Original article

How climate change will change the potential distribution of two wood-decaying fungi?

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ABSTRACT

Changes in climate, which can be understood as fluctuations in climate patterns as a reflection of natural or anthropic interventions, can generate changes in the environment and consequently affect the diversity of organisms. Fungi are extremely important in organic matter cycling in different environments, mainly forest areas, decomposing dead wood. To better understand the effects of climate change on two wood-degrading Agaricomycetes, their potential neotropical distribution was modeled using known occurrence data, available in the GBIF database and in specific literature, and associated with predictor variables extracted from Worldclim. A modeling package in R environment was used to analyze the present and future suitability for the optimistic and pessimistic scenarios. The results indicate the climate as an important factor in the distribution of *Auricularia brasiliana* and *Megasporoporia neosetulosa*. The suitability factors for the metrics used indicate that the models can be used to analyze climatic areas and that temperature and precipitation strongly influence the permanence of species in these locations. The results also indicate areas that can be affected by climatic effects, consequently causing a decrease in the occurrence and permanence of these fungi in the Neotropics. Our models can be useful as future guidelines in conservation studies for fungi.

Keywords: Agaricomycetes, Conservation, Neotropics, GBIF, Species distribution modelling.

Introduction

Over thousands of years, humans have been responsible for promoting changes in the environment causing significant ecological impacts and loss of its diversity, in addition to promoting the dispersion of species over long distances around the planet (Whittaker *et al*. 2005; Tylianakis *et al*. 2008; Bullock *et al*. 2018). Climate change (CC) is understood as changes in weather patterns caused by natural factors (Yue & Gao 2018) or by human action (Huang *et al*. 2020) that are mainly evident through the emission of gases into the atmosphere.

Changes in climate indicators are generally related to abiotic factors such as precipitation, temperature, rising levels and acidification of the ocean (Fawzy *et al*. 2020). These changes can trigger extreme natural phenomena and

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affect genetic diversity within populations (Pauls *et al.* 2012), causing extinction events for some ecological populations in tropical environments, including fungi (Sheldon 2019; Lughadha *et al.* 2020).

Fungi correspond to a group of organisms whose spatial patterns are still poorly explored compared to other groups of living beings (Hawksworth & Lücking 2017). In addition, they play an important role in recycling products resulting from their organic activity (Deacon 2006; Kendrick 2017) and are important bioindicators for conservation and management of forest areas (Jiménez *et al.* 2020).

Therefore, a fundamental question for conserving fungal diversity under the uncertainties of climate change would be the extent to which we will have compatible substitutes to perform the important ecological functions for the ecosystem dynamics in relation to genetic diversity (Nilsson *et al.* 2018). While the conservation of fungal species and ecosystems is the foundation of diversity preservation, there is a need to expand the concept of conservation to include new methodologies that add techniques and include an updated framework of new resources to track and catalog known species through potential predictions of their real functional and ecological diversity (Lofgren & Stajich 2021).

Species distribution model (SDM) is one of these new techniques, which uses existing species occurrence data associated with environmental predictor layers to generate presence probability models and suitable areas for new occurrences (Elith & Leathwick 2009; Guisan & Thuiller 2005). This technique has been recently developed and shows increasing use and applicability in delimitation of conservation areas (Guillera-Arroita *et al.* 2015; Keeley *et al.* 2017; Bosso *et al.* 2018), and that the Geographic Information System (GIS) tools can be useful in the management of areas and organisms relevant to their conservation and ecosystem balance, respectively (Brambilla & Saporetti 2014; Soberón *et al.* 2017; Kaky *et al.* 2020).

In recent years, studies have been intensified for most of organisms (Urbina-Cardona *et al.* 2019) mainly due to concerns related to climate change (Větrovský *et al.* 2019), species fertility (Walsh *et al.* 2019), expansion of invasive species in native areas (Barbet-Massin *et al.* 2018), divergence, conservation and niche delimitation of cryptic species (Culumber & Tobler 2016; Scriven *et al.* 2016; Zhao *et al.* 2019) and diversity through integrative taxonomy for wood-decomposing fungi (Fernández-López *et al.* 2019).

The number of works using SDM to analyze the distribution of fungi is currently increasing. Hao *et al.* (2020) recently reviewed 283 studies and highlighted three main approaches: 1) pathogenic fungi, 2) lichens and 3) mushrooms and other macro and microfungi of ecological importance. SDM showed to be a viable technique to analyze new potential areas of occurrence, as well as the relationship with the processes that influence them. Different methodologies and algorithms that incorporate

cataloged data available, mostly of them herbarium records, have already been used for Agaricales (Wollan *et al.* 2008), ectomycorrhizal fungi (González-Ávila *et al.* 2013; Guo *et al.* 2017; Pietras & Kolanowska 2019), lichens (Szczepańska *et al.* 2015; Dymytrova *et al.* 2016; Oh *et al.* 2019; Menezes *et al.* 2020), Hymenochaetaceae (Yuan *et al.* 2015; Fernández-López *et al.* 2019), *Ophiocordyceps* (Yan *et al.* 2017; Wei *et al.* 2021), Boletales (Banasiak *et al.* 2019) and other organisms similar to fungi, such as Myxomycetes (Almadrones-Reyes & Dagamac 2018).

These studies showed that the presence of sporophores in certain areas is more strongly related to climatic factors, although the distribution patterns of macrofungal communities can also be correlated with other factors depending on the modeled species, and that the processes of global transformation underway can affect the richness of these organisms (Andrew *et al.* 2019). Thus, we assess the potential impact of climate change for two wood-degrading Agaricomycetes species in the pessimistic and optimistic scenarios in the Neotropical area, through ecological modeling for suitable areas.

Materials and methods

Occurrence data

A dataset with the records of the Agaricomycetes *Auricularia brasiliana* Y. C. Dai & F. Wu and *Megasporoporia neosetulosa* C.R.S. Lira & Gibertoni available on GBIF – Global Biodiversity Information Facility (https://www. gbif.org/pt/) was used to SDM analysis. Occurrences for *A. brasiliana* from 1906 to 2021 were downloaded from GBIF.org on January 24, 2022 (https://doi. org/10.15468/dl.dqmgbz) and *M. neosetulosa* from 1887 to 2020 from GBIF. org on May 17, 2022 (https://doi. org/10.15468/dl.6nmbfx). We only included in our analyses records of samples deposited in herbaria and with coordinates or with information about locality/city/ municipality from which approximate coordinates could be found. Data with wrong or incomplete information, of doubtful reliability, *i. e.* arising from human, machine or empty observations, and of occurrence outside the Neotropics were excluded.

Due to the lack of reliable data on their actual absences, here we worked only with the presence data and pseudo-absence for model calibration and/or background points (Chefaoui & Lobo 2008; Phillips & Dudik 2008). In this sense, for this study, the environmental restriction method was used, which is based on the smallest suitable region predicted by a bioclimatic model (Engler *et al.* 2004). The application of this method has greater explanatory power in relation to models that randomly allocate pseudo-absences. Finally, the package reduced the number of duplicated points during the analysis.

Biology and taxonomic status of the species

Auricularia brasiliana belongs to Auriculariales and has effuse-reflexed basidiomata usually adhered to the substrate, monomitic hyphal system surrounded by a gelatinous matrix that gives the possibility of rehydration after periods of drought. *Megasporoporia neosetulosa* belongs to Polyporales and presents resupinate basidiomata, completely adhered to decomposing branches. Both species are ecologically important as angiosperm decomposers in Amazon, Atlantic Rain Forest, Caatinga, including montane forests, and Cerrado. *Auricularia brasiliana* is potentially edible, since other species of the genus are traditionally used for food.

Auricularia brasiliana was segregated from the *A. mesenterica* complex and is only known in Brazilian biomes so far (Wu *et al.* 2015), while *M. neosetulosa* was described as a new species, phylogenetically separated from the morphologically similar *M. setulosa* (Henn.) Rajchenb., from which differs in the slightly larger basidiospores, and the occurence in the Neotropics, while *M. setulosa* seems to be restricted to Africa (Lira *et al.* 2021). However, the databases have not yet been updated and the cited records appear as *A. mesenterica* and *M. setulosa*. Thus, previous records of these species in the Neotropics are considered as *A. brasiliana* and *M. neosetulosa*, respectively.

Bioclimatic variables

All 19 environmental climate layers were included, as well as the topographic variable (Elevation) in two sets (current and future), available in WorldClim (Fick & Hijmans, 2017, available at: https://www.worldclim.org/). For future projections (2061~2080), the CNRM-CM6-1 climate model was used with a spatial resolution of 2.5 minutes, from the National Center for Meteorological Research. The package used, detailed below, carried out the current model and the future projection simultaneously.

Two scenarios of Shared Socio-economic Pathways, SSP1-2.6 – optimistic scenario and SSP5-8.5 – pessimistic scenario were assumed. SSP 1-2.6 represents the imposition of policies to mitigate global CO_2 emissions, with temperature rise stabilizing at around 1.8°C by the end of the century, while SSP 5-8.5 represents one of the sets of scenarios that describe the highest emissions of CO_2 gases until 2050. In this scenario, the world economy grows rapidly, driven by the exploitation of fossil fuels, with an increase in the average temperature of the planet by up to 4.4 °C to 2100 and with emissions high enough that they will produce a radioactive forcing of 8.5 W m-2 (O'Neill *et al.* 2016). The data used here were obtained from the Coupled Model Intercomparison Project Phase 6 (CMIP6) (Eyring *et al.* 2016, available at https://www.worldclim.org/). Finally, the study was conducted only for the Neotropics, here defined according to One Earth (https://www.oneearth.org/bioregions-2020/, accessed in April/04/2023). Thus, the environmental variables were cut with a focus on the studied area, through the Q-GIS program version 3.16.14 (https://www.qgis.org/pt_BR/site/forusers/download.html).

Algorithms and model calibration

For the species modeling process, the "ENMTML" package (Andrade *et al.* 2020) was used in the R environment (R Core Team 2023) which is divided into three stages: pre-processing, processing and post-processing (Andrade *et al.* 2020). In the pre-processing stage, the occurrences and predictor variables were inserted. No parameter was used to reduce the autocorrelation of the occurrence data. An important point for the construction of the model is the reduction of the collinearity of the predictor variables, since the use of many climatic variables can generate misleading models and, consequently, an increase in the commission errors of the predicted distributions, that is, the area climatically adequate where the species does not actually occur (Beaumont *et al.* 2005). In this sense, the Variance Inflation Factor (VIF) was used to reduce the collinearity of the predictor variables and the final set of climatic predictors used for modeling had VIF values >2 (Marquaridt 1970). The script can be accessed in https://github.com/ailtonm4th3us/Script-for-modelling-distribuition-species.

The argument (sp_accessible_area) that defines the hypothetical geographically accessible area for the species over time was also used for the construction of the models in relation to what is already known about their ecology and biogeography (Barve *et al.* 2011; Peterson *et al.* 2011). This area can be represented by the BAM (Biotic interactions, Abiotic conditions, and Movement) diagram (Soberón & Peterson 2005) which demonstrates the main factors that influence the distribution patterns of the species. However, this information is not available for the species studied here, so for this study we defined the accessible areas in a single shape-file of the ecoregions for the Neotropics, extracted from the World Wildlife Fund website (https://www.worldwildlife.org/biomes, accessed in April/26/22) in the modeling process (Peterson *et al.* 2001; Andrade *et al.* 2020). The extrapolation of the model is controlled by this method, as the SDM adjust the models based on the conditions in which the occurrences, pseudo-absence and/or background data are found. In this sense, when forecasts are made, the models will present new conditions, especially when projections are made for different time periods and/or geographic regions. In this case, as there is uncertainty, the models will perform extrapolations, as they were not adjusted for the conditions found in the occurrence data (Fitzpatrick & Hargrove 2009; Andrade *et al.* 2020).

Modeling process

Here, to perform the data partitioning, the Bootstrap method was used, which comprises a random partition between the training and test subsets (Fielding & Bell 1997; Andrade *et al.* 2020). Thus, 10 replicates of each model were performed, with 70% of the data destined for the

training models and 30% for the validation of the models. In the processing step, we consider three algorithms for modeling: 1) Maximum Entropy (MXS) (linear and quadratic characteristics), 2) Support Vector Machine (SVM), both Machine Learning methods (Karatzoglou *et al.* 2004; Phillips *et al.* 2017) and 3) Random Forest (RDF), a classification method and linear regression (Liaw & Wiener 2002).

In the post-processing stage for evaluating the models, the metrics Area Under the Curve (AUC, Fielding & Bell 1997), Kappa (Cohen 1960), True Skill Statistics (TSS, Allouche *et al.* 2006), Jaccard (Leroy *et al.* 2018) and Sorensen (Leroy *et al.* 2018) were used. AUC, Kappa and TSS range from 0 to 1, and the closer to 1, the most excellent performance has the model, while the closer to 0, the poorer. Jaccard and Sorensen metrics, which refer to the similarity index, indicate that, if the value is close to 1, the predictions are similar to the observations, while the inverse indicates a higher number of errors, with possible extrapolations, thus, a lower similarity with a greater number of false positives and false negatives (Leroy *et al.* 2018). As the similarity indexes are not influenced by the prevalence of the species and by the unequal number of pseudo-absence (Leroy *et al.* 2018; Nascimento *et al.* 2022), we used the threshold that maximizes the Jaccard values, thus considering the values of sensitivity and specificity as limits for creating binary maps (Allouche *et al.* 2006). To adjust the models with the different algorithms and create an ensemble model, we used the Mean of the Best Models (SUP, acronym used in the ENMTML package, Andrade *et al.* 2020), which evaluates the best algorithms based on Jaccard values, that is, those algorithms that presented the Jaccard index above the average (Velazco *et al.* 2019). Subsequently, the maps generated were edited in the Q-GIS.

Results

Species data processing

We modeled the current distribution of two wood-degrading Basidiomycota species using SDM to predict suitable areas for their occurrence. We designed the models to analyze two future scenarios and understand which areas are expected to change over the 2061 to 2080 range due to the effects of climate change. Initially, *A. brasiliana* had 176 and *M. neosetulosa* 237 occurrence records downloaded from the database and the consulted literature. After the removal of incomplete data or incorrect information regarding the place of collection, the number of records was reduced to 55 records to *A. brasiliana* and 157 to *M. neosetulosa*. However, for the species modeling process, 40 occurrence points were used for *A. brasiliana* and 72 for *M. neosetulosa*, according to the spatial resolution of 2.5 minutes.

Model performance

The species presented a good performance of the explanatory values of suitability for all algorithms in the construction of the binary maps (Table 1). For AUC, the three algorithms presented training values of 0.946 and SVM had the best performance. For Kappa, the algorithms totaled a SUP average of 0.842, whereas the value of TSS was close to 1, with SVM once again being the algorithm with the highest performance value. For Jaccard, the average was 0.861 and for the Sorensen index the adequacy value was 0.922. For these two adequacy metrics, SVM also presented the best contribution values, so it seems that the SVM algorithm presents better applicability to the data training provided for these species.

The product of the training data thus represents the suitability in known and potential areas for the two species. Low values represent areas with less suitability and correspond to paler colors in the maps (Fig. 1), while those that correspond to stronger colors have greater climatic suitability for the occurrence of fungi and represent optimal values, which approach to 1.

Contribution of biovariables

Of the 20 variables used to perform the analysis, 10 were selected by the model during execution for the two species in relation to the three algorithms used. For *A. brasiliana*, five predictors presented better performance in

Table 1. Contribution values of the algorithms with the best performance for the models of *A. brasiliana* and *M. neosetulosa* in bold.

Species	Model Evaluation					
	Algorithms	AUC	Kappa	TSS	Jaccard	Sorensen
Auricularia brasiliana	MXS	0,854	0,550	0,550	0,681	0,808
	RDF	0,916	0,775	0,775	0,797	0,883
	SVM	0,926	0,792	0,792	0,827	0,901
	SUP	**0,946**	**0,842**	**0,842**	**0,861**	**0,922**
Megasporoporia neosetulosa	MXS	0,827	0,577	0,577	0,678	0,805
	RDF	0,919	0,745	0,745	0,774	0,870
	SVM	0,849	0,577	0,577	0,685	0,811
	SUP	**0,920**	**0,755**	**0,755**	**0,782**	**0,876**

the execution of the model, being the predictor Bio2 (Mean diurnal range) with the highest corresponding value for the three algorithms, while *M. neosetulosa* had its performance with the best correspondence for Bio3, Bio9, Bio18, Bio19 and Elev, being Bio18 (Precipitation of warmest quarter) and Bio19 (Precipitation of coldest quarter) with higher values for the SVM algorithm, Bio18 for the MXS and Bio19 for RDF (Table 2). The climatic suitability for *A. brasiliana* seems to have the temperature as the greatest climatic factor influencing its occurrence, while *M. neosetulosa* would have the precipitation.

Species climate scenarios

The models showed three scenarios that allow visualization of the climatic suitability of the species in the present and over time in an optimistic and pessimistic perspective, respectively (Fig. 1).

In the Neotropical region, *A. brasiliana* currently has a wide distribution from Central America to the central region of South America, with points of greater climatic suitability also in the Caribbean islands (Fig. 1A). The Amazon rainforest stand out as areas of countries with a hot-humid climate. Some of these areas seem to have greater aptitude for the permanence of this species and consequently other potential areas are predicted by the model.

In an optimistic future scenario, there would be a significant reduction in the suitability of *A. brasiliana*, observed by the color differences (Fig. 1B). For the pessimistic scenario, most areas that maximize suitability are drastically reduced to some points at the coastal strip of South America, corresponding to the Atlantic Forest in Brazil, thus comprising a diminution in the niche of this species (Fig. 1C).

For *M. neosetulosa*, its current distribution is more concentrated in southern South America, in Central America and the Caribbean Islands (Fig. 1D). Brazil has a greater number of suitable areas compared to other South American countries, which, however, also have potential points of suitability for the current scenario (Fig. 1D). We were able to identify that, in addition to the humid tropical forests
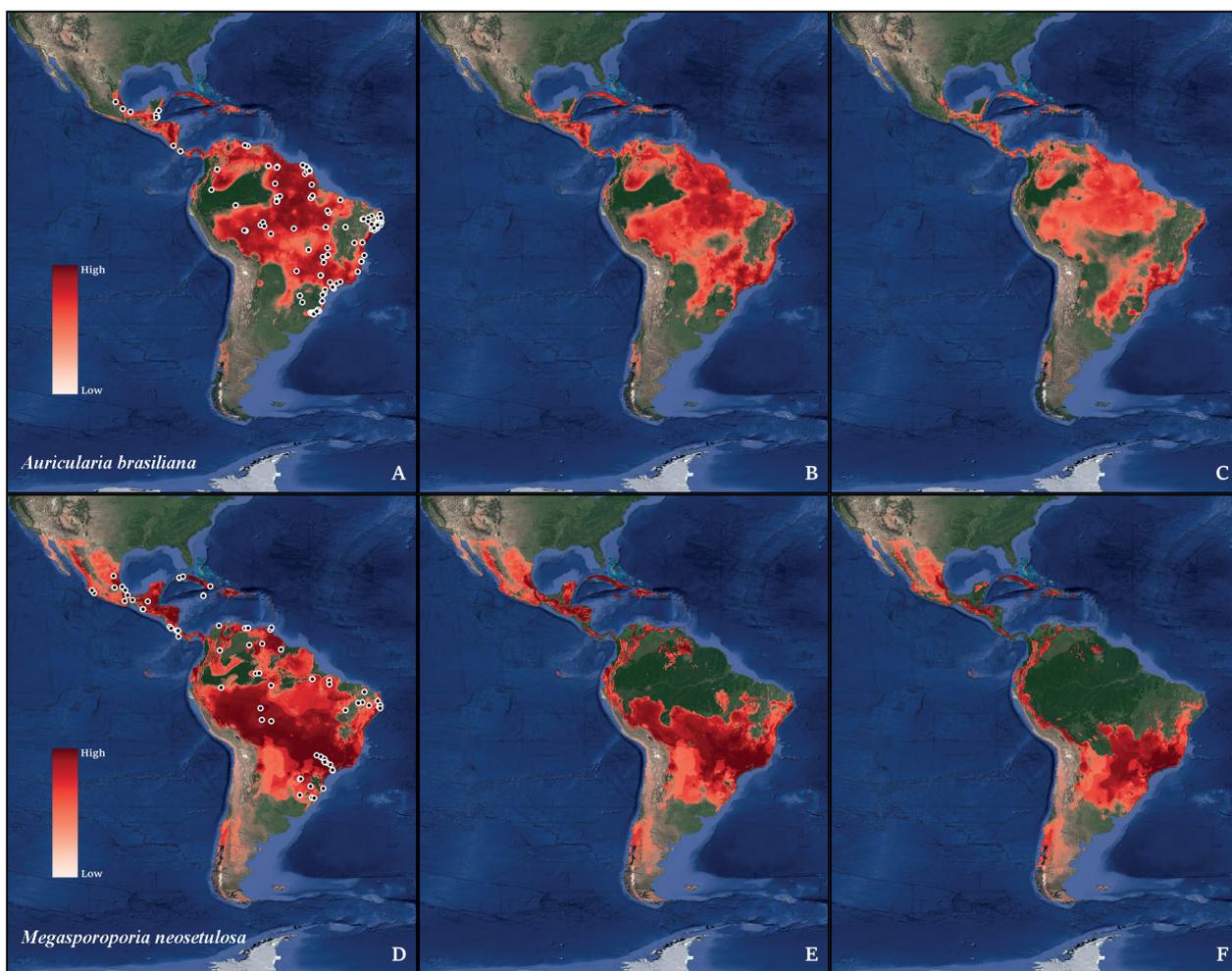
Figure 1. Climate scenarios for *A. brasiliana* and *M. neosetulosa*. **A**- Current scenario, **B**- Optimistic scenario and **C**- Pessimistic scenario for *A. brasiliana*. **D**- Current scenario, **E**- Optimistic scenario and **F**- Pessimistic scenario for *M. neosetulosa*.

Table 2. Contribution of predictor variables for each algorithm to *A. brasiliana* and *M. neosetulosa*. **Bio2:** Mean diurnal range (mean of monthly (max temp–min temp); **Bio3:** Isothermality (bio2/bio7) (x100); **Bio8:** Mean temperature of wettest quarter; **Bio9:** Mean temperature of driest quarter; **Bio13:** Precipitation of wettest month; **Bio14:** Precipitation of driest month; **Bio15:** Precipitation seasonality (coefficent of variation), **Bio18:** Precipitation of warmest quarter; **Bio19:** Precipitation of coldest quarter Elev: Elevation.

Species	Variables	Algorithms		
	ID	MXS	RDF	SVM
Auricularia brasiliana	**Bio2**	**0.390**	**0.226**	**0.236**
	Bio3	0.009	0.088	0.053
	Bio8	0.041	0.055	0.069
	Bio9	0.029	0.038	0.112
	Bio13	**0.130**	**0.154**	**0.161**
	Bio14	**0.106**	**0.107**	**0.126**
	Bio15	**0.022**	**0.154**	**0.074**
	Bio18	**0.160**	**0.078**	**0.039**
	Bio19	0.027	0.067	0.100
	elev	0.080	0.034	0.025
Megasporoporia neosetulosa	Bio2	0.078	0.052	0.059
	Bio3	**0.065**	**0.073**	**0.096**
	Bio8	0.089	0.052	0.042
	Bio9	**0.152**	**0.228**	**0.106**
	Bio13	0.086	0.091	0.000
	Bio14	0.022	0.097	0.097
	Bio15	0.031	0.124	0.035
	Bio18	**0.196**	**0.098**	**0.238**
	Bio19	**0.153**	**0.135**	**0.237**
	elev	**0.124**	**0.051**	**0.087**

of Brazil, Central America, Caribbean and South America, the species seems to be well adapted to Cerrado, which is characterized by a seasonal tropical climate, with rainy periods and well-delimited drought.

In the optimistic scenario, the species has its niche reduced almost entirely in the northern region of South America, being most likely to be restricted to dry regions in the Andes and the southern region of South America (Fig. 1E). We also found that for northern South America, a small area of the Guiana plateau remained suitable for the species, which could lead to the isolation of the species (Fig. 1E). The niche was also significantly reduced to the central region on the map which previously presented several potential areas for the species. For the pessimistic future scenario, the model admits that this reduction to the north could be even more severe, and that the species will only occur in small fragments along Central and South America, and the Cerrado with greater potential of its occurrence, in addition to the coastal strip of the country where we find the Atlantic Forest (Fig. 1F).

Our analyses showed that the two species share, in some cases, equal access points for each suitability grid, but with different values for each distribution range, although *A. brasiliana* seems to be better distributed in the northern part of the Neotropics while *M. neosetulosa* in the southern part. Our suitability values for both models performed excellently and the maps indicate that most suitable areas are in Amazonian Forest for *A. brasiliana* and Cerrado and mountainous areas for *M. neosetulosa*. Furthermore, some areas of Atlantic Forest in Brazil would remain suitable for both species in different scenarios.

Discussion

Although the distribution of fungi is still poorly explained and there are difficulties in predicting climate change for these organisms, the use of SDM presents a good technique to predict the occurrence of these organisms in space over time (Hao *et al.* 2020). We found that the challenges to apply SDM to fungi are linked to detection and sampling, as well as the taxonomic changes underway. This is due to the inclusion of genetic data to better delimit and identify the species, which causes uncertainties in the choice of the taxa to be modeled (Stefani *et al.* 2014; Hawksworth & Lücking 2017) Therefore, the species in this study were selected following recent literature that confirmed their taxonomic position and delimitation from

DNA sequences. Although *A. brasiliana* and *M. neosetulosa* have phylogenetic support that justify their delimitation to the Neotropics, the confirmation of their distribution is not fully resolved and new complementary studies with broader DNA sampling of material collected in other regions of the Neotropics other Brazil are needed. Furthermore, revising deposited material in herbaria and updating the databases is of paramount importance to optimize this process. Despite being an initial study, our work paves the way for the ecological understanding and the limits of the distribution of the studied species, knowing that for fungi the effects of taxonomic inaccuracies have been little studied when dealing with distribution models (Elith *et al.* 2013; Fernández-López *et al.* 2019).

There is currently an emerging interest in predicting new environments in which fungal species have not been observed, mainly to guide biodiversity management and conservation processes (Sequeira *et al.* 2018). Studies show that the areas modeled according to the points of occurrence correspond to places in which the species already exists and that the models introduce new areas climatically similar (Nascimento *et al.* 2022) which can be reached by the species and serve as potential areas for their establishment depending on their dispersion capacity (Barve *et al.* 2011). The planet is undergoing transformations resulting from climate change, which are a reflection of different impacts. Among these, forest deforestation is one of the aggravating factors that lead to loss of substrate and temperature rising, generating extreme phenomena and atypical events that can lead to the extinction of organisms such as fungi (Walker *et al.* 2018; Lughadha *et al.* 2020). Additionally, other important factors may be already affecting the distribution of these organisms more than climate changes, such as land and sea use that reduces biodiversity on the planet, followed by the exploitation of natural resources and pollution (Jaureguiberry *et al.* 2022). However, the results obtained here demonstrate the current panorama of the distribution caused by the effect of climate change and alert to the causes of alterations in the future, which come from the set of successive actions and events listed above that drive the global loss of biodiversity and compromising the conservation of organisms.

Our models show that the areas of greatest climatic suitability are reduced and that for *A. brasiliana* and *M. neosetulosa* the potential range will change in some regions, mainly central and northern South America in response to climate change. Although these areas remain suitable for both species over the years, the decrease in suitability for central-northern regions including countries in this territorial range, especially Brazil, is worrying, as they are areas that hold a large part of Amazon Forest and shelter a good part of the diversity of fungi (Gazis & Chaverri 2015) that act in different roles in ecosystem dynamics (Fukasawa & Matsukura 2021).

With the reduction of the Amazon Forest in these areas, it is assumed that the occurrence of *A. brasiliana* will drastically be reduced, since dependence on climatic conditions can alter its presence and interfere with ecological interactions with plants due to its role as a decomposer, and also affecting its diversity (Větrovský *et al.* 2019; Naranjo-Ortiz & Gabaldón 2019). For *M. neosetulosa*, the Cerrado biome in Brazil seems to have the highest percentage of suitable areas, which indicates that the conditions present in this environment may favor the permanence of the species in this habitat. The Cerrado is the second largest biome in Brazil, a hostspost that has suffered strong pressure from agribusiness through legal and illegal deforestation and has few protected areas compared to other biomes in the country such as the Amazon (Colli *et al.* 2020; Rajão *et al.* 2020). Even for an optimistic future scenario, the suitability of this species seems to disappear in the central-north region of South America, leaving few areas appropriate for its occurrence.

In addition, areas of the Atlantic Forest biome show to be suitable for both species even in the pessimistic scenario. It is worth mentioning that this Brazilian hotspot is currently undergoing changes in its remnants as a result of habitat reduction and fragmentation that negatively impact species richness (Püttker *et al.* 2020). It is, therefore, an area that urgently needs conservation. This concern extends to climate change that can further exacerbate and reduce the size of distribution areas for fungal species (Bidartondo *et al.* 2018).

Areas of importance for conservation in South America, such as the islands of the Caribbean Sea, the Chilean forests, the coastal zone of Colombia, the Amazon rainforest and the Brazilian Cerrado are considered biodiversity hotspots and constantly suffer from threats over the years that reflect in the reduction of existing lives in these environments (Higgins 2007; Brum *et al.* 2019; Zabel *et al.* 2019; Rosa *et al.* 2021). The two future scenarios show that suitable biomes in Brazil for the analyzed species appear to be the most important centers for conservation. It can be seen that even for the optimistic scenario, the reduction of climatically suitable habitat is dramatic and with that, our models suggest climate impacts on the populations of *A. brasiliana* and *M. neosetulosa*. Finally, we dialogue with the need for actions that prioritize the conservation of areas and biodiversity in order to avoid future devastation and disturbances that affect the diversity of wood-decomposing fungi (Fukasawa & Matsukura 2021) and, consequently, the ecological relationships they establish mainly with plants in the Neotropics.

The application of ecological modeling to wood-decomposing fungi brings a new perspective to analyze the distribution of species in areas of ecological importance. These areas have a high degree of biological diversity, showing strong signs of disturbance. Our models indicate climatic suitability for regions considered hostspots of biodiversity in the Neotropics and the need for intervention

to preserve, at least, the species modeled here. The values of the tests performed were explanatory and reliable, showing that the annual temperature and the level of quarterly precipitation are strongly influencing the species in the study and that all these factors may probably be associated with the effects of anthropic changes and consequently of the climate change.

The species mostly occur in places of climatic vulnerability, with more critical points for the north of South America, as well as for the Central America region. In both optimistic and pessimistic future scenarios, *A. brasiliana* will have its niche drastically reduced, while *M. neosetulosa* will be restricted to dry regions of the Andes and southern South America. Thus, our models may serve as guides for conservation plans that seek to protect areas from their expansive reduction, as well as presenting factors associated with climatic interferences that impact the occurrence of fungal species and their ecosystem biodiversity.

Acknowledgments

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