



Current and potential geographic distribution of red palm mite (*Raoiella indica* Hirst) in Brazil

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ABSTRACT

The red palm mite, *Raoiella indica* Hirst, is the most invasive pest, having spread quickly to several countries. In Brazil it is already present in several regions and has a high potential for dispersion to other regions, which could severely affect the cultivation of coconuts, bananas, native and exotic palm trees, and tropical flowers, such as those of the Heliconiaceae family. Thus, we aimed to determine the regions of Brazil most prone to the occurrence of *R. indica* using Maxent with updated data on its occurrence and a selection of bioclimatic variables that may influence its establishment. The occurrence data used were obtained through a literature search, online databases, and surveys carried out in the field. The model indicated a high potential for the establishment of *R. indica* in the following locations: a large part of the State of Roraima, the eastern part of the State of Amazonas, the northern and central-western parts of the State of Pará, and parts of the states of Acre and Amapá (North Region); the coast of Brazil from Rio Grande do Norte to the states of Paraíba, Pernambuco, Alagoas, Sergipe and Bahia (Northeast Region); the states of Rio de Janeiro and Espírito Santo, the far east of Minas Gerais, and almost the entire state of São Paulo, except the northern part (Southeast Region); most of the State of Mato Grosso do Sul and the most southern portion of the State of Mato Grosso (Midwest Region); and the northern part of the State of Paraná and small parts of the states of Santa Catarina and Rio Grande do Sul (South Region). The bioclimatic variables that most influenced the potential geographical distribution of *R. indica* were precipitation of driest month (Bio14), precipitation of wettest month (Bio13), mean diurnal range (Bio2), and isothermality (Bio3). The parameterization for the Maxent model provides an updated model to prevention invasion of *R. indica* due updated data on its occurrence used. Thus, potential geographic distribution of *R. indica* in Brazil should be consider from this study.

1. Introduction

The red palm mite, *Raoiella indica* Hirst (Tenuipalpidae) was introduced to the Americas 15 years ago (Flechtmann and Etienne, 2004). It spread quickly across the continent to several islands in the Caribbean (Etienne and Fletchmann, 2006; Kane et al., 2005), south Florida (Welbourn, 2006), Mexico (NAPPO, 2009), Venezuela (Vásquez et al., 2008), Colombia (Carrillo et al., 2011a) and northern Brazil (Navia et al., 2011; Rodrigues and Antony, 2011). *Raoiella indica* is a

phytophagous mite that can be found in the leaves of infested plants, which later become necrotic, leading to significant yield losses in economically important crops (up to 70%), such as coconuts in the Caribbean (Roda et al., 2012) and Mexico (Otero-Colina et al., 2016), and coconuts and bananas in Brazil (Gondim Jr. et al., 2012).

In the Americas, *R. indica* not only spread quickly, forming large populations, but also expanded its host range, attacking several species of exotic or native palm trees (Arecaceae) and plants from several families of monocotyledons, such as Cannaceae, Cycadaceae,

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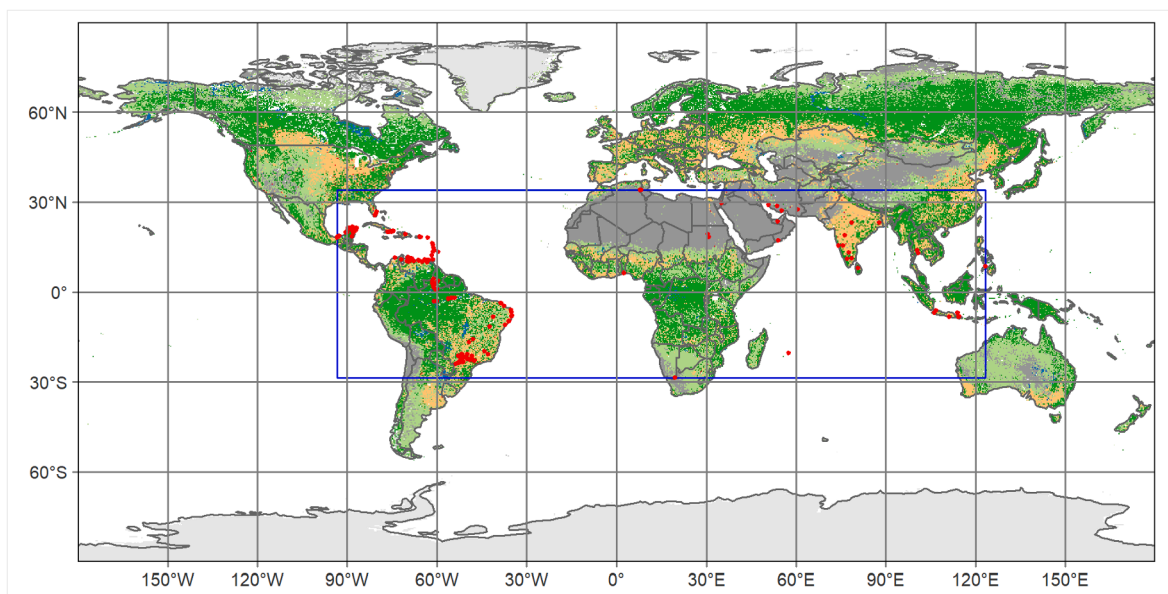


Fig. 1. Distribution of *Raoiella indica*: occurrence points (217, red dots) and study area (blue rectangle, rectangular bounding box buffer around the species extent of occurrence). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Heliconiaceae, Musaceae, Pandanaceae, Strelitziaceae, and Zingiberaceae (Carrillo et al., 2011a, Gondim Jr. et al., 2012, Navia et al., 2015, Gómez-Moya et al., 2018).

Brazil is the third largest fruit producer in the world, according to the Brazilian Association of Exporters of Fruit and Derivatives (Abrafrutas). In 2018, the production of coconut was 1,564,500 tons, and banana production was 6,752,171 tons of bunches, based on the Municipal Agricultural Production Survey (PAM) by the Brazilian Institute of Geography and Statistics (IBGE). According to data from the Foreign Trade Secretariat (Secex) compiled by Abrafrutas, exports grew 21% compared to the same period in 2018, to 429,700 tons, while revenue increased 15%, to US \$384.4 million. Banana exports increased by 57% in the first half of 2019 alone.

Brazilian banana production is distributed nationwide, with the Northeast region being the largest producer (34%), followed by the Southeast (32%), South (15%), North (14%) and Midwest (4%), according to IBGE production data. The leading producing states in Brazil are Bahia (16%), São Paulo (16%), Minas Gerais (11%), Santa Catarina (10%), and Pará (9%). In addition, banana cultivation plays an important social role in generating income for family farming, representing a strong component of agroforestry systems (SAFs) in the Brazilian Amazon (Amaro, 2010; Arco-verde, 2008; Calvi, 2009; da Freitas, 2008; de Sá et al., 2008; Gama, 2003) and other integrated production systems, as established under Embrapa's Productive Transition and Environmental Services Project.

World coconut production is concentrated in Asia (over 83%). Brazil is the fourth-largest producer, according to FAO data (<http://faostat3.fao.org>), with a volume of more than 2,8 million tons in 2013, approximately 2 million fruits. Of this, approximately 70% of the fruit were produced in the Northeast Region, according to IBGE, with the main coconut producing states being Bahia (29%), Sergipe (12%), Pará (11%), Ceará (11%), and Espírito Santo (9%). Studies indicate that 90% of the world's coconut production comes from small farms less than 5 ha. 70% of worldwide coconut cultivation in properties less than 10 is

often consumed internally (Siqueira et al., 2002).

The prediction of potentially suitable habitats for *R. indica* is important to support and assist in the planning and implementation of phytosanitary control policies. The development and reproduction of *R. indica* are related to climatic variables (Fidelis et al., 2019), and establishing the effects of climatic parameters, especially temperature, on its development and reproduction is extremely useful for defining prevention and control measures.

Species distribution modeling (SDM), in which predictive models of the geographical distribution of species are developed based on the environmental conditions where they occur, have applications in the planning of conservation policies, ecology, evolution studies, epidemiology, and invasive species management (Corsi et al., 1999; Peterson et al., 1999; Peterson and Shaw, 2003; Scott et al., 2002; Welk et al., 2002; Yom-Tov and Kadmon, 1998).

Most SDM applications consider that the ecological niche is the basic model that supports predictions about the occurrence of species (Elith et al., 2006; Peterson, 2001; Thuiller et al., 2005). The ecological niche is defined as the geographical space that presents the most suitable conditions and resources under which a species can survive, grow, and reproduce. Therefore, knowledge of these conditions and resources can be used to predict the locations of species occurrence.

Semi-mechanical modeling packages, such as CLIMEX, have been preferred for determining seasonal variations for different species, such as *R. indica* (da Silva et al., 2020). However, there is still a lack of research on the use of other methods, such as Maxent, for *R. indica* using local data of its occurrence in Brazil. The maximum entropy algorithm (Maxent) allows the use of only presence data and categorical predictors and has been widely used (Phillips et al., 2006). Elith et al. (2006), Ashraf et al. (2017), and Ray et al. (2018) demonstrated that Maxent performed better than other established methods, such as BIOCLIM, GARP, GAM, and GLM. Barry and Elith (2006) observed that Maxent, GLM, and GAM were similar in their ability to adjust non-linear response surfaces that are often seen in biological data. Hernandez et al. (2006)

Table 1

Bioclimatic variables (WordClim, version 2) used for modeling the species distribution of *Raoiella indica* in Brazil.

Codes	Description	VIF	Contribution %	Permutation importance
Bio01	Annual mean temperature			
Bio02	Mean diurnal range	21,538	35,1200	17,0300
Bio03	Isothermality ^a	23,521	19,7300	13,3900
Bio04	Temperature seasonality ^b			
Bio05	Max temperature of warmest month			
Bio06	Min Temperature of Coldest month			
Bio07	Temperature Annual range ^c			
Bio08	Mean Temperature of Wettest quarter	15,192	31,990	12,830
Bio09	Mean Temperature of Driest quarter	28,736	11,390	16,580
Bio10	Mean Temperature of Warmest quarter			
Bio11	Mean Temperature of Coldest quarter			
Bio12	Annual precipitation			
Bio13	Precipitation of Wettest month	24,553	36,470	15,8300
Bio14	Precipitation of Driest month	44,670	24,2500	41,7900
Bio15	Precipitation seasonality ^d	29,906	12,4800	60,670
Bio16	Precipitation of Wettest quarter			
Bio17	Precipitation of Driest quarter			
Bio18	Precipitation of Warmest quarter	35,631	0,3625	26,940
Bio19	Precipitation of Coldest quarter	37,792	0,0734	0,2616

The variable with codes in bold were used to model. The ones with permutation importance in bold were bioclimatic variables that most influenced the potential geographical distribution of *R. indica*, as stated in results.

^a (Bio2 / Bio7) × 100.

^b Standard deviation × 100.

^c (Bio5–Bio6).

^d Coefficient of variation.

tested four modeling methods and demonstrated that Maxent obtained the most robust results, performing well and maintaining the accuracy of its estimates across all categories and sample sizes, with maximum levels for smaller sample sizes.

MaxEnt have been used in a thousand of investigation of the effects of climate on the potential distribution of the pest species to prevent their invasion and spreading on climate suitable agriculture areas in current time or climate change predictions. A few notable studies have been performed to predict potential distributions of important pests using MaxEnt, such as, *B. tabaci*, *Dalbulus maidis*, *Tuta absoluta*, *Euplatypus parallelus*, *Batocera lineolata*, *Planococcus ficus*, *Diaphorina citri*, *Lobesia botrana*, *Stenotarsonemus spinki*, *Schistocerca gregaria* and 58 species in an alpine ecosystem (Ji et al., 2020; Kimathi et al., 2020; Li et al., 2020; Negrini et al., 2020; Ramos et al., 2018; Rank et al., 2020; Santana Jr et al., 2019; Santana et al., 2019; Tang et al., 2019; Li et al., 2021; Li et al., 2020).

Therefore, we aimed to determine the regions of Brazil most prone to the occurrence of *R. indica* using Maxent with updated data on its occurrence and the bioclimatic variables that may further influence its establishment.

2. Material and methods

2.1. Occurrence data for *R. indica*

Occurrence data for *R. indica* were obtained from databases (CABI/EPPO, 2019), literature (Adepará, 2016; Arbabi et al., 2002; CABI, 2019; Carrillo et al., 2011b; CAPS/FFD, 2008; Carrillo et al., 2011a; Benito et al., 2009; de Santana et al., 2010; Dowling et al., 2012; Estrada-Venegas et al., 2010; Etienne and Fletchmann, 2006; EPPO, 2019; Gómez-Moya et al., 2018; Flechtmann and Etienne, 2004; Giliomee and Ueckermann, 2016; Hirst, 1924; Hountondji et al., 2010; IPCC, 2010; Kamali et al., 2001; Kane et al., 2005; Melo et al., 2018; Mendes et al., 2015; Moraes et al., 2017; Moutia, 1958; NAPPO, 2009; Navia et al., 2011; Nusantara et al., 2017; Oliveira et al., 2016; Rodrigues et al., 2007; Rodrigues and Antony, 2011; Silva et al., 2016; Souza et al., 2016; IPCC, 2010; Kamali et al., 2001; Kane et al., 2005; Kohavi, 1995; Moraes et al., 2017; Morales et al., 2017; NAPPO, 2009; Welbourn, 2006; Zouba and Raeesi, 2010; Vásquez and de Moraes, 2013; Welbourn, 2006; Zannou et al., 2010; Zouba and Raeesi, 2010) and field sample data from the states of Roraima and Amazonas. A total of 220 occurrence points were obtained. We performed spatial filtering of the data using the R software package spThin (Aiello-Lammens et al., 2015) to minimize spatial autocorrelation. Spatial autocorrelation is the degree of spatial association present in the datasets, and it may prevent the separation of the points used for testing. The treatment of these data is necessary to avoid points outside the boundaries of the region and points with unreal values. A total of 217 points were used for the development of the model (Fig. 1). The study area was determined based on the geographical extent of the records: a rectangular bounding box buffer around the species extent of occurrence, as in El-Gabbas and Dormann (2018) and Hijmans and Elith (2017), should contain only locations where the species is equally likely to reach (Saupe et al., 2012).

2.2. Environmental data layers

Bioclimatic variables (Nix, 1986) are the most ecologically sensitive to demarcate physiological tolerances of habitats (Hijmans et al., 2005; Thompson et al., 2009) and are used for SDM. Data from 19 bioclimatic variables, considered potential predictors of the distribution of the ecological niche of *R. indica*, were selected (Table 1). The data were downloaded as layers of matrix data (raster) from the WorldClim database, version 2, which contains annual averages from 1970 to 2000 (Fick and Hijmans, 2017), represented in a generic grid of 5 arcmin.

The variables with Pearson's correction coefficient ($r > |0.80|$) (significant at alpha level = 0.05) were grouped according to hierarchical cluster analysis (Fig. 2). The values of the variables were then tested for collinearity using the variance inflation factor (VIF), which points out how much of the variance of a regression coefficient estimated by one variable is inflated due to the collinearity with all the others (Naimi and Araújo, 2016). The procedures for selecting the variables were performed using the functions vif.corr and vif.step from the usdm package (Naimi et al., 2014) in the R environment (R Core Team, 2019). Although collinearity decreases efficiency and increases uncertainty in species distribution models, the difference in performance between collinear and non-collinear environmental datasets is low for methods such as Maxent, which may support the claim that during the adjustment process this type of model benefits from collinearity (De Marco Júnior and Nóbrega, 2018). Variables with VIF > 10 (Naimi et al., 2014) were excluded after evaluating their probable biological significance (Fitzpatrick et al., 2013) based on Fidelis et al. (2019). The use of all environmental variables was criticized based on the effects of collinearity during the construction of the species distribution model. However, according to De Marco Júnior and Nóbrega (2018), this is not a problem for modeling algorithms such as Maxent and SVM, which take advantage of collinearity for parameter estimation. Thus, the following bioclimatic variables were used in the models (codes highlighted in

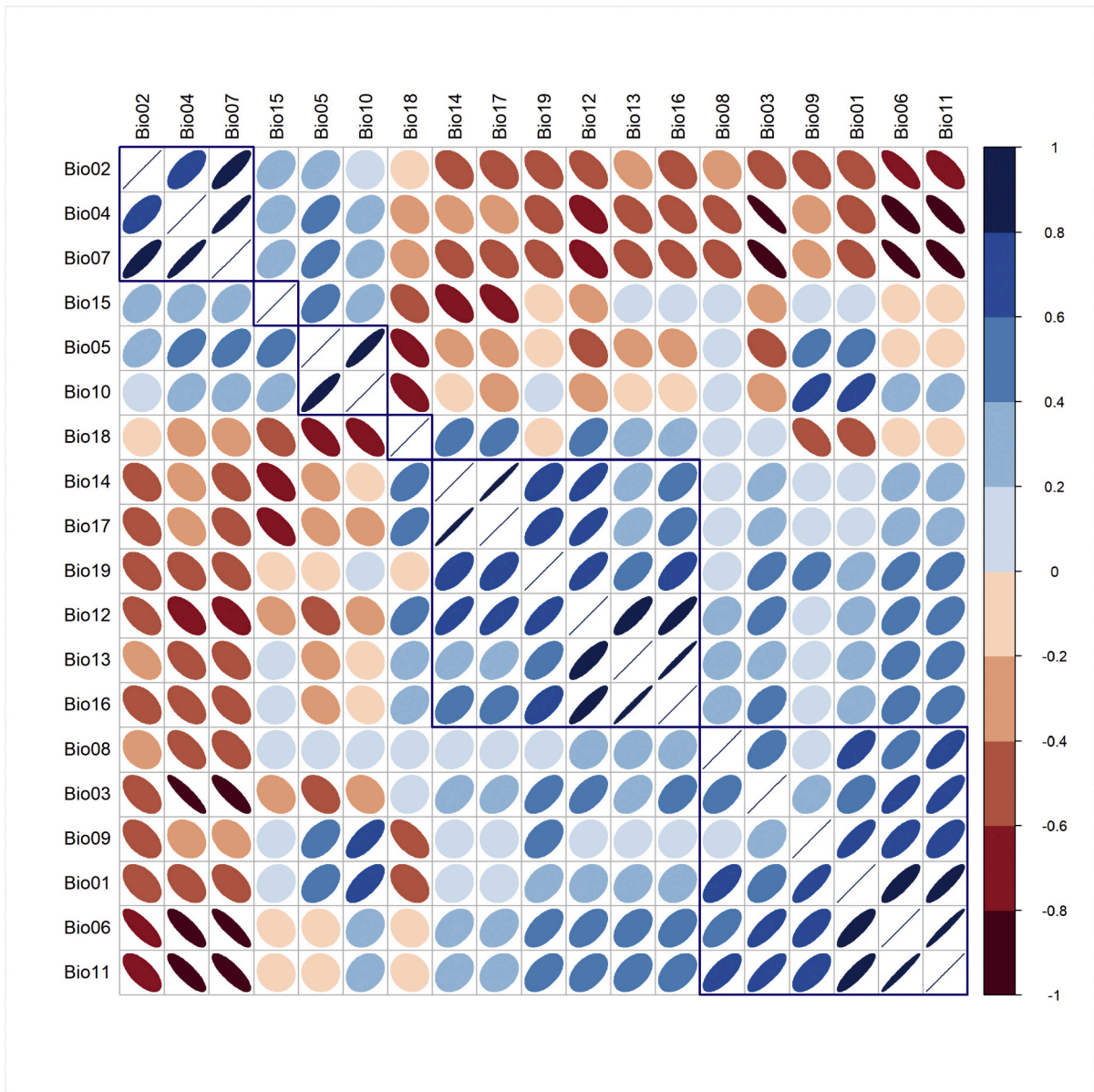


Fig. 2. Correlation between bioclimatic variables. Blue colour with right slope indicates positive correlation, while red colour with left slope indicates negative correlation. The intensity of Pearson's correlation coefficient (r) increases from the circle ($r = 0$) to the ellipse ($r =$ intermediate) to the line ($r = 1$). Correlated variables, $r > 0.80$, were grouped with hierarchical cluster analysis. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Table 1 in bold bold): average variation of daytime temperature (Bio02), isothermality (Bio03), average temperature of the wettest quarter (Bio08), average temperature of the driest quarter (Bio09), precipitation of the wettest month (Bio13), precipitation of the driest month (Bio14), seasonality of precipitation (Bio15), precipitation of the coldest quarter (Bio18), and the warmest quarter (Bio19).

2.3. Model development and validation

Maxent (Maximum Entropy, version 3.4.1, Phillips et al., 2004; Phillips et al., 2006; Phillips et al., 2017; Phillips and Dudík, 2008) was used, executed from the sdm package (Naimi and Araújo, 2016). Maxent was chosen for the nature of the data (points of presence only) and its performance compared with other models. The principle of maximum

entropy proposed by Jaynes (1957) is the fundamental idea behind the Maxent algorithm. The model uses the principle of maximum entropy in presence data to estimate a set of functions that relate to the environmental variables (covariates or predictors) of the habitat in order to approximate the potential geographic distribution of the species (Phillips et al., 2006). The Maxent software implements features, which are an expanded set of transformations of the original predictor covariates, of five classes: linear (L), quadratic (Q), product (P), threshold (T), and hinge (H, similar to threshold but with the inclusion of a linear function). These functionalities restrict the means, variances, and covariance of the variables to correspond to their experimental values (Phillips et al., 2006). Each of these types allows a different possible shape of the response curves and has different implications for the constraints. To obtain a solution, Maxent maximizes the gain function, a maximum

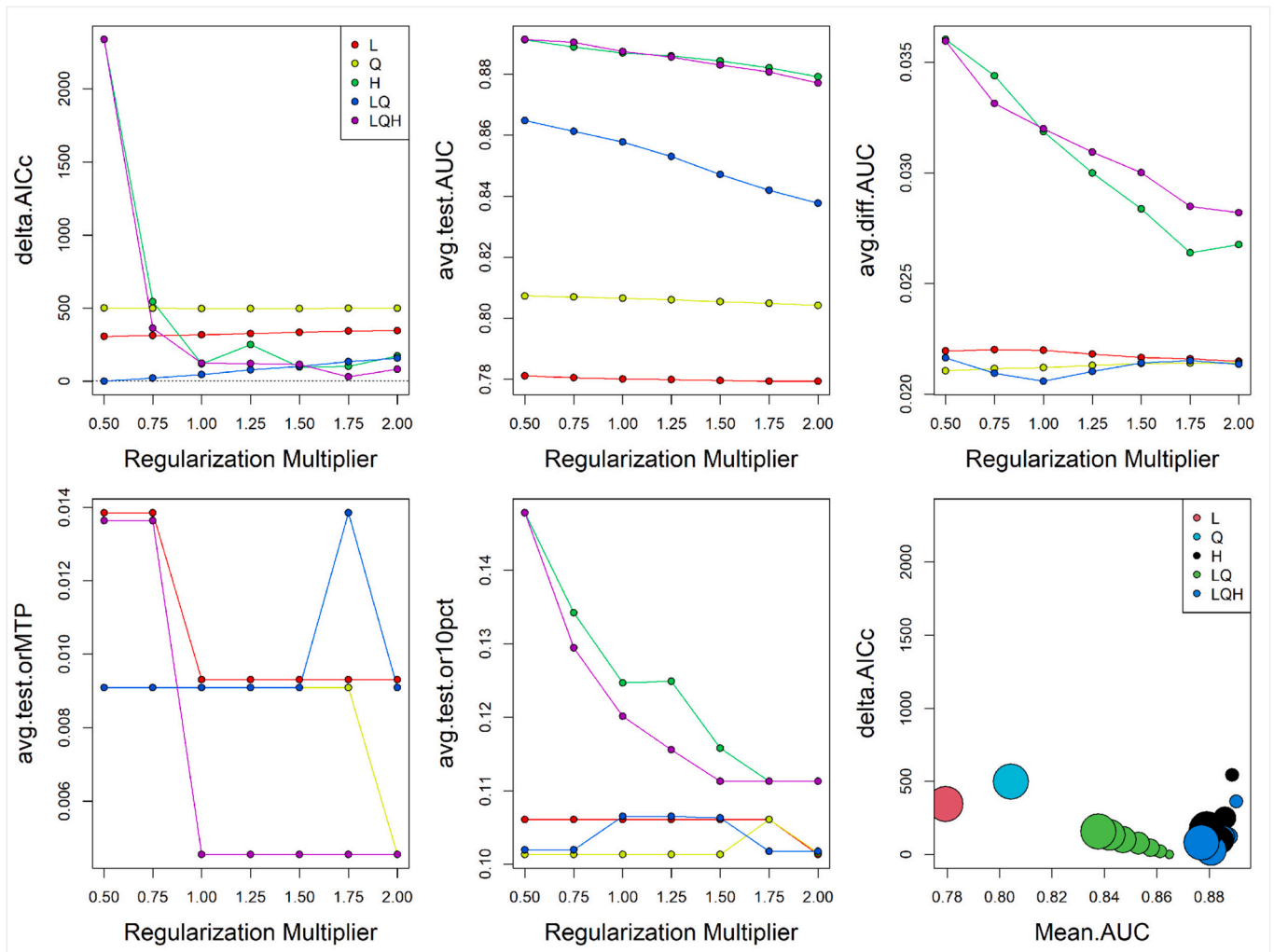


Fig. 3. Metrics for selection of the feature sets and regularization multiplier value for the final model.

likelihood function that has a penalty term to reduce the model's over-parameterization (Merow et al., 2013; Phillips et al., 2006). Regularization coefficients can be adjusted by multiplying by a user-defined constant, the regularization multiplier (RM), to produce more or less complicated models (Elith et al., 2011). As models based only on points of occurrence can be highly susceptible to sample bias (Pearce and Boyce, 2006), background points are used. The Maxent algorithm compares the locations of where a species has been found to all the environments that are available in the study area. It defines these available environments by sampling a large number of points throughout this area, which are referred to as background points. Because background points can include locations where the species is known to occur, background points are not the same as pseudo-absence points in the sense that they define the available environment. In this way, 10,000 (Maxent standard) random points were generated within the species extent area of occurrence (red rectangle in Fig. 1), according to Phillips (2008), using the random points function of the dismo package (Hijmans et al., 2015) in R. Although Maxent's current default settings are based on an extensive study of empirical tuning (Phillips and Dudík, 2008), recent work has shown that its use may result in models with poor performance (Radosavljevic and Anderson, 2014; Shcheglovitova and Anderson, 2013). In addition, artificial spatial autocorrelation between training and test data partitions (for example, due to sampling bias) can increase the metrics used to assess model

performance (Radosavljevic and Anderson, 2014; Veloz, 2009; Wenger and Olden, 2012). The selection of the best settings for the regularization multiplier and which features to use, which determines the complexity of the model, requires quantitative assessment (Phillips, 2008). It is essential to analyze combinations of parameters to select the best model (Morales et al., 2017); therefore, the ideal parameters of the model were adjusted using the ENMevaluate function of the ENMeval package (Muscarella et al., 2014) in R, and the following combinations of features were evaluated: L, Q, H, LQ, LQH, LQHP, and LQHPT. The regularization multipliers ranged from 0.50 to 2.00 in increments of 0.25 (half and double of Maxent's default = 1.00). To partition the data set into 10 groups for training and testing the model, the K-fold method (Burman, 1989) of cross-validation was used according to Fielding and Bell (1997) and Peterson et al. (2011). This method is suitable for studies that involve transferring models in space or time, including the possibility of finding non-analogous conditions (for example, native regions versus invaded regions, effects of climate change; Wenger and Olden, 2012). Groups of 5, 10, or 20 are recommended to be statistically stable, and the choice of group size is determined by the size of the study population (Kohavi, 1995; Salzberg, 1997). Thus, considering the total set of features ($s = 7 + 7 = 14$ parameters) — including the regularization multipliers — and the data partitioning ($k = 10$), $s(k + 1)$, according to Muscarella et al. (2014), resulting in 154 models to be compared in order to determine the best model to be calibrated. The

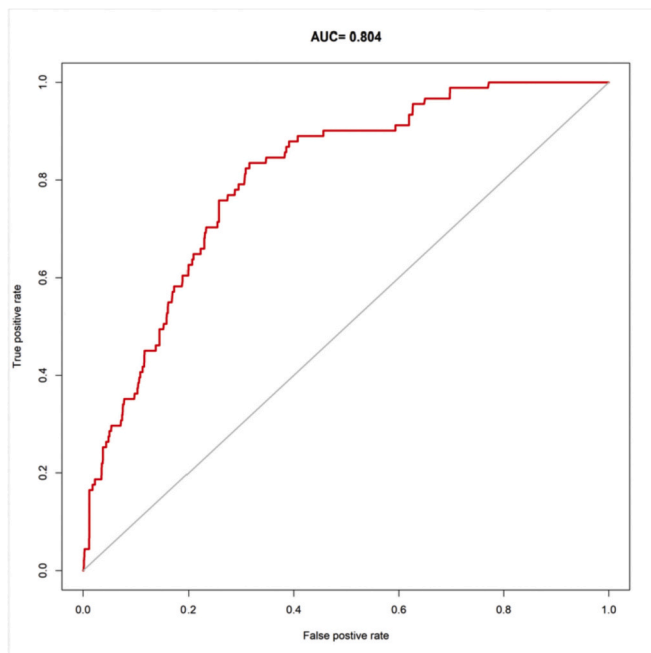


Fig. 4. Receiver Operating Characteristic (ROC) graph for the potential geographical model for *Raioidella indica* in Brazil.

various models generated were classified using the corrected Akaike Information Criterion (AICc) (Hurvich and Tsai, 2008), the best being the one with the lowest AICc value, as suggested by Morales et al. (2017). Although the model selection was made based on the AICc, there is currently no consensus on the most appropriate metric or approach to assess the performance of SDMs (Fielding and Bell, 1997; Lobo et al., 2008; Peterson et al., 2011; Warren and Seifert, 2011). Therefore, other evaluation indicators were also determined. The True Skill Statistic (TSS) was introduced by Allouche et al. (2006) as an alternative to Kappa (Cohen, 1960; Shao and Halpin, 1995), seeking to correct the latter's prevalence problems. In the authors' own words, "TSS is a special case of Kappa, maintaining all the benefits of this metric and mitigating the prevalence problem". There are some minor criticisms of the TSS, but the problems appear to be extreme cases, not systematic (Leroy et al., 2018). The AICc is a comparison of the model's complexity and adjustment. It is a variation of the complete AIC metric, with adjustments to the formula to take into account small sample sizes (Burnham and Anderson, 1998, 2002). Under the statistical principle of parsimony, the AICc seeks to find a balance between too little and too much complexity in the model, while considering the general adjustment of the model. Models with lower AICc scores are desirable as they indicate less complexity and a better fit. In addition to these more traditional metrics, the results presented by the ENMeval package include additional metrics used to evaluate SDMs. The *avg.test.orMTP* (Minimum Training Presence Omission Rate), *avg.test.or10pct* (10% Training Omission Rate), and *var.diff.AUC*, which is the difference between the AUC of the training data and that of the test data, indicate potential over-adjustment. The *avg.test.orMTP* and *avg.test.or10pct* metrics are measures based on thresholds, suggested by Radosavljevic and Anderson (2014), with the *avg.test.orMTP* indicating the proportion of species presence sites in the test data that are below the lowest training sites.

Likewise, *avg.test.or10pct* sets the test limit at the level of 10% of the training data. The *var.diff.AUC* measure is simply the difference between the AUC of the training data and the AUC of the test data (Warren and Seifert, 2011). High values indicate that the model is over-adjusted.

3. Results and discussion

The resulting metrics of the different combinations of feature classes (FC) with different regularization multipliers (RMs) are shown in Fig. 3. Based on the AICc, the best combination was obtained using linear and quadratic features (LQ), with a regularization multiplier of 0.5. The metrics (ENMeval) of evaluation for the test data with this model were: $\Delta AICc = 0$, $AICc = 5490$, $train.AUC = 0.8722$, $avg.test.AUC = 0.8648$, $avg.diff.AUC = 0.02163$, $avg.test.orMTP = 0.009091$, $avg.test.or10pct = 0.1019$, and $TSS = 0.3077$.

The ROC curve of the final model (Fig. 4), the result of evaluating true positive predictions (sensitivity) and false-positive predictions (1 - specificity), demonstrated high predictive capacity. A good model is defined by a curve that maximizes sensitivity for low values of the false-positive fraction. The significance of this curve is quantified by the area under curve (AUC) and has values that typically range from 0.5 (no better than random) and 1.0 (perfect fit). Values less than 0.5 indicate that the model fit is worse than random (Baldwin, 2009; Engler et al., 2004; Fielding and Bell, 1997; Hernandez et al., 2006).

The AUC values obtained indicate that the model can discriminate between the conditions at the retained occurrence sites (for testing) and those at the background locations (ranking the first higher than the second, based on their predicted suitability values). The low *avg.diff.AUC* value obtained indicates that the model does not suffer from overfitting problems (Warren and Seifert, 2011), which was also confirmed by the *avg.test.orMTP* and *avg.test.or10pct* values (Pearson et al., 2007).

The bioclimatic variables that most influenced the potential geographical distribution of *R. indica*, according to permutation importance, were precipitation of driest month (Bio14), precipitation of wettest month (Bio13), mean diurnal range (Bio2), and isothermality (Bio3), which can be seen in Table 1. This fact is observed in the field where the amplitude of climatic factors influences occurrences of *R. indica* population. In Brazil, lowest population is observed with the high intensity of precipitation (da Silva et al., 2020; Fidelis et al., 2019). Precipitation is one factor that can cause mortality of *R. indica* by removing adults, eggs, and nymphs from plants.

The response curves (marginal effect of changing values) for all bioclimatic variables used are shown in Fig. 5. This figure presents the response curves illustrating the relationship between the Maxent predicted probability of occurrence and the environmental variables. The values shown on the y-axis are the predicted probability of suitable conditions, as given by the logistic output format, with only the predictor variables used to develop the Maxent model.

According to the response curves, the following trends in predicted suitability were observed: it remains stable at 0.8 with an average daytime temperature variation (Bio2) of -5 to 5 °C, then decreases; reaches its peak when the isothermality (Bio3) is around 70; increases, with the average temperature of the wettest quarter (Bio08) around 15 °C to 40 °C and then remains stable; it increases until the average temperature of the driest quarter (Bio09) is around 40 °C; decreases rapidly from small increases in precipitation in the wettest month (Bio13); it presents a peak with precipitation of the driest month (Bio14) close to 80 mm; it reaches its peak when the seasonality of precipitation (Bio15) is around 80 mm and the precipitation in the coldest quarter (Bio18) is around 1200 mm; and increases linearly with the

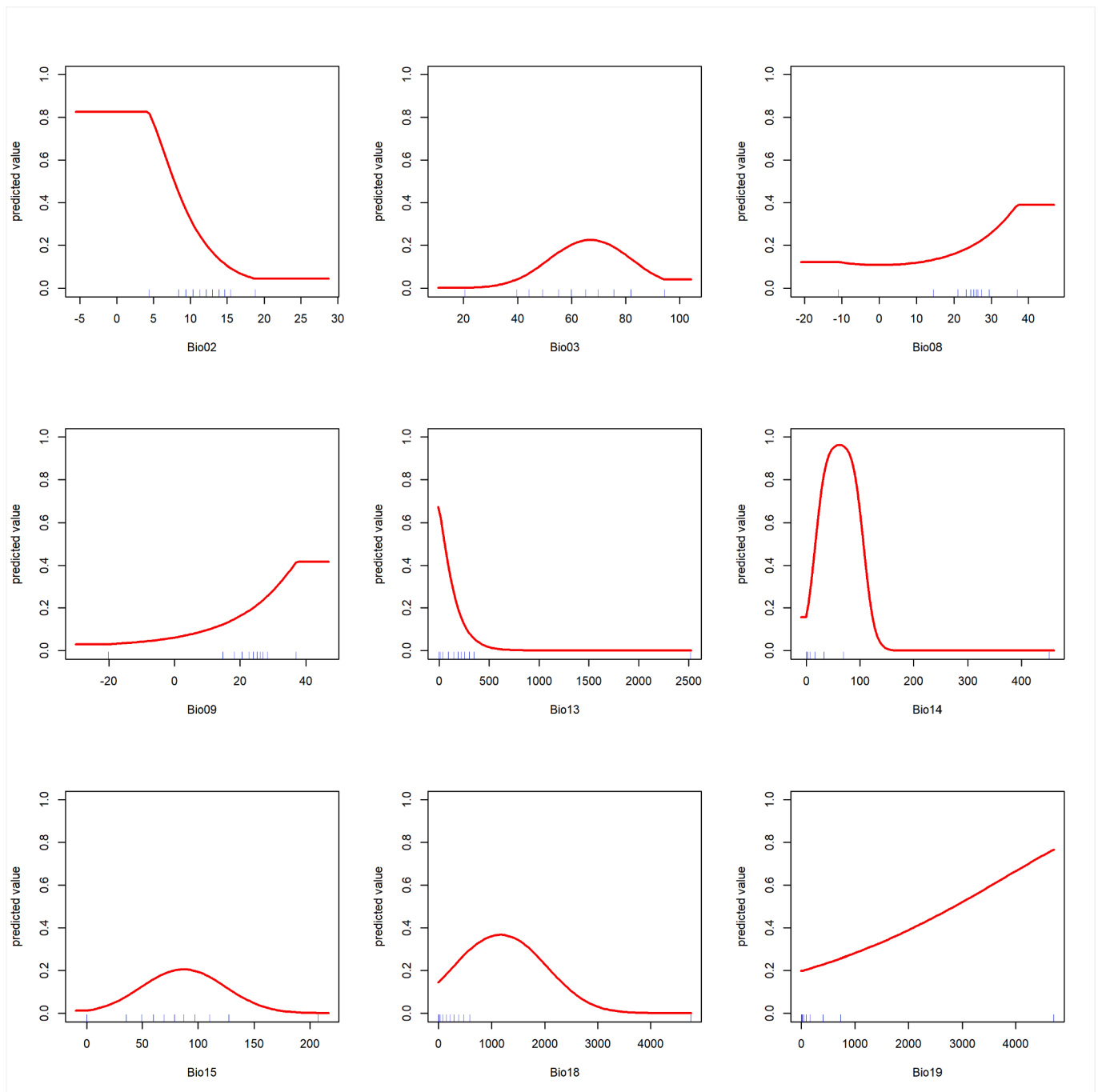


Fig. 5. Response curves for nine bioclimatic variables used as predictors in SDM for *Raiella indica* in Brazil.

precipitation of the warmest quarter (Bio19).

The potential distribution of *R. indica* in Brazil, resulting from the adjustment of the occurrence points to the environmental variables using the parameterized Maxent as described, is shown in Fig. 6. The areas with appropriate habitat exceeded the areas of reported occurrence. Similar results were obtained by Amaro and de Moraes (2013) with fewer points of presence and a different parameterization for the Maxent model. Here using updated data on its occurrence, the model results are better than last one, once location of the samples is important as incomplete sampling affects interpolation and extrapolation (Jarnevich et al., 2015). This model results provide a useful tool to prevention

invasion of *R. indica* in areas where now shows increase of suitability for *R. indica* due updated data on its occurrence used. Thus, potential geographic distribution of *R. indica* in Brazil should be consider from this study.

The full life cycle of *R. indica* depends on temperatures between 20 and 30 °C (Fidelis et al., 2019), which has also been proven in population dynamics studies (Taylor et al., 2012). Our model corroborates this, showing that the regions most suitable for the establishment of this mite had higher temperatures and lower variations in climate. Also, the bioclimatic variables that most influenced the potential geographical distribution of *R. indica* were precipitation of driest month (Bio14),

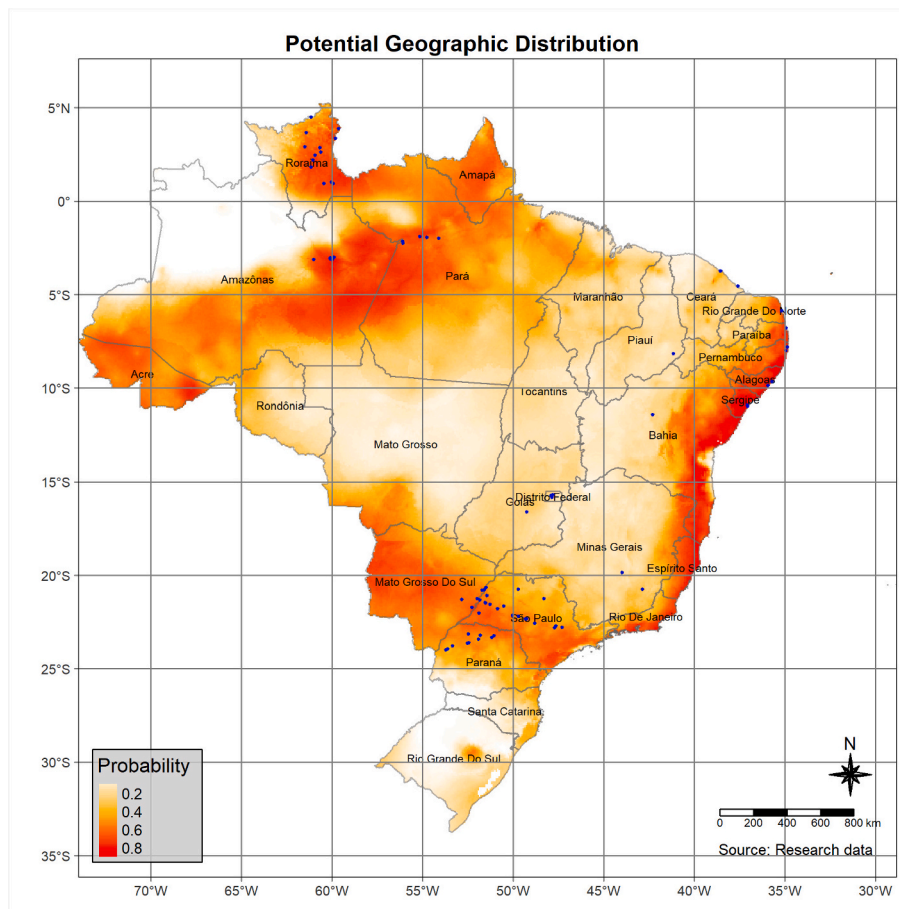


Fig. 6. Potential geographic distribution of *Raiella indica* in Brazil, according to the adjusted Maxent model (probability of occurrence from 0 to 1: warmer colors represent areas with better environmental conditions), based on the occurrence records (blue dots). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

precipitation of wettest month (Bio13), mean diurnal range (Bio2), and isothermality (Bio3). This fact is observed in the field where the amplitude of climatic factors influences occurrences of *R. indica* population. In Brazil, lowest population is observed with the high intensity of precipitation (da Silva et al., 2020). Precipitation is one factor that can cause mortality of *R. indica* by removing adults, eggs and nymphs from plants.

The model prediction shows a high probability of suitable conditions for *R. indica* in the following locations: a large part of the State of Roraima, the eastern part of the State of Amazonas, the northern and central-western part of the State of Pará, and parts of the states of Acre and Amapá (North Region); the coast of Brazil from Rio Grande do Norte to the states of Paraíba, Pernambuco, Alagoas, Sergipe and Bahia (Northeast Region); the states of Rio de Janeiro and Espírito Santo, the far east of Minas Gerais, and almost the entire state of São Paulo, except the northern part (Southeast Region); most of the State of Mato Grosso do Sul and the most southern portion of the State of Mato Grosso (Midwest Region); and the northern part of the State of Paraná and small parts of the states of Santa Catarina and Rio Grande do Sul (South Region).

Predictions of the model, considering a threshold that maximizes the sum of sensitivity and specificity (Liu et al., 2005; Liu et al., 2015), are shown in Fig. 7, indicating the areas with the highest potential for establishment (or invasion). These areas are relevant for the production

of bananas, coconuts, and other economically important palm species, such as açai, buriti, and pupunha, which may be economically impacted if invaded by *R. indica*.

4. Conclusions

This work presents a model for the potential distribution of *R. indica* in Brazil. The maximum entropy algorithm in the R environment was used to create the model, representing an approximation of the potential ecological distribution of *R. indica* based on its niche. The bioclimatic variables that most influenced the potential geographical distribution of *R. indica*, according to permutation importance, were precipitation of driest month (Bio14), precipitation of wettest month (Bio13), mean diurnal range (Bio2), and isothermality (Bio3).

The projected model indicates a high potential for the establishment of *R. indica* in the following locations: a large part of the State of Roraima, the eastern part of the State of Amazonas, the northern and central-western part of the State of Pará, and parts of the states of Acre and Amapá (North Region); the coast of Brazil from Rio Grande do Norte to the states of Paraíba, Pernambuco, Alagoas, Sergipe and Bahia (Northeast Region); the states of Rio de Janeiro and Espírito Santo, the far east of Minas Gerais, and almost the entire state of São Paulo, except the northern part (Southeast Region); most of the State of Mato Grosso do Sul and the most southern portion of the State of Mato Grosso

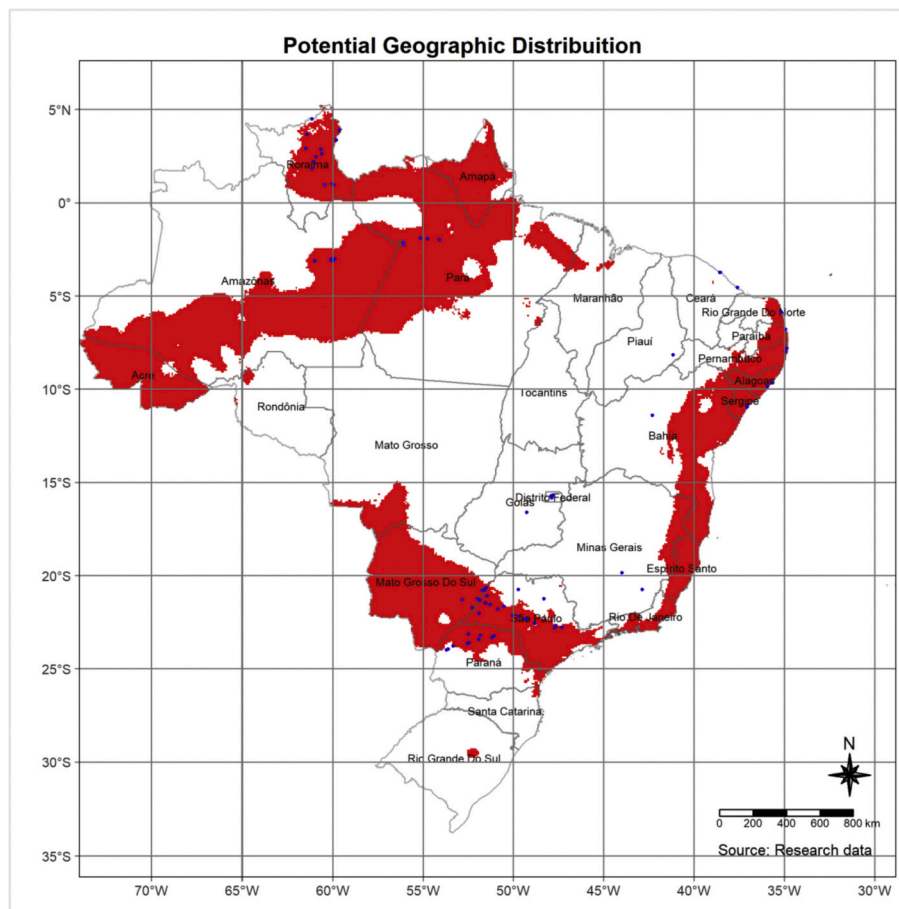


Fig. 7. Potential geographic distribution of *Raoiella indica* in Brazil, considering a threshold that maximizes the sum of sensitivity and specificity (0.444), in red, together with the occurrence records (blue dots). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

(Midwest Region); and the northern part of the State of Paraná and small parts of the states of Santa Catarina and Rio Grande do Sul (South Region).

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Declaration of Competing Interest

None.

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