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Bioclimatic modeling for the prediction of the suitable regional geographical distribution of selected bright-spored myxomycetes in the Philippine archipelago

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Abstract. *Limbo-Dizon JE, Almadrones-Reyes KJ, Macabago SAB, Dagamac NHA. 2022. Bioclimatic modeling for the prediction of the suitable regional geographical distribution of selected bright-spored myxomycetes in the Philippine archipelago. Biodiversitas 23: 2285-2294.* Myxomycetes communities in the Philippines have been well studied in terms of diversity patterns projected by their enigmatic fructifications. To predict potential suitable geographical distributions of three different bright-spored myxomycetes with known variations in its occurrences, namely, *Arcyria cinerea*, *Perichaena depressa,* and *Hemitrichia serpula,* species distribution modeling was utilized. Three different modeling approaches employing MaxEnt were performed in this study and have calculated high model performances based on the AUC values generated (0.778-0.873). In all of the modeling approaches, the three myxomycetes species were predicted to have an expansion of their localized fundamental niches pointing to the influence of isothermality (BIO3) as an important macroclimatic predictor for modeling approaches 1 and 2. Highly suitable habitats for the three bright-spored species were discovered primarily in terrestrial landscapes on the regions of Luzon Island, as well as in small parts of the Visayas and Mindanao Islands. The predicted models in this study do not tell missing geographical information but rather may use as tools for the exploration of potentialities, such as understanding the possible distribution patterns of the three bright-spored myxomycetes species in the Philippines. This can serve as a useful baseline to enhance the conservation efforts for most habitats in the country that are directly affecting microbial communities due to rampant habitat loss and rapid urbanization.

Keywords: Distribution, environmental niches, mapping, maximum entropy, protist

INTRODUCTION

Knowledge of how individual species respond to varying environmental conditions and understanding of the mechanisms involved in how species can be distributed spatially in suitable habitats are just some of the venerable goals that are associated with community ecology (Mertes and Jetz 2018). Ecological niches of species are important features to address most ecological and biogeographical issues, i.e., species persistence, spatial distribution, and range shifts. Abiotic factors such as temperature, precipitation, etc., have been proven to be affecting the distribution of species at different geographical scales (Belguidoum et al. 2021; Gonzáles-Salazar et al. 2013; Sosa and Loera 2017). For the last few years, modeling biogeographic patterns and distributional ranges have become an important topic for identifying the responses of many species to changing climates. The most commonly used strategy to estimate the potential geographic distribution of a target species is to characterize the environmental conditions known to be suitable from confirmed records and identify all regions that meet these conditions (Araujo and Guisan 2006). The precision of this correlative approach depends critically on the set of environmental variables that may affect the probability of persistence for the species.

Modeling the potential distribution of many macroecological organisms like plants and animals (Cabral et al. 2017; Connolly et al. 2017; Guisan and Rahbek 2011) has been widely tackled in many kinds of literature, including those organisms that are ephemeral in nature, such as fungal reproductive structures (see Ocampo-Chavira et al. 2020; Yuan et al. 2015; Rohr et al. 2011) or fungal allies (see Duque-Lazo et al. 2016, Aguilar and Lado. 2012) that are once classified as species belonging to the Kingdom Fungi. In fact, species distribution models are an emerging tool in the study of fungi, and their use is expanding across species and research topics (Hao et al. 2020). However, despite the growing interest in this important tool to be utilized, most of the reported studies concentrated on macrofungi (see Sato et al. 2020), lichens (see Dymytrova et al. 2016, Braidwood and Ellis 2012), and fungal pathogens (see Bosso et al. 2017; Narouei-Khandan et al. 2017). Very limited species distribution modeling (SDM) studies have been reported so far, especially on fungus-like protists that are widely known to be an important microbial predator on the soil biota. Among these protists, myxomycetes are one of the few groups with macroscopically visible fruit bodies that are found in a wide array of ecological habitats. Unlike the true fungi, myxomycetes are predominantly sexual (Feng et al. 2016; Shchepin et al. 2022) and the fructifications of these protists have very limited diagnostic morphological characters which can easily be withered (Shchepin et al. 2019). Moreover, myxomycetes are classified as a monophyletic taxon within the Amoebozoa (Adl et al. 2012, 2019; Ruggiero et al. 2015) and are classified into two clades: bright-spored and dark-spored, which are now officially called Lucisporomycetidae and Columellomycetidae, respectively. Rostafiński (1875) established the first classification based on comprehensible criteria, dividing myxomycetes into two "subdivisions" based on the color of the spore mass: the dark-spored and bright-spored. This classification was based on a combination of fructification morphological characteristics, although plasmodium appearance and fruiting body growth were also taken into account to some degree (Ross 1973).

In the case of the myxomycetes, there are only a few papers that have reported the utilization of SDM. All of these papers have exploited the Maximum Entropy (MaxEnt) algorithm, a statistical model perfect for predicting the distributions of rare species because it is responsive to the changes in sample size, with strong predictive efficiency even if the sample size is small (Hernandez et al. 2006; Wisz et al. 2008; Garcia et al. 2013). Rojas et al. (2015) applied this modeling technique to gain a better understanding of the five most common myxomycetes species occurring in Costa Rica. In addition, to further prove the speculation about moderate endemicity among myxomycetes, this approach was also used for some myxomycetes species (*Badhamia melanospora*, Aguilar et al. 2014; *Hemitrichia serpula*, Dagamac et al. 2017a). SDM has also been used to show the global distribution limits of *Barbeyella minutissima* (Stephenson et al. 2019) and the nivicolous myxomycetes, *Physarum albescens* (Dagamac et al. 2021).

Among the countries in Southeast Asia, the Philippines have been able to document the greatest number of records of plasmodial slime molds (myxomycetes) for the region (Macabago et al. 2020). Over the last decades, since the myxomycetes surveys have been conducted in the Philippines, most of the assessments were able to show the following: (i) major terrestrial ecosystems harbor a diverse myxomycete flora for the country (Bernardo et al. 2018), (ii) variation on the diversity of most myxomycetes assemblages randomly collected on different substrates collected on priority areas for conservation in the Philippines occurs (Macabago et al. 2017; Pecundo et al. 2017), and (iii) clear differences on the occurrences of myxomycete assemblages exist (Dagamac et al. 2017b). So far, there is only a single study that used SDM for Philippines myxomycetes. In the paper of Almadrones-Reyes and Dagamac (2018), the suitable habitat for the common dark-spored myxomycetes in the tropics, *Diderma hemisphaericum*, was determined. It also predicted the range expansion of the species in other islands of the Philippines in response to two climate change scenarios (A2 and B1). With many reported myxomycetes species in the country, none have tried to predict the geographical niches suitable for bright-spored myxomycetes. Hence, this study is conceived to (i) fill the distribution gaps of tropical bright-spored myxomycete assemblages in the Philippines and (ii) employ different modeling approaches using the MaxEnt software.

MATERIALS AND METHODS

Occurrence data and environmental layers

For this study, three bright-spored myxomycete species were selected based on their known occurrence in the Philippines: *Arcyria cinerea* (Bull.) Pers. representing the abundantly/cosmopolitan occurrence, *Perichaena depressa* Lib. depicting common occurrence, and *Hemitrichia serpula* (Scop.) Rostaf. ex Lister as the occasionally occurring slime molds. The distribution of these bright-spored representatives was surveyed using all known local historical occurrence data published as reports, grey publications, and personal records accounted by the third and last author of this study accounting from the reports starting in the earliest publications in the1970s up to the year 2021 (for the comprehensive list of literature used, see Table S1). An initial list of all the known records with clearly described localities and coordinates was included in this study. Reports that have an unclear description of the distribution data were excluded from the study. It is important to note that most of these records come from the intense surveys concentrated only on the middle and southern part of mainland Luzon Island. So far, the missing patches found in the islands of Mindanao (Southern Philippines) and the Northernmost mountain ranges of the Luzon Island have remained unsampled for any myxomycete survey. To verify the accuracy of all the 201 geographic coordinates used for this correlative modeling study, an initial data checking was conducted. All the coordinates were initially transformed into a CSV file that was then overlaid on a Philippine map using ArcGIS ver. 10.3. All points that were eliminated on the base map were then rechecked and corrected.

The environmental layers for this study were the 19 bioclimatic variables in the Philippines with a raster resolution of 1km obtained from the PhilGIS website (http://philgis.org/). Since the downloaded environmental layers from PhilGIS were all in GeoTIFF format, the ArcGIS software was utilized to convert all the 19 GRID file layers into an ASCII extension (file format compatible with the modeling software used for this study).

Modeling procedures

MaxEnt software (ver. 3.4.4) was initially downloaded from https://biodiversityinformatics.amnh.org/opensource/maxent/. The software generalizes individual observations of species presence using entropy and does not require or even include points where the species is absent within the theoretical context. MaxEnt ranks a species' habitat suitability on a scale of 0 to 1, with 0 being the least suitable and 1 being the most suitable (Kamyo and Asanok 2020). In this study, three approaches (Table 1) were used for each bright-spored myxomycetes species. Firstly, with the use of MaxEnt's default settings (see Table 1). Secondly, to provide pseudo-absence correction, the input files were subjected to an ENMeval analysis performed using R Studio. Lastly, the autocorrelations among the 19 bioclimatic variables were analyzed, reducing now the possible environmental layers that can be used for the correlative modeling.

For the first model, the transformed CSV file of the occurrence records of each bright-spored myxomycetes and the converted ASCII format of the 19 bioclimatic environmental layers were used as input files in the MaxEnt software. The model was run using the default regularization settings (regularization multiplier = 0, feature type = Auto) in Maxent. To determine the significance of each biophysical variable, the following settings were chosen: (i) “*Create a response curve*” and “*Do jackknife test to measure variable importance*,” and (ii) the output format was set to “*logistic*”. In accordance with Yang et al. (2013), the random test percentage was adjusted to 30% and the file format turned into logistics for all models. A total of 10 runs were set for each model approach. The algorithm runs either 1000 iterations of these processes or continues until it reaches a convergence threshold of 0.00001 (Yuan et al. 2015).

In the second model, ENMeval was used to optimize model complexity to balance the goodness of fit and predictive ability. In addition, the use of this R-based modeling evaluation modifies the models to improve predictive ability and avoids issues of possible overfitting (Muscarella et al. 2014). For this approach, the fine-tuned setting generated from the ENMeval analysis (method = randomkfold, kfold=10) suggested the adjustment of a regularization multiplier (RM) and feature type (FT) for each bright-spored myxomycetes as follows: *A. cinerea* (2.5 [RM] / LQHPT [FT]); *P. depressa* (1 [RM]/ LQ [FT]) ; *H. serpula* (2.5 [RM] / H [FT]).

For the third approach, the SDMToolbox in ArcMap 10 was utilized to check for autocorrelations among the environmental variables. The ASCII file of 19 environmental layers was uploaded in ArcMap 10.3 and the tool “*Remove highly correlated variables*” was used under the SDMToolbox. Variables with correlation coefficients of >0.8 were chosen following the Spearman correlation for a total of 9 variables (BIO2, BIO4, BIO7, BIO8, BIO12, BIO16, BIO17, BIO18, and BIO19). These variables were used to produce the ENMeval analysis for each species in the third model approach. In this case ENMeval suggested the following settings: *A. cinerea (*2 [RM] / LQH [FT]); *P. depressa* (0.5 [RM]/ LQ [FT]); *H. serpula* (2.5 [RM] / LQHPT [FT]). The random sampling process was performed ten times for all the models to make sure that the results were not affected by the random collection of points and the average of those ten runs was used in this study.

The resulting models were then evaluated using the receiver operating characteristic (ROC) analysis, which eventually generated the area under the curve (AUC) scores (Phillips and Dudik 2008) to determine the model’s goodness-of-fit. A *Jackknife* procedure was used to calculate the contribution of the variables used for the model prediction. The final output of all models produced a distribution map with potential incidence values for each grid cell, ranging from 0 to 1. For better visualization, the ASCII output file format from MaxEnt was imported into ArcMap 10.3 software. The map was then divided using a defined interval as a classification method. Based on projected habitat suitability, the habitat suitability of each species was divided into five categories, which are as follows: Very low suitability (0-<0.2), Low Suitability (0.2-<0.4), Moderate Suitability (0.4-<0.6), High Suitability (0.6-<0.8), Very High Suitability (0.8-1).

RESULTS AND DISCUSSION

A total of 201 occurrence points (98 for *A. cinerea*, 67 for *P. depressa*, and 36 for *H. serpula*) found in different geographical ranges in the Philippines were used for this study (Figure 1). The maximum entropy algorithm, which was used for species distribution modeling for three bright-spored myxomycete species, suggested several important bioclimatic variables that could affect the species' predictive local distribution in the Philippines. The results show in all three cases a potential distribution pattern centering in the middle part of the archipelago, with low to very low incidences in the North and in the south.

In the first model approach, isothermality (BIO3) has the highest percentage contribution for all three bright-spored species, with 32.6% for *A. cinerea*, 32.0% for *P. depressa*, and 29.7% for *H. serpula* (Table 1). In terms of permutation importance, the model calculated that isothermality (BIO3) was the highest for *H. serpula* with 39.2% and annual temperature change (BIO7) was the highest for the two other bright-spored species with 26.5% and 23.7% for *A. cinerea* and *P. depressa*, respectively (Table 2). Furthermore, the Area Under the Curve (AUC) values derived from maximum entropy-based results for the three bight-spored species are (i) 0.873 for *A. cinerea*; (ii) 0.841 for *P. depressa;* and (iii) 0.824 for *H. serpula*, indicating strong predictive model efficiency (Figure 2). For the second model approach, isothermality has the highest percent contribution for both *A. cinerea* and *H. serpula* with 38.9% and 50.7%, respectively. But for *P. depressa* precipitation of the driest quarter contributed the most accounting for 31.3% (Table 1). When it comes to permutation importance, the three species ranked isothermality (BIO3) as the highest (Table 2). For the values of AUC, *A. cinerea* has an AUC of 0.850, *P. depressa* has an AUC of 0.793, and *H. serpula* has an AUC of 0.816 (Figure 2).

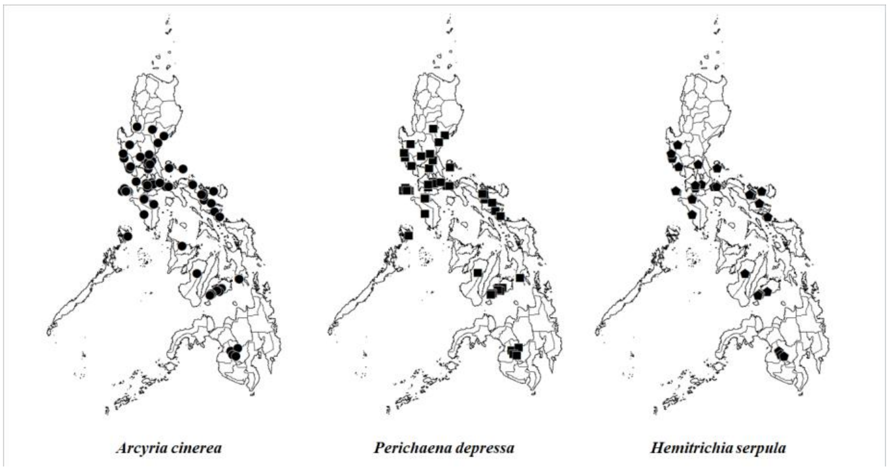

Figure 1. Occurrence points of three bright-spored species in the Philippines based on the published geographic coordinates of species occurrences where each of the three bright-spored species was recorded

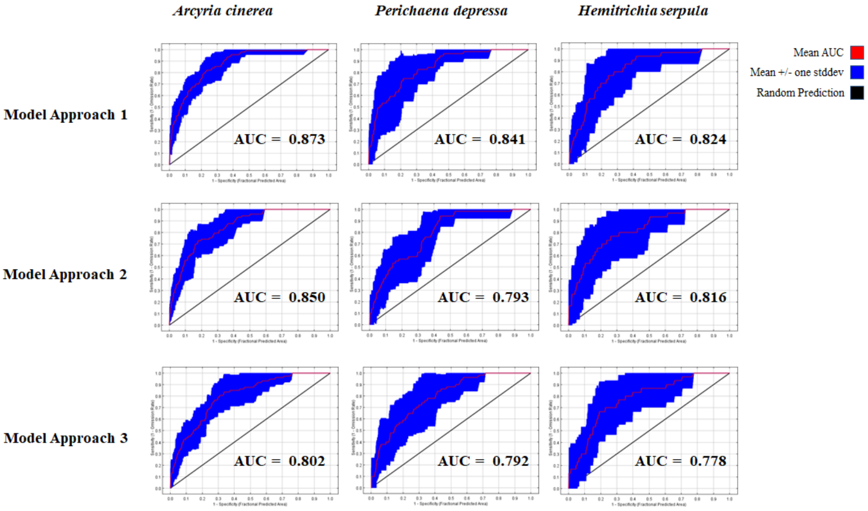

Figure 2. Results of the area under the curve (AUC) analysis, including mean AUC values for each bright-spored species obtained using the three model approaches

Highest percent contribution for both *A. cinerea* and *H. serpula*, with 41.1% and 43.5%, respectively. While the precipitation of the driest quarter (BIO17) contributed the most to *P. depressa*, accounting for 56.8% (Table 1). In terms of permutation importance, the model calculated that annual temperature change was the highest for *A. cinerea* with 55.7% and temperature seasonality was the highest for the two other bright-spored species with 36.4% for *P. depressa* and 33.5% for *H. serpula* (Table 2). *Arcyria cinerea*, *P. depressa*, and *H. serpula* each had AUC values of 0.802, 0.792, and 0.778, respectively (Figure 2).

Based on current species occurrence data of the selected bright-spored myxomycetes, the predictive model recommended areas in the Philippines with favorable bioclimatic conditions for the three bright-spored species (Figure 3). According to the first modeling approach, the three species are predicted to be found in (i) areas of the southernmost part of the main island of Luzon, specifically CALABARZON Region, Bicol Region, the coastal provinces of Central Luzon Region and (ii) some parts of Visayas Island. In the second model, there is only a small change in the possible suitable habitats for *A. cinerea*; however, the possible suitable habitats have been extended with the inclusion of the northern island provinces (Ilocos region) and southeastern areas of the country (a region in the country abbreviated as MIMAROPA) for *P. depressa*. In the case of *H. serpula*, the predicted models showed that the suitable local habitats expanded in the northern and southern part of Luzon, particularly the Ilocos Region, the Cordillera Administrative Region, and the islands of MIMAROPA. For model approach 3, *A. cinerea*'s possible suitable habitats were extended to the Ilocos region and MIMAROPA, while the two other species have a slight change in their possible suitable habitats. Furthermore, areas in Northern Mindanao are predicted to have a moderately high probability of suitable habitats for the three bright-spored species.

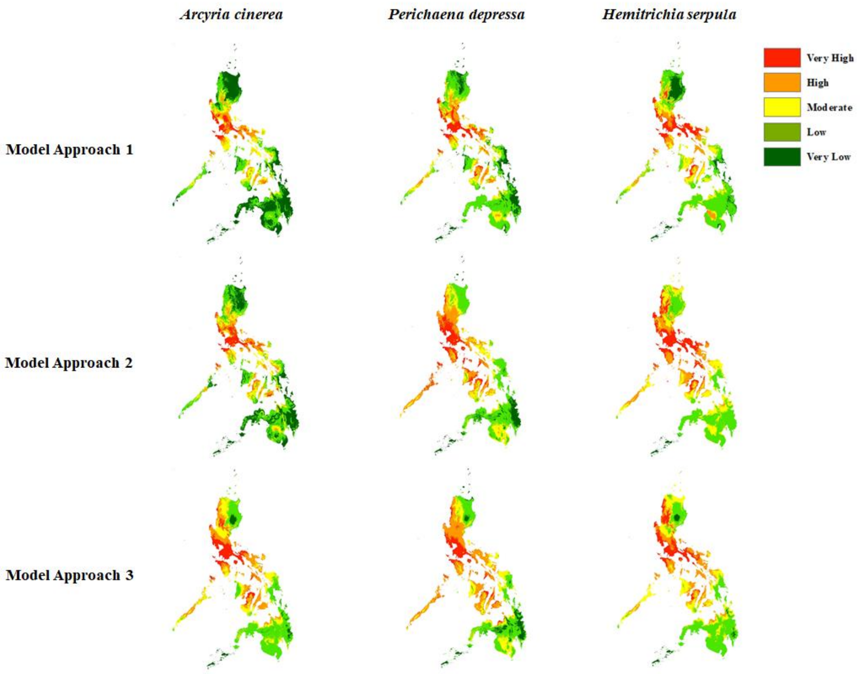

Figure 3. Species distribution models for the three bright-spored species of myxomycetes showing a map of the Philippines and the predicted suitable habitat areas under the three model approaches generated by the maximum entropy algorithm. Based on the calculated probability of occurrence for the three bright-spored species, a heatmap is presented. Dark Green indicates very low suitability (0-<0.2), light green indicates low suitability (0.2-<0.4), yellow indicates moderate suitability (0.4-<0.6), orange indicates high suitability (0.6-<0.8) and red indicates very high suitability (0.8-1)

Discussion

The predictive models generated by MaxEnt utilized in this study were employed on three selected bright-spored myxomycetes, which have been reported to have varying occurrence in many surveys in the Philippines (Figure 1): the cosmopolitan and abundantly occurring *A. cinerea,* the commonly occurring *P. depressa,* and the occasionally occurring *H. serpula.* So far, only dark-spored myxomycetes species, *D. hemisphaericum,* an abundantly occurring species that thrives in many moist chamber collections in the Philippines, is the sole predictive modeling study that has been reported for the country and utilized only a default setting of MaxEnt models to see areas where this species is most likely to thrive (Almadrones-Reyes and Dagamac 2018). Hence, this study is conducted to fill the missing gaps in the range distribution of these myxomycete communities in the country and to compare different modeling approaches that can be used to explain the habitat suitability of their distribution. In accordance with Naimi et al. (2014) and Moudrý and Šímová (2012), since most of our records are either recent or have relatively identified precise geographical coordinates, the direct influence of spatial uncertainty was not investigated for this study.

Comparing the modeling approaches

The climatic variables from the PhilGIS database set certainly do not immediately reflect such complex interactions that might really happen in natural conditions. Therefore, we should first be cautious in interpreting any models that are predicted, especially in addressing the question to which extent the macroclimatic factors that are used can effectively explain the fundamental niche of the three bright-spored myxomycetes identified in this study. Predicted models do not tell missing geographical information, but rather, models are used as tools for the exploration of potentialities (Dagamac et al. 2021). Nevertheless, the high mean AUC values calculated from the three different modeling approaches indicate the excellent performance of the model but certainly do not indicate a high level of accuracy for the prediction (Phillips et al. 2006). It is important to note that model evaluation is assessing the generality by means of penalizing the model for complexity using a cross-validation scheme. Therefore, model precision can be improved if (1) appropriate choices for the background sample are reflective of prior assumptions and (2) environmentally biased sampling has been considered (Merow et al. 2013). Moreso, only conducting more ground-truthing (in areas as suggested by the models) can verify the “correctness” of the models and test if the absence of the species is really a product of true absence or just an indication of pseudo-absence. Furthermore, the results of the analyses of the three modeling approaches for the three myxomycetes species were projected to have an expansion of their localized distributional range in the archipelago, which may be attributed to varying reasons. For model approach 1, it all showed the highest AUC values for the three bright-spored-myxomycetes (see Figure 2) - here, no correction for pseudo-absence was introduced and the default setting has a stricter regularization multiplier of 0.5. The AUC values slightly decreased in model approach 2 (Figure 2). It is important to take note that correction for pseudo-absence was considered and hence ENMeval was added in the model calibration step to avoid issues of overfitting. Moreover, using multicollinearity of predictor variables, i.e. including all the 19 bioclimatic variables, as seen in model 1 and model 2 can affect the omission rates (Feng et al. 2019) hence producing overly complex distribution models (Halvorsen et al. 2016). Model approach 3, which reduced the number of variables using the principles of autocorrelation among the 19 environmental layers, provided the lowest AUC values. In spite of the robust performance of the predictive maps (Figure 3), the percent contributions of single variables shift among the model approaches and the myxomycete communities (Table 1), probably due to the high correlation between some of the macroclimatic (1-19) variables as what was similarly observed in the recent paper of Dagamac et al. (2021). Removing correlated variables in model 3 have slightly changed the fit of the model in comparison to model 1 and 2 but did not affect the performance of the model. This now proves the ability of the MaxEnt algorithm to regulate complexities in the model by restraining the role of redundant predictive variables (Feng et al. 2019; de Marco Junior & Nobrega 2018). Furthermore, when autocorrelated variables are implemented in the model, like in the case of model 3, we can expect that there will be an increase in the species distribution model's efficiency, reducing now possible predictive uncertainties (Naimi et al. 2014). Hence, among the three approaches, model approach 3 has showcased practically the best approach to explain species distribution for this study, especially in accounting for priority conservation areas for the Philippines.

Comparing now the different model approaches concerning percent contributions of the variables used for every model, the first and second model approach shows that among the 19 macroclimatic variables, *isothermality* (BIO3) had the highest contribution for *A. cinerea* and *H. serpula*. When looking at the third model approach, both myxomycete species also showed that the strongest contribution comes from the temperature seasonality (BIO4). These results are similar to another Philippine myxomycete case study by Almadrones-Reyes and Dagamac (2018), which also portrayed the two abiotic factors, *isothermality* and *temperature seasonality*, as the main contributors to the predictive model using a similar approach. Except for the *annual temperature change* (BIO7), the model generated by Rojas et al. (2015) among the five most abundant Costa Rican myxomycetes also indicated how isothermality is an important predictor for the models generated in that study. It seems that most tropical myxomycetes communities (regardless of their spore color) follow this pattern of being influenced by isothermality to fruit. However, for the case of *P, depressa*, both model approaches 2 and 3 indicated the highest contribution of the *precipitation of the driest quarter* (BIO17). This is interesting to note of since most of the recorded occurrence for *P, depressa* in the Philippines comes from moist chamber collections that might have been collected in areas wherein they are experiencing the seasonal period of the year described be dry and humid.

Ecological relevance of the model to understand tropical myxomycete communities at a local scale

The correlative approach employed in the MaxEnt algorithm suffers from at least two shortcomings: first, the set of abiotic data is limited to an easily scalable set of abiotic factors; complex, especially biological, interactions are not considered. Second, the model is static (Convertino et al. 2014) and does not regard (i) possible dispersal limitations (Rodriguez-Rey et al. 2013) and (ii) local genetic adaptation or any other within-species differentiation (Merow et al. 2013). Admittedly, most of the knowledge in the study of the Philippine myxomycetes is concentrated only on surveys and assessments of species diversity. Most of these myxomycetes assessments have been intensely done on the easily accessible areas found in the lowland forest in the central islands of Luzon, Philippines, which possibly explains now the low suitability on the Northern and Southern parts of the country as generated by all of the modeling approaches for the three myxomycete species. Moreover, the distribution patterns in myxomycetes do not depend exclusively on climatic factors and some other factors must be considered, such as the availability of substrate. Needless to say, the interpretation of the potential distribution patterns found for this study depends critically on the availability of current records and should be treated carefully. However, with the attempt to create a possible ecological explanation of the distributional patterns and variations on the occurrence of selected bright-spored myxomycetes that exists in major areas surveyed in the Philippines, the models nevertheless help identify major "white patches" of habitats and localities that are classified to be a suitable niche for these bright-spored myxomycetes (Figure 3). This modeling approach has also been used to shift the paradigm on the restricted distribution of the myxomycete, *B. minutissima*, since for many years, it has been believed to occur only in temperate areas with pronounced dominance *Picea* species. However, the global modeling approach that utilized MaxEnt showed that it could have a geographically wider distribution, as supported by the recent study of Stephenson et al. (2019) that verified the appearance of this species in the highlands of Australia and Vietnam. Moreover, the recent worldwide modeling conducted by Dagamac et al. (2021) about nivicolous myxomycetes confirms that not all mountainous areas of the world harbor this distinct ecological guild but rather identified other putative areas that will help many myxomycete field workers to limit the mountain ranges, i.e., Himalayas, the coastal mountains of Alaska, or the Atlas Mountains of Morocco, they can explore in the future. But in comparison to these cases, our study showed that in all of the three cases studied, the models had proposed a distribution that is rather close to a pattern you would assume if the surveying intensity were high and uniform over the whole archipelago, which is certainly impossible on the standpoint of myxomycetes ecology. Perhaps, due to the current available limited data, the model is assuming (from the known distribution) a narrower ecological niche of the (complex) species than realized in nature. This now points out that to verify this model, these "white patches" should be urgently investigated and also go to the areas that have remained untapped or unexplored for myxomycete surveys.

Table 1. List of environmental variables in the Philippines used for the three model approach performed for this study and its percent contribution and Mean AUC values. Model approach 1 included all 19 bioclimatic variables with default regularization setting; model approach 2 increased the regularization multiplier suggested after ENMeval calculations; Model approach 3 included the selected 9 bioclimatic variables after autocorrelation

	Model Approach 1			**Model Approach 2**			**Model Approach 3**		
	Arcyria cinerea	***Perichaena depressa***	***Hemitrichia serpula***	***Arcyria cinerea***	***Perichaena depressa***	***Hemitrichia serpula***	***Arcyria cinerea***	***Perichaena depressa***	***Hemitrichia serpula***
Feature type	Auto	Auto	Auto	LQHPT	LQ	H	LQH	LQ	LQHPT
Regularization multiplier	0.5	0.5	0.5	2.5	1	2.5	2	0.5	2.5
Bio1 Annual Mean Temperature	0	0	0.5	1.2	0	0.5	~	~	~
Bio2 Mean Diurnal Range	0.8	0.2	0.4	3.7	0.6	0	1.2	0.3	0.6
Bio3 Isothermality	32.6	32	29.7	38.9	14.2	50.7	~	~	~
Bio4 Temperature Seasonality	0.8	0.7	0.2	2.3	9.9	0	41.1	18.9	43.5
Bio5 Max Temperature of Warmest Month	0.9	3.7	3.7	1.5	2.3	4.4	~	~	~
Bio6 Min Temperature of Coldest Month	2.2	2.3	0.1	2	0.1	0	~	~	~
Bio7 Temperature Annual Change	19.7	23.7	27	20.1	1.2	25	33.6	2.7	25.7
Bio8 Mean Temperature of Wettest Quarter	0	0.1	0	0.1	0	0	0.4	0.8	0.6
Bio9 Mean Temperature of Driest Quarter	1.1	3.5	1.6	1.5	0.7	0	~	~	~
Bio10 Mean Temperature of Warmest Quarter	1	2.5	0.3	1.6	0.5	0	~	~	~
Bio11 Mean Temperature of Coldest Quarter	0.1	0.3	0.9	0.1	0.2	0	~	~	~
Bio12 Annual Precipitation	0.6	0.5	0	2.6	0.9	0	0.6	2.9	0
Bio13 Precipitation of Wettest Month	5	2.5	5.3	1.6	0.3	0.5	~	~	~
Bio14 Precipitation of Driest Month	10.1	5.1	14.1	5.1	19.6	15.5	~	~	~
Bio15 Precipitation Seasonality	3.8	1.5	1.1	2.9	3.9	1.4	~	~	~
Bio16 Precipitation of Wettest Quarter	0.3	0.1	0.9	0.3	2	0.1	1.2	4.4	1.1
Bio17 Precipitation of Driest Quarter	2.1	3.1	0.8	2.5	31.3	0.3	12.2	56.8	21.2
Bio18 Precipitation of Warmest Quarter	14.4	16.7	12.1	8	10.4	1.3	6.9	10.4	3.4
Bio19 Precipitation of Coldest Quarter	4.5	1.6	1.4	4.1	1.8	0.2	2.9	2.7	3.9
Mean AUC Value	0.873	0.841	0.824	0.850	0.793	0.816	0.802	0.792	0.778

L = Linear, Q = Quadratic, H = Hinge, P = Product, T = Threshold

Table 2. List of environmental variables in the Philippines used for the three model approach performed for this study and its permutation importance. Model approach 1 included all 19 bioclimatic variables with default regularization setting; model approach 2 increased the regularization multiplier suggested after ENMeval calculations; Model approach 3 included the selected 9 bioclimatic variables after autocorrelation

	Model Approach 1			**Model Approach 2**			**Model Approach 3**		
	Arcyria cinerea	***Perichaena depressa***	***Hemitrichia serpula***	***Arcyria cinerea***	***Perichaena depressa***	***Hemitrichia serpula***	***Arcyria cinerea***	***Perichaena depressa***	***Hemitrichia serpula***
Feature type	Auto	Auto	Auto	LQHPT	LQ	H	LQH	LQ	LQHPT
Regularization multiplier	0.5	0.5	0.5	2.5	1	2.5	2	0.5	2.5
Bio1 Annual Mean Temperature	0	0	0	0.7	0	0	~	~	~
Bio2 Mean Diurnal Range	4.3	0.7	2.6	1.8	10.3	0	16.2	0.1	0
Bio3 Isothermality	19.3	13.2	39.2	38.6	35.4	55.3	~	~	~
Bio4 Temperature Seasonality	3.5	7.3	1.6	2.1	6.2	0	14.7	36.4	33.5
Bio5 Max Temperature of Warmest Month	5.2	8.2	9.2	9.1	14.6	9.1	~	~	~
Bio6 Min Temperature of Coldest Month	0.9	1.9	1.6	1.7	0	0	~	~	~
Bio7 Temperature Annual Change	26.5	23.7	30.9	13.8	15.7	33.7	55.7	13.5	32.2
Bio8 Mean Temperature of Wettest Quarter	0	0.3	0	0.1	0	0	1.1	0.8	1.6
Bio9 Mean Temperature of Driest Quarter	5.8	16.1	3.7	5.8	10.2	0	~	~	~
Bio10 Mean Temperature of Warmest Quarter	2.7	9.2	1.5	2.5	0	0	~	~	~
Bio11 Mean Temperature of Coldest Quarter	0.3	2.2	4.7	0.2	0	0.1	~	~	~
Bio12 Annual Precipitation	2	4	0	3.7	0.9	0	1.1	10.1	0
Bio13 Precipitation of Wettest Month	0.1	0.8	0.1	0.5	0.2	0.1	~	~	~
Bio14 Precipitation of Driest Month	3.5	3.7	0.5	2.2	0.1	0.8	~	~	~
Bio15 Precipitation Seasonality	14.3	1.5	0.1	9.2	0.1	0.4	~	~	~
Bio16 Precipitation of Wettest Quarter	3.1	0.2	0.8	0.1	0	0	2.9	2	4.2
Bio17 Precipitation of Driest Quarter	0.9	0.6	0.7	0.9	0	0.4	0.1	2.6	28.1
Bio18 Precipitation of Warmest Quarter	2.3	3.4	1.5	4	5.3	0	5.3	27.1	0.1
Bio19 Precipitation of Coldest Quarter	5.4	2.9	1.5	3	0.8	0.2	2.9	7.5	0.3

The contribution of these models to the conservation of Philippine myxomycete communities

Several Southeast Asian myxomycetes studies (the Philippines, Dagamac et al. 2012; Thailand, Ko et al. 2011; Vietnam, Novozhilov et al. 2018) are also indicating the relationship between seasonality and myxomycete diversity. These findings revealed that the amount of successful fruiting varies between dry and wet seasons, as it is common in tropical regions (Rojas and Stephenson 2007; Lado et al. 1999). Furthermore, the habitat suitability using the three model approaches of all myxomycete species clearly suggest the range expansion to the northern part of Luzon and the Southern part of Visayas. Interestingly, suitable areas range from moderate to very high suitability, particularly in the region of Northern Mindanao, where there are limited myxomycete surveys conducted until this date (Buisan et al. 2019; Buisan et al. 2020). This study can help understand the possible distribution patterns of the three bright-spored myxomycetes species and will now provide the most important baseline data that can serve as a useful model for better conservation efforts in many of the country’s terrestrial habitats. The more generalist species, like in the case of *Arcyria cinerea*, might not be directly affected byany anthropogenic disturbance since high tolerance of species occurrence (which may include phenotypic plasticity as a means of adaptation) has been accounted for the species. However, various human activities such as deforestation, land-use change, and urbanization which are already occurring in the majority of the predicted suitable habitats, can have a significant impact on the current predicted species distribution of the more occasionally occurring myxomycetes like *Perichaena depressa* and *Hemitrichia serpula*. As a response, several precautions must be put in place to protect the habitats of these microorganisms in locations where they might be expected to flourish.

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