

Climate Change Impact on Fungi – can species distribution modeling indicate shiitake's (*Lentinula boryana*) reaction to a changing climate?

By Rachel Pringle

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Introduction

Apart from being an important crop in agriculture and medicinal cultivation, fungi play many essential roles in the ecosystem. For example, saprotrophic fungi perform ecosystem functions such as decomposition which drives many geochemical processes (A'Bear, Jones & Boddy, 2014). In addition, other fungi – such as mycorrhizal fungal communities - are an important resource for forests to fight infection as well as access nutrients and develop tolerance to environmental stressors via their symbionts and relationships (Jansa, Smith & Smith, 2008). Undoubtedly, fungal biodiversity and conservation is essential for maintaining ecosystem health and resilience which is of increasing importance in a world affected by climate change.

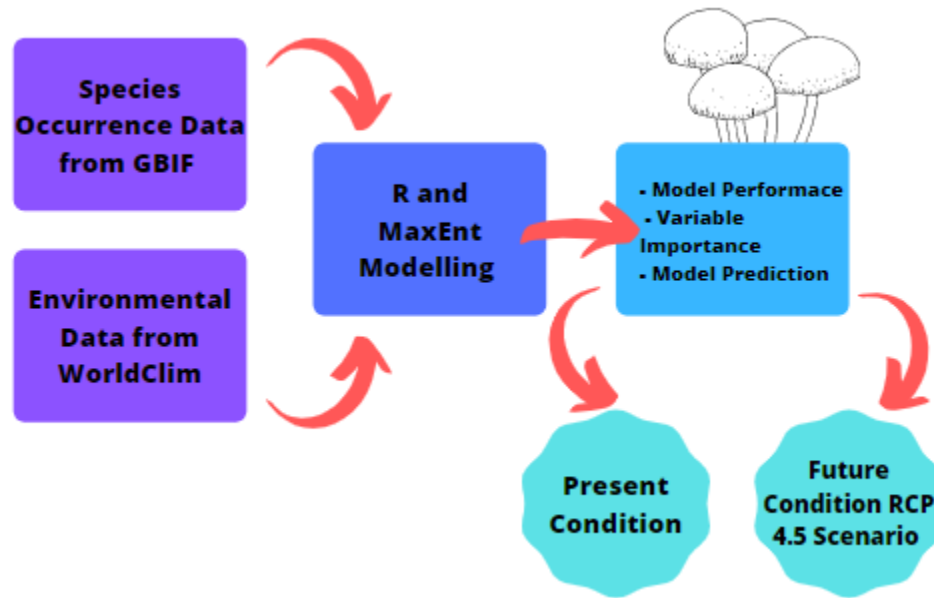
Despite their critical role in the environment as well as their agricultural value, fungi are rarely considered in climate modelling and predictions. This is primarily due to their complex interactions with other soil-dwelling microorganisms and the fundamental lack of fungal biodiversity knowledge. Because of this, there is a demanding need for fungi to be explicitly included in climate scenario and species distribution modelling. As an attempt to fill this gap in ecological knowledge, this research will focus on species distribution modelling of the shiitake species *Lentinula boryana* – a relative of the widely cultivated East-Asian *Lentinula edodes* – found in the Americas. As a saprotrophic fungal species, *L. boryana* is expected to contribute towards driving many geochemical processes, for example, by decomposition. Additionally, the shiitake (*Lentinula* spp.) is an important agricultural product for human consumption and medicine causing it to comprise approximately 22% of all fungiculture world-wide (Royse, Baars & Tan, 2017).

The purpose of this research is to determine the distribution of *Lentinula boryana* (fig 1) using occurrence data from the GBIF database. Additionally, the distribution of *Lentinula boryana* will be used to predict the species response to certain bioclimatic variables under the IPCC5 RCP45 scenario using MaxEnt. Due to the contribution of slope aspect on fungal distribution, it can be inferred that bioclimatic factors such as precipitation and temperature will have an impact on *Lentinula boryana* distribution and will be important variables for predicting climate change impacts (Geml, 2019, Asemaninejad, Thorn, Branfireun & Lindo, 2018). Therefore, it is hypothesized that with increasing temperature and precipitation changes in the tropical Americas in the RCP 45 scenario, *Lentinula boryana* will experience a shift and change in distribution decreasing its habitat suitability.



Figure 1: Photo of *Lentinula boryana* collected in Mexico and preserved by the University of Tennessee fungal herbarium

Methodology & Results



Occurrence data

As reported by Thon, M. & Royse, D in their 1999 paper, *Lentinula boryana* is primarily found in the tropical Americas. This was confirmed by the species occurrence data obtained from GBIF. Human observations as well as material samples, living specimens, and preserved specimens were used as occurrence data (fig 2). Once the occurrence data was obtained, it was cleaned and all excess information – such as repeats, unrelated data, and occurrences with no coordinates – were removed in excel. Additionally, a singular occurrence in Russia was removed due to the unlikelihood that it truly occurred there and to optimize the area of interest to the tropical Americas. After cleaning the data, *L. boryana*'s distribution was mapped using R against the WGS84 coordinate system and bioclimatic variable 1 – the mean annual temperature (fig 3).



Figure 2: Map of *Lentinula boryana* distribution obtained from GBIF indicating its distribution primarily in the tropical Americas as well as spots in North America. One occurrence was documented in Russia but was later determined to be a false occurrence

Spatial Bias

Unfortunately, there is a lack of fungal biodiversity knowledge globally. On top of this, most fungal biodiversity knowledge resides in Scandinavian regions and other first-world countries (Heilmann-Clausen et al., 2014). Due to *L. boryana*'s distribution occurring primarily in the tropical Americas, occurrence data could be skewed due to a lack of ecological data collected within the Amazon. It should be noted that the occurrence data of *L. boryana* may be biased due to *L. boryana*'s niche being found in central America/south America which are areas that are difficult to conduct research in and vastly understudied. Despite the risk of spatial bias, it is confirmed in literature that *Lentinula boryana* exhibit an ecological niche in tropical America. Due to *L. boryana*'s saprotrophic nature, it's ecological niche would most likely be realized in an environment with high biomass production and one that requires rapid nutrient cycling – such as the tropical Americas. Lastly, because of *Lentinula* spp. dependence on certain woody forests, the distribution of *Fagaceae* trees in Central America could account for the high abundance of *L. boryana* present (Manos & Stanford, 2001).

Environmental data

Obtained from WorldClim Global Climate Database, nineteen bioclimatic variables were tested for autocorrelation. Of the nineteen, five environmental variables had an autocorrelation value below 0.7 and were interpreted as important for *L. boryana* distribution (table 1). These five variables, again seen in table 2, included Bio08 (Mean Temperature of Wettest Quarter), Bio14 (Precipitation of Driest Month), Bio15 (Precipitation Seasonality), Bio18 (Precipitation of Warmest Quarter), and Bio19 (Precipitation of Coldest Quarter).

Because fungal distribution is heavily dependent on slope aspect, one method to determine which bioclimatic variables are relevant in *L. boryana* distribution is to identify the variables along the slope (Geml, 2019). Environmental factors that vary among these gradients is precipitation and temperature driving the distribution of fungal communities (Geml et al., 2014). Therefore, after ensuring that they



Figure 3: Map of *Lentinula boryana* distribution obtained from GBIF mapped in ArcGis.

were not autocorrelated, the environmental variables in table 2 were chosen. Furthermore, the five bioclimatic variables were tested for multicollinearity via the variance inflation factor test which confirmed – with a value below 10 – that they were independent variables.

	Bio08	Bio14	Bio15	Bio18	Bio19
Bio08	1	0.07012	0.034913	0.283597	0.192968
Bio14	0.07012	1	-0.67902	0.561105	0.573271
Bio15	0.034913	-0.67902	1	-0.27656	-0.28873
Bio18	0.283597	0.561105	-0.27656	1	0.212968
Bio19	0.192968	0.573271	-0.28873	0.212968	1

Table 1: Autocorrelation table with Pearson correlation values.

*Table 2: (bottom left) Bio08, Bio14, Bio15, Bio18, and Bio19 were used from WorldClim to predict future distribution of *L. boryana*. All had a VIF below 10*

Environmental Variable	Description	VIF
Bio08	Mean Temperature of Wettest Quarter	1.17
Bio14	Precipitation of Driest Month	3.80
Bio15	Precipitation Seasonality (Coefficient of Variation)	2.00
Bio18	Precipitation of Warmest Quarter	1.75
Bio19	Precipitation of Coldest Quarter	1.69

Model settings

For this SDM, the data from the IPCC5 climate projections for the representative concentration pathway (RCP) 4.5 was used. Under the 4.5 scenario, it is assumed that emissions of carbon dioxide will peak around the year 2040 and steadily decrease thereafter. The data was obtained from the WorldClim database with a five-minute resolution. The future models would then be representative of the species distribution in the year 2050.

Model output

Using the occurrence data from GBIF, present climate, and future RCP 4.5 climate scenarios from WorldClim, the following output was generated in MaxEnt. The MaxEnt output was replicated five times and resulted with an average AUC of 0.847 indicating that the model had high reliability (*fig 4*). According to the analysis of variable contribution, variable Bio08 contributed most in the MaxEnt model (32%) with Bio15 and Bio18 trailing close behind it (27% and 23% respectively). The response curves generated by MaxEnt demonstrated that Bio8 exhibited an optimal value for mean temperature of the wettest quarter while Bio14 and Bio15 demonstrated threshold values for precipitation of the driest month and precipitation seasonality (*fig 5*). These response curves can be reinforced by literature; for example, it is known that this distribution of certain fungal species is heavily dependent on temperature (Geml et al., 2014) and increased precipitation is linked to a decrease in fungal abundance and diversity providing a threshold for survival (Hawkes et al., 2010). Aside from potential spatial bias, much of the model contains predictions in regions that can be trusted. As indicted by MaxEnt, predictions made in regions such as

north-west Africa and Greenland must be treated with caution; however, very few *L. boryana* occurrences are predicted in the regions (fig 6).

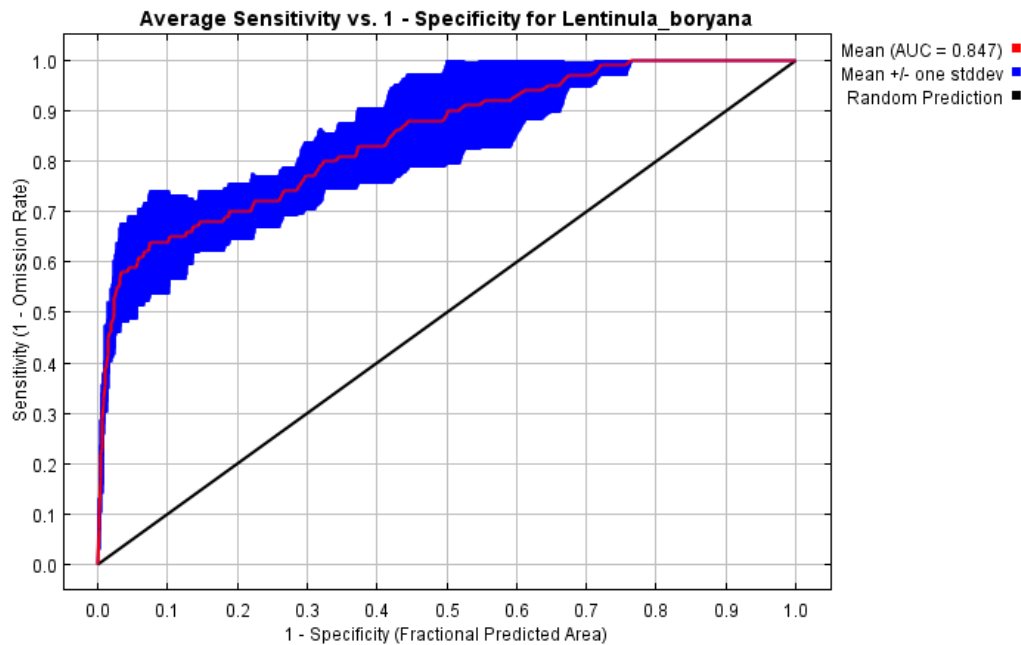
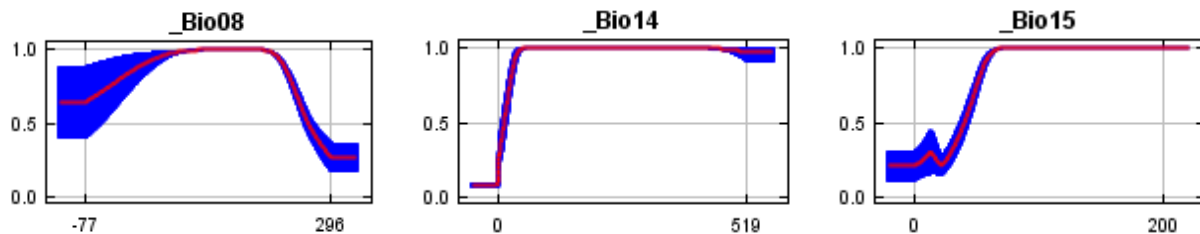


Figure 4: (above) Area Under the Curve (AUC) graph indicating high reliability of model with an average AUC of 0.847

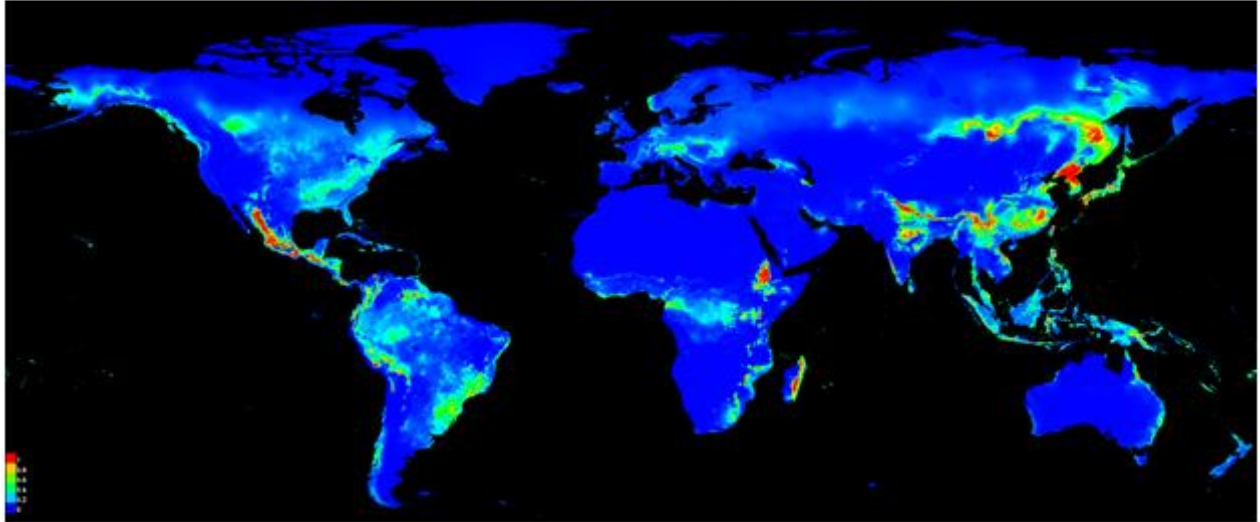
Figure 5: (below) Response curves generated by MaxEnt demonstrating an optimal value for Bio8 and threshold values for Bio14 and Bio15



SDM Projections

After running in MaxEnt, present-climate potential distribution maps and future-climate potential maps based on the RCP 4.5 climate scenario were generated as an average of all five replicates (fig 6). This scenario is based on carbon-dioxide emissions reaching a peak in 2040 and declining thereafter. In addition to *L. boryana*'s realized distribution in the tropical Americas, MaxEnt also predicted a possible fundamental niche in areas of Asia and Oceania. The future SDM of *L. boryana* predicts a shift in distribution such as a decrease in population in south-east Brazil and a decrease in abundance around Mexico. The model appears to have not predicted a substantial change in distribution in Asia and Oceania. Looking at *L. boryana*'s area of interest, the decrease in species abundance in Mexico as well as in Brazil can be seen more clearly (fig 7).

Present SDM of *L. boryana*



Future SDM of *L. boryana* RCP 4.5

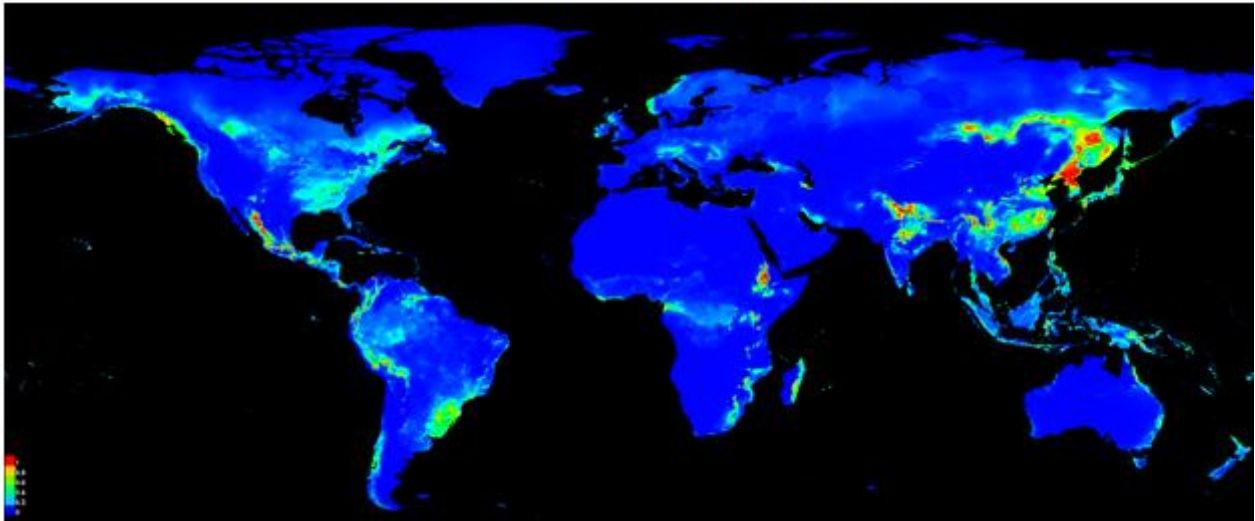


Figure 6: MaxEnt output of *L. boryana* species world-wide fundamental niche distribution model based on five replicates. The top map represents the fundamental niche based on present bioclimatic variables. The bottom map represents the predicted fundamental niche based on the RCP 4.5 climate scenario.

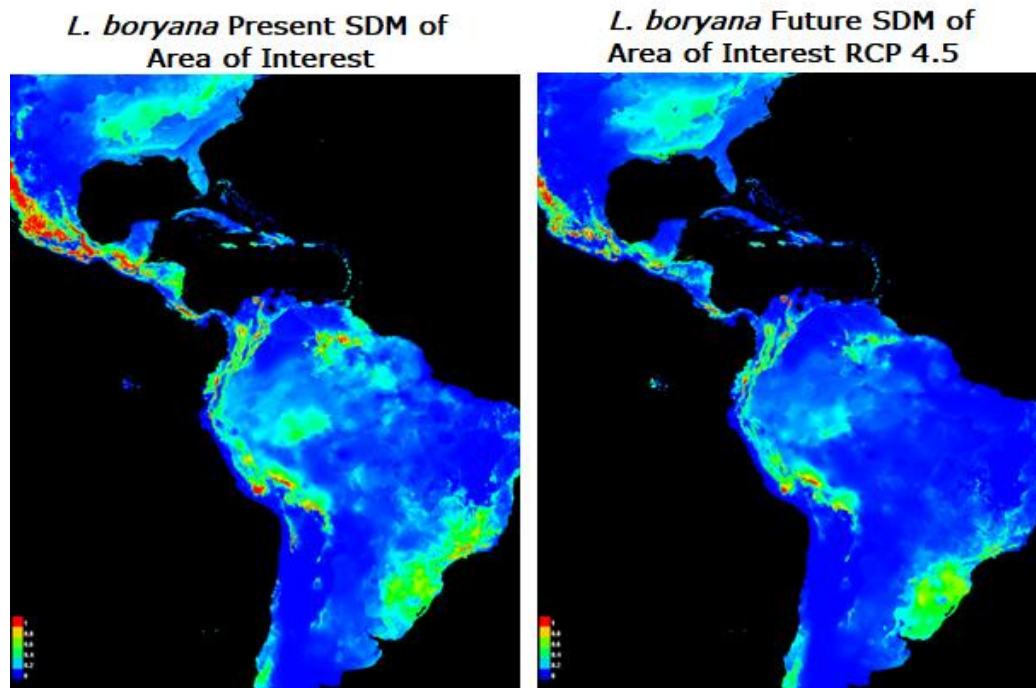


Figure 7: MaxEnt output of *L. boryana* species area of interest fundamental niche distribution model based on five replicates. The left map represents the fundamental niche based on present bioclimatic variables. The right map represents the predicted fundamental niche based on the RCP 4.5 climate scenario.

Change in Habitat Suitability

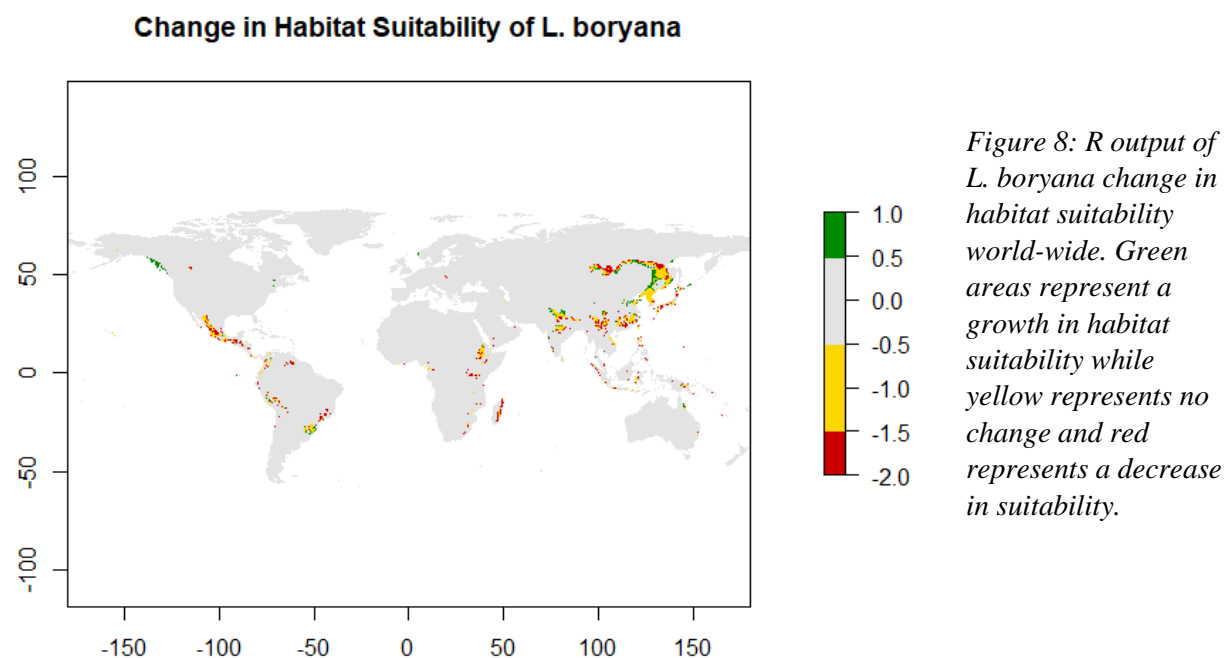


Figure 8: R output of *L. boryana* change in habitat suitability world-wide. Green areas represent a growth in habitat suitability while yellow represents no change and red represents a decrease in suitability.

Changes in Habitat Suitability of *L. boryana*

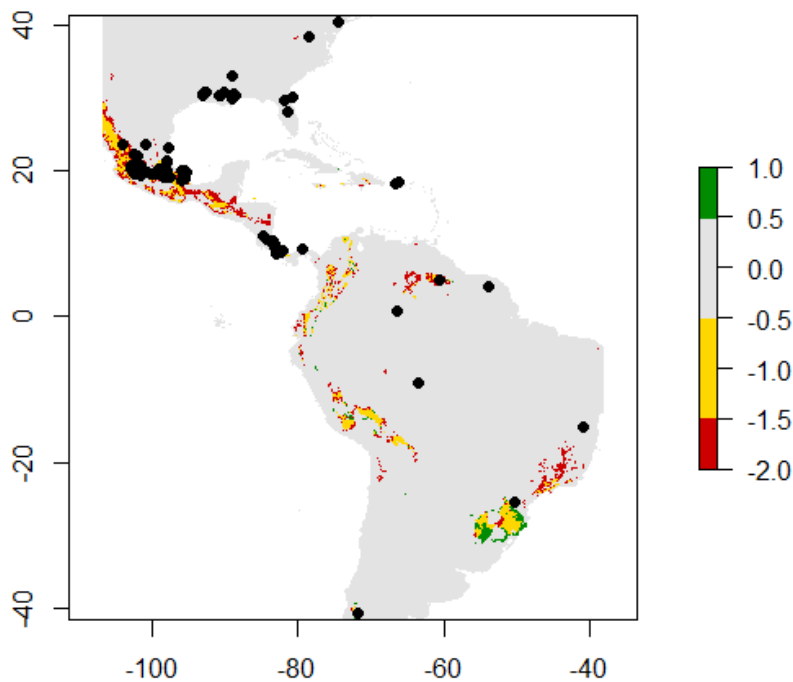


Figure 9: R output of *L. boryana* change in habitat suitability in the area of interest. Green areas represent a growth in habitat suitability while yellow represents no change and red represents a decrease in suitability. Black dots represent occurrence data from GBIF.

As predicted by MaxEnt, there will be a change in habitat suitability for *L. boryana* world-wide as well as locally. Indicated in figure 8, there appears to be no net-increase in *L. boryana* abundance world-wide. When focusing in on the area of interest of *L. boryana*, there appears to be net-decrease in abundance in areas around Mexico (fig 9). Areas in South America vary in *L. boryana* abundance remaining the same as well as decreasing. Overall, *L. boryana* habitat suitability does not increase and appears to have a net-decrease. These results were not quantified.

Threshold Table

To reinforce the credibility of the MaxEnt SDM, threshold values were used to determine how severely *L. boryana* was affected by climate change under the RCP 4.5 scenario. For this model, the threshold “maximum test sensitivity plus specificity” was chosen due to it having the lowest p-value in all five replicates (rep0 = 1.825E-16, rep1 = 1.776E-6, rep2 = 2.736E-15, rep3 = 3.166E-12, rep4 = 2.237E-11). Using an average threshold value of 0.517, a present threshold SDM and future threshold SDM under the RCP 4.5 scenario were generated (fig 10). Due to very little difference between the present and future threshold distributions. It can be inferred that climate change is not the biggest threat to *L. boryana* biodiversity and abundance.

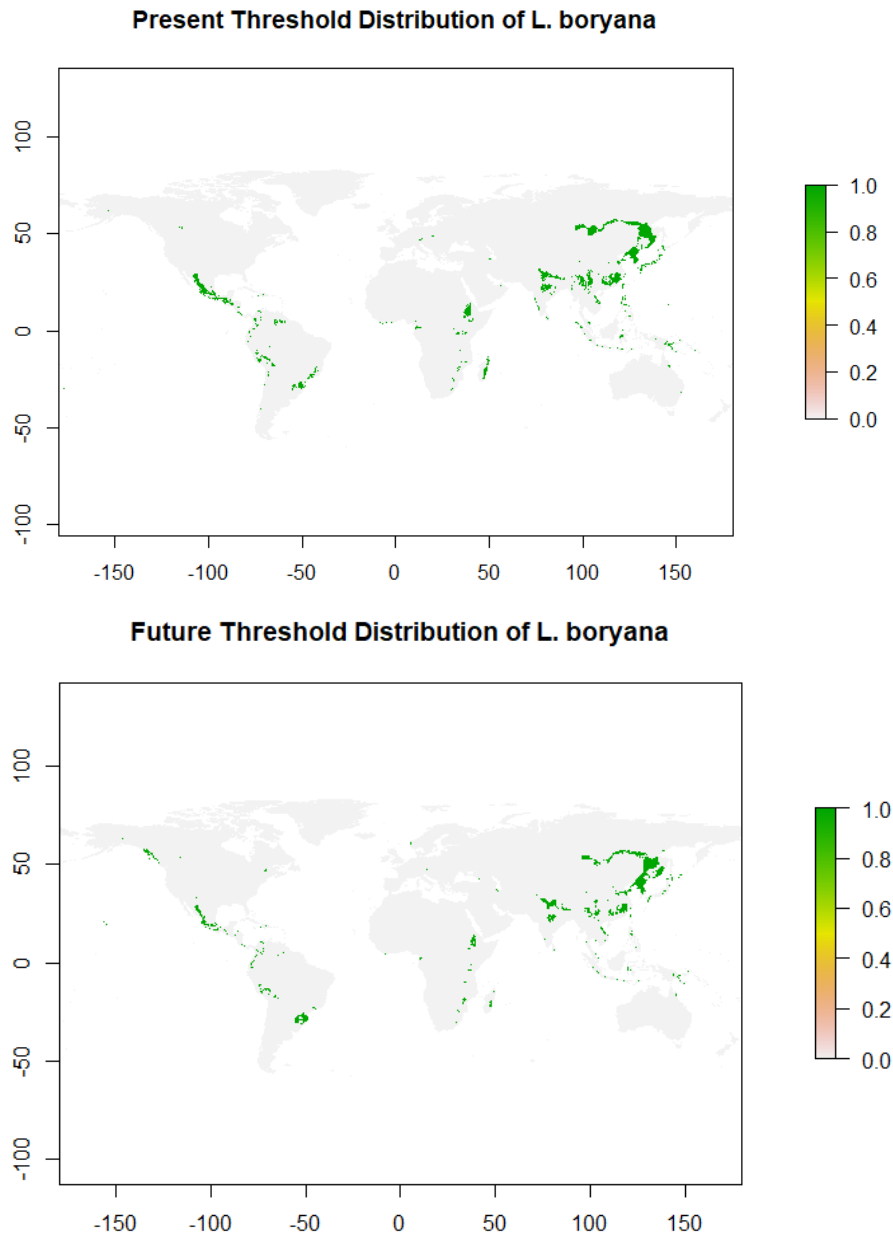


Figure 10: Output of *L. boryana* threshold distribution in R. Green areas indicate presence data. The threshold used was “Maximum Test Sensitivity plus specificity” from the MaxEnt output.

Species Relocation

As indicated by the world SDM of *L. boryana* by MaxEnt, a suitable habitat for this species could potentially be in Asia and Oceania. Given the chance to relocate – by anthropogenic means – it has a possibility of occupying these predicted regions. However, it should be noted that an ally of *L. boryana* – *Lentinula edodes* (the common shiitake) – already exists in these regions of Asia and Oceania (Thon & Royse, 1999). Therefore, *L. boryana* may not be suitable to compete with the native shiitake. Further research needs to be done to address the possibility of *L. boryana* relocation to Asia and Oceania.

Discussion & Conclusion

It is well known that fungi play essential roles in the ecosystem such as driving geochemical pathways and forming intricate relationships with surrounding plant-life and other organisms. However, despite their importance, very little is known about how they will be affected by anthropogenic influences such as climate change. This research was an attempt to identify the distribution of the shiitake species *Lentinula boryana* and clarify how climate change could potentially influence its habitat suitability and distribution.

The occurrence data obtained from GBIF indicated that *L. boryana*'s distribution occurs primarily throughout tropical America with high concentrations in Mexico. Using bioclimatic data from the WorldClim database, the RCP 4.5 climate change scenario was combined with GBIF occurrence data and modelled in MaxEnt to determine how *L. boryana* would be impacted on the basis of Bio08 (Mean Temperature of Wettest Quarter), Bio14 (Precipitation of Driest Month), Bio15 (Precipitation Seasonality), Bio18 (Precipitation of Warmest Quarter), and Bio19 (Precipitation of Coldest Quarter). The purpose of choosing these variables were due to fungi's distribution primarily depending on slope aspect which includes environmental factors such as altitude, precipitation, and temperature.

After modeling in MaxEnt, it was found that *L. boryana* had a potential fundamental niche in not only the tropical Americas but also Asia and Oceania. This was interesting because *L. boryana*'s close ally – *Lentinula edodes* – is known to occupy these regions. After generating the future RCP 4.5 models, a change in *L. boryana*'s distribution was found mostly indicating a shift in habitat in the tropical Americas. Therefore, the null hypothesis was rejected due to the visible decrease in habitat suitability. This data was not quantified but was drawn based on observation.

Because the kingdom fungi are vastly understudied, various complications and spatial biases could be encountered during species distribution modelling. One potential source for spatial bias is the lack of observations made for this species due to its niche location existing in areas with a lack of access to modern laboratory equipment and difficult terrain. Additionally, very little fungal taxonomy has been conducted as compared to other organisms partially due to difficulty in locating and identifying species. Fortunately, this is likely to change with the help of environmental DNA and DNA metabarcoding.

References

- A'Bear, A., Jones, T., & Boddy, L. (2014). Potential impacts of climate change on interactions among saprotrophic cord-forming fungal mycelia and grazing soil invertebrates. *Fungal Ecology*, 10, 34-43. doi: 10.1016/j.funeco.2013.01.009
- Asemaninejad, A., Thorn, R., Branfireun, B., & Lindo, Z. (2018). Climate change favours specific fungal communities in boreal peatlands. *Soil Biology And Biochemistry*, 120, 28-36. doi: 10.1016/j.soilbio.2018.01.029
- Geml, J. (2019). Soil fungal communities reflect aspect-driven environmental structuring and vegetation types in a Pannonian forest landscape. *Fungal Ecology*, 39, 63-79. doi: 10.1016/j.funeco.2018.12.005
- Geml, J., Pastor, N., Fernandez, L., Pacheco, S., Semenova, T., & Becerra, A. et al. (2014). Large-scale fungal diversity assessment in the Andean Yungas forests reveals strong community turnover among forest types along an altitudinal gradient. *Molecular Ecology*, 23(10), 2452-2472. doi: 10.1111/mec.12765
- Hawkes, C., Kivlin, S., Rocca, J., Huguet, V., Thomsen, M., & Suttle, K. (2010). Fungal community responses to precipitation. *Global Change Biology*, 17(4), 1637-1645. doi: 10.1111/j.1365-2486.2010.02327.x
- Heilmann-Clausen, J., Barron, E., Boddy, L., Dahlberg, A., Griffith, G., & Nórdén, J. et al. (2014). A fungal perspective on conservation biology. *Conservation Biology*, 29(1), 61-68. doi: 10.1111/cobi.12388
- Jansa, J., Smith, F., & Smith, S. (2008). Are there benefits of simultaneous root colonization by different arbuscular mycorrhizal fungi?. *New Phytologist*, 177(3), 779-789. doi: 10.1111/j.1469-8137.2007.02294.x
- Manos, P., & Stanford, A. (2001). The Historical Biogeography of Fagaceae: Tracking the Tertiary History of Temperate and Subtropical Forests of the Northern Hemisphere. *International Journal Of Plant Sciences*, 162(S6), S77-S93. doi: 10.1086/323280
- Royse, D., Baars, J., & Tan, Q. (2017). Current Overview of Mushroom Production in the World. *Edible And Medicinal Mushrooms*, 5-13. doi: 10.1002/9781119149446.ch2
- Thon, M., & Royse, D. (1999). Evidence for Two Independent Lineages of Shiitake of the Americas (*Lentinula boryana*) Based on rDNA and β -Tubulin Gene Sequences. *Molecular Phylogenetics And Evolution*, 13(3), 520-524. doi: 10.1006/mpev.1999.0677