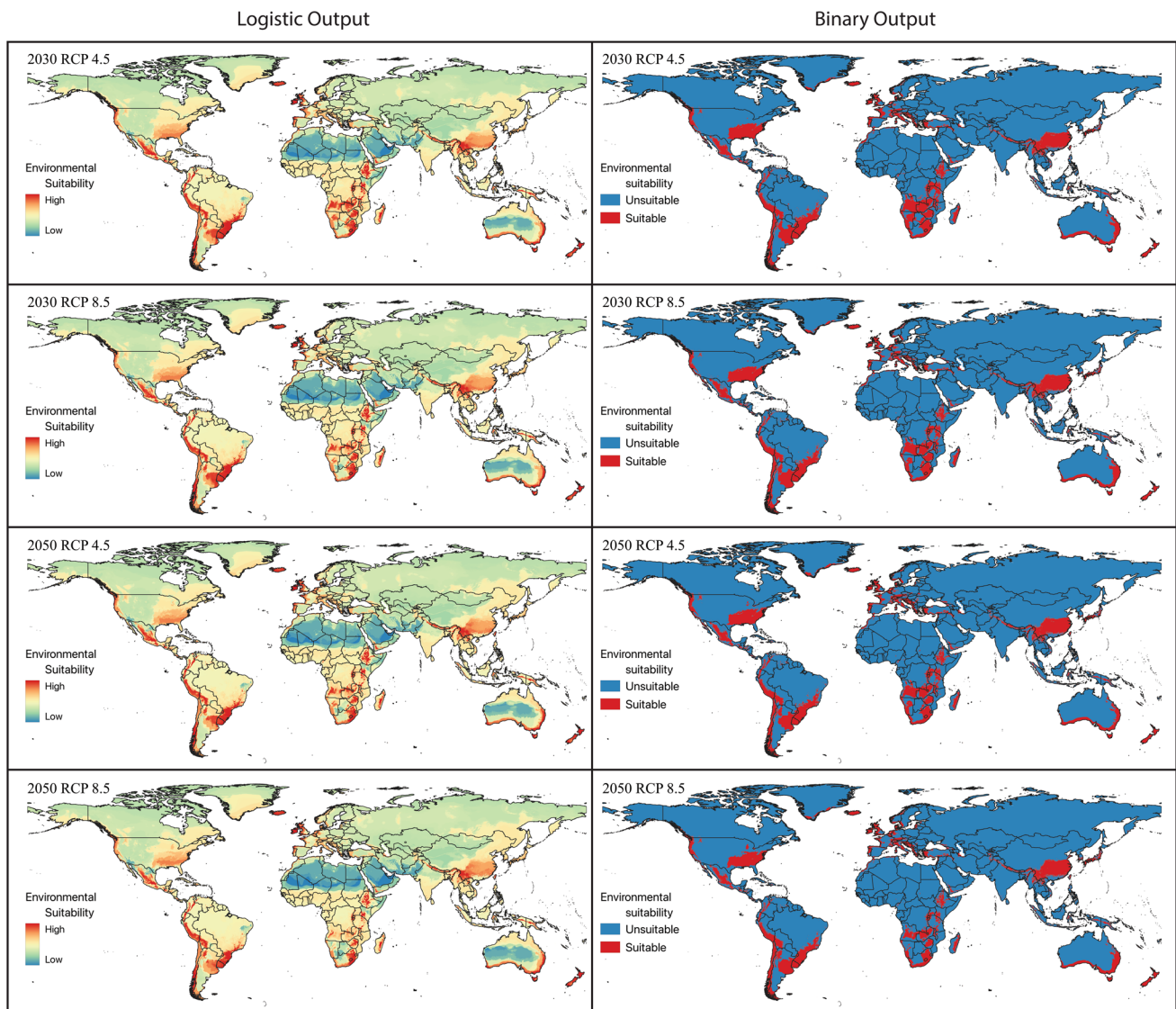
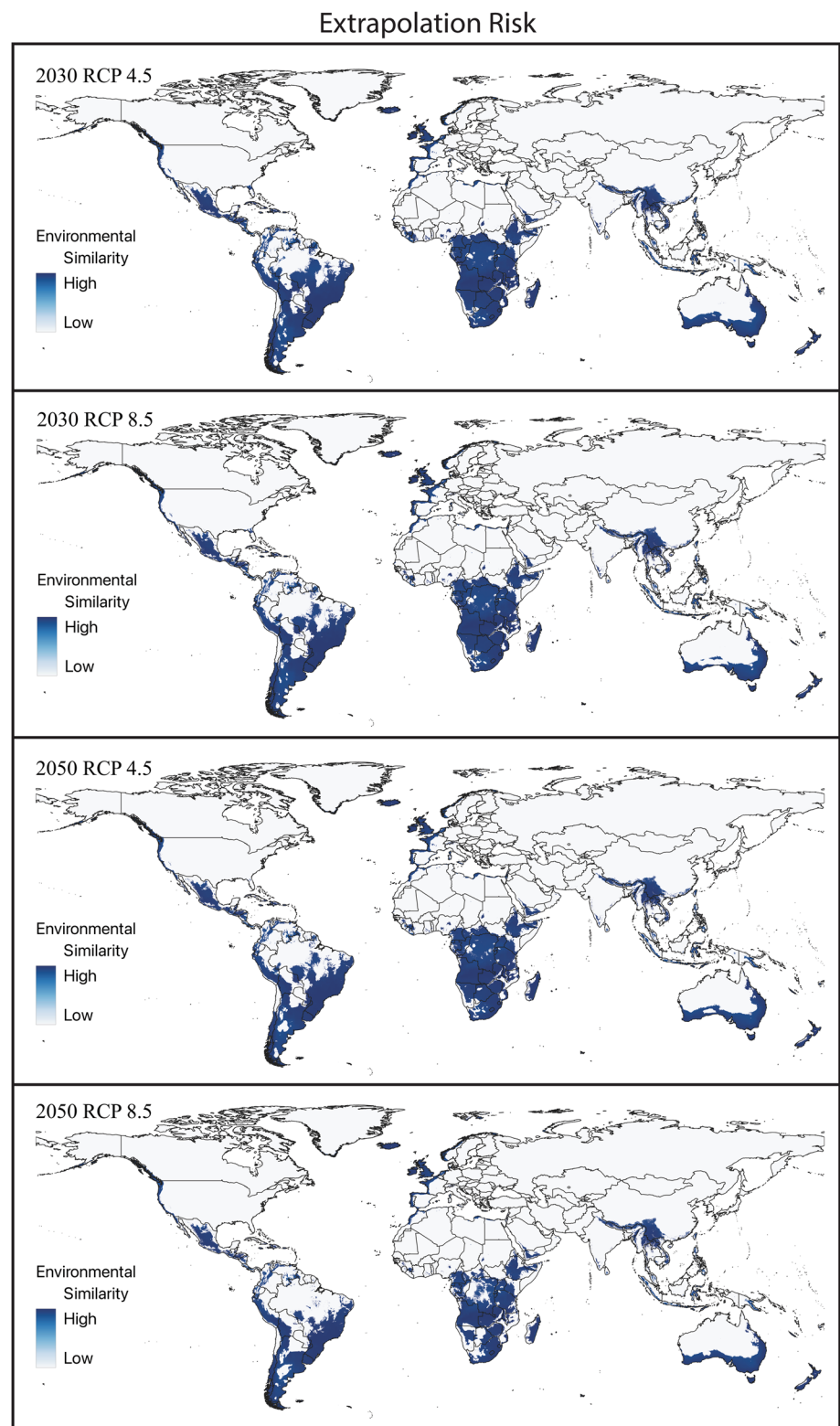


Fig. 7 Environmental suitability map in future projections based on logistic and binarized outputs of the final 4 SDM models meeting the selection criteria OR_AICc through the entire world using the ccs4 GCM and RCP 4.5 and RCP 8.5 pathways, allowing extrapolation and clamping

33 countries across North America, Africa, Europe, Asia, and Australia. The environmental similarity is present in broad areas around the world. The North American region is of particular interest due to an increased trade of honey-derived products between South America and the USA.

Otherwise, with increasing trade with China, a great potential exists for that country, particularly in its southern region. Figure 8 evaluates more robustly the extrapolation risk for *B. dracunculifolia* in future scenarios worldwide. As a result, a high invasiveness potential is present in the same regions

Fig. 8 Extrapolation risk map in future projections (MOP results) using the ccsm4 GCM and 4.5 and 8.5 pathways. Legend indicates environmental similarity where higher values indicate broad areas of strict extrapolation for *B. dracunculifolia*



displayed in Fig. 7. However, there is an evident increase of risk in the African continent and a slight risk decrease in North America (the USA) and the Asian continent. This extrapolation confirms that this species can proliferate over time. Nonetheless, it also shows a loss of environmental conditions in RCP 8.5, especially in the African continent, which suggests that an increase of greenhouse gas emissions negatively affects ideal conditions that allow *B. dracunculifolia* to proliferate.

The best way to combat an invasive species is prevention (Richardson and Thuiller 2007). Once established, eradicating an invasive species is extremely difficult or impossible (Koch et al. 2006). Thus, there must be efforts to predict the entry of an invading species in a given territory (Committee on the Scientific Basis for Predicting the Invasive Potential of Non-indigenous Plants and Plant Pests in the United States 2002). We propose that given the risk of invasion by *B. dracunculifolia* discussed earlier, projects of introduction of this species should be monitored.

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Author contributions GWF, NPUB, and UOP conceived and designed the study. UOP, NPUB, and GWF performed the modeling analyses. UOP, NPUB, and GWF analyzed the data and performed statistical analyses. UOP, NPUB, and GWF wrote the paper. All authors completed and approved the final manuscript.

Declarations

Conflict of interest The authors declare no competing interests.

Data and source code availability Occurrence data and source code for (1) cleaning and preparing occurrence data, (2) selecting and crop bioclimatic variables, and (3) calibrating models, extrapolation, and risk assessment are available in the following GitHub repository https://github.com/HpcDataLab/B.dracunculifolia_Invasion.

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