

Wood-Inhabiting Fungi of the Eastern Ecuadorian Cloud Forest: Fungal diversity comparison along an altitudinal gradient in the Rio Zuñac reserve

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Abstract

Wood-inhabiting fungi are responsible for the degradation of dead wood, playing a role in nutrient cycling and nutrient transport making them indispensable to their ecosystem's health. Fungi are generally understudied, specifically in the tropics despite its proven hotspot in diversity and the importance of conservation. Wood-inhabiting fungi were investigated in the eastern Andean montane cloud forest of Ecuador to determine the biodiversity, distribution, and relation to an altitudinal gradient. Along multiple ridges of EcoMinga's Rio Zuñac reserve, 13 20x20 meter (0.1-hectare) quadrants between the altitudes of 1300 to 2000 meters were sampled for wood-inhabiting fungi. A total of 175 samples were taken comprised of 36 families and 152 species demonstrating extremely high diversity and low species coverage. Species abundance estimations suggest a much higher quantity of species in the Ecuadorian montane cloud forest than are currently described. Six different altitudes were compared, and it was found that, on a spectrum, communities were neither distinct nor the same provoking the need for more study on the complete effect of altitude and different biotic and abiotic factors.

Resumen

Los hongos que habitan en la madera son responsables de la descomposición de los troncos, siendo la base en el ciclo de nutrientes, además son indispensable para el desarrollo del ecosistema. Generalmente los hongos son poco estudiados, especialmente en los trópicos, donde existe una alta biodiversidad de especies y que se debería prestar más atención sobre la importancia y conservación. La investigación sobre los hongos se realizó en el bosque nublado, en una zona comprendida entre la población de Baños y Puyo, al oriente del Ecuador, para biodiversidad, distribución y tendencia existente en esta zona. La muestra se produjo en la reserva del Rio Zuñac, donde la altura del lugar oscila entre los 1300 a 2000 msnm. Dentro de la investigación se determinaron 13 cuadrantes de 20x20 metros (0.1 ha) dentro de ellos se encontraron 152 especies de 36 diferentes familias en 175 muestras colectados. A pesar de haberse encontrado una alta cantidad de especies, esta muestra representa un bajo porcentaje de la cobertura de especies existentes en la zona. En la investigación se tomó en cuenta seis diferentes altitudes para comparar las comunidades de hongos. Se encontró que las comunidades no fueron lo mismo ni distinta.

Keywords: fungal diversity – species coverage – Ecuador – species accumulation – cloud forests

1 INTRODUCTION

1.1 Background

The kingdom of fungi is one of the most important types of living organisms in the world due to the vital roles to the ecosystem and the influence on human related activities. Fungi are crucial for their tasks in decomposition, nutrient transport, and nutrient cycling making them indispensable to their ecosystem's health¹. Fungi also have great importance in the economy due to their domestic use in baking, brewing, the pharmaceutical

industry, industrial fermentation, and the millions of dollars lost to building material degradation and food spoilage². Their worldwide impact is representative of their massive breadth of taxa with approximately 100,000 described species³. It has been an accepted yet debated hypothesis that there are 1.5 million species of fungus on Earth, but subsequent estimates have ranged from 500,000 to 9.9 million⁴.

The fungal kingdom is comprised of a broad range of sizes, from single celled eukaryotes, in the case of yeast, to the largest and oldest known living organism,



Figure 1. *Gloephyllum* sp1

Armillaria solidipes. The largest known *A. solidipes* has been estimated to cover an area of 9.6 km² and have an age between 1,900 and 8,650 years old⁵. The study of all types of fungus is a daunting endeavor with difficulties finding mycelium networks and identifying individuals. For that reason, this study will only be examining macrofungi. Macrofungi are defined by having fruiting structures, or fruiting bodies, visible to the naked eye².

Macrofungi are comprised of a few structural components. The most rudimentary component is hyphae, thread-like strands that form an interconnected network known as mycelium⁶. Mycelium is the vegetative system of the fungus, responsible for growth and the absorption of nutrients from the environment. Nutrient absorption occurs in two steps. First, hyphae secrete enzymes which break down macromolecules or polymers into monomers. Second, the broken-down nutrients are absorbed into the mycelium by active transport and facilitated diffusion, providing the energy to expand and reproduce⁶. Reproduction of macrofungi is performed by the fruiting body, a spore producing mass of mycelium. Fruiting bodies, commonly called mushrooms, are the classical way to identify fungi according to their characteristics such as gills, pores, teeth, volva, and annulus. Fruiting bodies release spores, the reproductive entity that are commonly dispersed by wind but also by explicit fauna⁷. The fruiting body and spore characteristics described will be used to identify the fungi in this study. When dispersed, spores can land on a variety of substrata including soil, leaf litter, dead wood, and live trees. The spore will successfully germinate if ecological conditions are favorable, and the species has the biological processes necessary to grow on the substratum.

This study focuses specifically on the substratum of wood and their corresponding macro-wood-inhabiting fungi. Certain wood-inhabiting fungi grow discriminately on different host species, level of decay, and ecological position of substrata². These fungi have the ability to grow and decompose wood due to their enzymes



Figure 2. *Macromytilidia* sp1.

that break down lignin, the compound that physically protects cellulose⁷. Thus, they are known as lignicolous fungi. The process of wood decomposition involves several groups of organisms: bacteria, nematodes, protozoa, arthropods, and insects but under normal conditions fungi are the primary agents⁸.

Dead wood has proven to be an essential component of forest ecosystems due to its contributions to organic soil matter, reduction of erosion, and service as a reserve for nutrients and water⁹. The input of dead wood to mature forest ecosystems represents 30-40% of total biomass and it is the job of the wood-inhabiting fungi to recycle this mass¹⁰. There have been numerous studies studying the relationship between wood decay in temperate forests but there is a gap in knowledge around non-pathogenic tropical wood-inhabiting fungi. There is strong conservational need for this information due to the global decomposition of wood releasing CO₂ at 6-9.5 Pg C/year, comparable to fossil-fuel combustion at 9.5 Pg C/year¹¹. Therefore, diversity of wood-inhabiting fungi controlling decomposition could hold broad importance to carbon cycle-climate feedback and implications of climate change¹¹.

Poroid and corticoid wood-inhabiting fungi are macrofungi that have been recognized as a valuable reference point for biodiversity, conservation value, and wood decomposition, likely due to their visibility¹². Unlike temperate zones, little is known surrounding the factors affecting polypore diversity and distribution in the neotropics, hence the conservation of these organisms is difficult¹³.

No individual, species, or population lives in ecological isolation without interactions with the biotic and abiotic components of their complex ecosystem, and fungi is no exception¹⁴. Consequently, the ecological structure of their communities must be studied to detect patterns in fungal diversity. These include host species diversity, precipitation, latitude, soil composition, elevation, and the presence of human activities¹⁵. This investigation will focus on patterns along an elevation gradient while taking into account the effects of human

disturbance on the geographic location.

1.2 Location

This study was conducted in the Rio Zuñac reserve, located inside the Rio Pastaza watershed in the eastern Andean cloud forest of Ecuador. The private reserve belongs to the EcoMinga Foundation, an organization that protects the valley lying between Parque Nacional Sangay and Llanganates. The Rio Zuñac reserve is located on the Andes ridge closest to the Ecuadorian Amazon. The Eastern Andes of Ecuador, specifically at the latitude that the reserve lies, are comprised of montane cloud forests with an elevation range of 1300 to 3000 meters above sea level¹⁶.

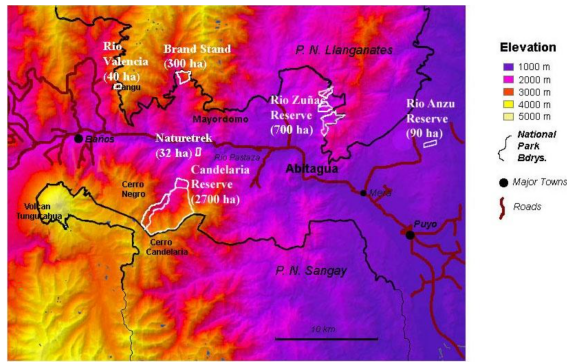


Figure 3. Elevation map of the upper Rio Pastaza watershed with six of the ten EcoMinga reserves indicated¹⁷

The eastern Andes mountain range in Ecuador acts as a barrier to the trade winds that converge on the equator moving west to east. When the prevailing winds meet the eastern Andes, the water vapor condenses to form clouds resulting in consistently high humidity and precipitation¹⁸. The elevational and precipitation gradients in this valley apply varying abiotic factors, influencing niches and biotic diversity. These unique montane cloud forests are filled with lichens, climbing ferns, epiphytes, mosses, and orchids that form thick layers around trees creating microclimates¹⁹. This valley has a greater number of endemic botanical species than the Galapagos Archipelago in a smaller area¹⁶.

This complex ecosystem and geographic location provide optimal conditions for high fungal diversity. A study hoping to disentangle the roles of climatic, edaphic, floristic, and spatial parameters on fungal diversity on a global scale found that distance from the equator and mean annual precipitation had the strongest effects on richness while fungal diversity and endemism peaked in tropical ecosystems²⁰. Additionally, a study in the eastern Andean montane cloud forest in Argentina found that an elevation gradient differentially affected distribution and species richness of four orders of Agaricomycetes³. Despite, Ecuador capturing

practically all the proven parameters of high fungal diversity there are only 845 documented species while China contains approximately 27,900 species in the *Checklist of Fungi in China* database²¹. That being said, there is a massive need for mycological investigations in this unique area of Ecuador to start to unravel the distribution and diversity of fungi for the purpose of conservation and the understanding of the ecosystem as a whole.

1.3 Objectives & Hypotheses

The main objective of this study is to sample and determine the richness and diversity of the fungi that inhabit the wood in the Zuñac river reserve. The altitudinal gradient was studied, the communities at each elevation were compared according to the abundance of families and species. The similarities or differences in the communities provided information on the fungal distribution of macro fungi based on the altitude gradient.

This information forms the basis for a better understanding of the distribution of the fungi that inhabit the wood in a montane cloud forest, the results of which will contribute to the knowledge of wood fungi for future studies and the conservation of the reserve. The results of this abiotic gradient compared to future studies of abiotic factors, such as precipitation, will provide a more complete picture of the diversity and ecology of fungi in tropical montane forests.

2 METHODS

Classic methods were used to study wood macro-fungi specifically classical substrate-based methods, the study was conducted between November 11th and 28th, 2019. The classic methods consist of taking samples while recording the characteristics of the fruit body and the substrate and then proceed to taxonomic identification. Regardless of the recent popularity and advancements in molecular methods, classical methods have advantages in the inventory of fungi in a clearly defined area or substrate as well as the creation of a species list²². Species list can then be used for conservation or comparing communities across regions. Consistent with classical methods, a plot-based study was combined with opportunistic sampling with the purpose of representing the fungi region as a whole and identification of communities.

2.1 Plot-based Study

For the fungus collection, 13 quadrants of 20x20m were established until reaching 0.1-hectares, to effectively cover the entire established area in a reasonable period of time, the methodology was completed with 5 transects of 20-meter near the quadrants. All four sides of

the quadrant were measured with a field measuring tape and cut as limits for the search for macro fungi. The elevation and coordinates of the four corners of each quadrant were recorded using the "My Altitude Application". Each of the fallen, sloping, and vertical dead trees were specifically screened for fungi, without ignoring the live trees. The first two quadrants were reviewed for three hours, therefore, all the remaining quadrants were examined at the same time to apply the same search effort. Clarifying, that the time to describe, measure and take photos of each sample was often the longest to the established time. Therefore, the quadrants with more samples had less search effort.



Figure 4. The distribution of quadrants and transects according to meters above sea level.

With the purpose of the study being to identify changes in fungal community according to altitude, locations for the quadrants were placed about every 100 meters of elevation, always near the trail. Two quadrants were performed for each 100 meters of elevation

besides 1400, 1600, and above 2000m. The fluctuations to every 100 meters and duplicate quadrants were due to the high variability of the region. Some stretches, specifically the altitudes below 1700 meters, were recently disturbed in the interest of accessibility for cattle and agriculture, therefore dense in low vegetation. On the other hand, high altitudes were extremely steep making it impossible to navigate uniformly in search of fungi. Thus, the primary forest search consisted of 8 quadrants between 1700-2000m. The secondary forest search consisted of 4 quadrants from 1300-1500m. To effectively represent the extent of the region five transects were performed between 2092-2210m following the same methods without the physical quadrant for equal sample effort.

Sampling was done with the purpose of fungal identification. When a fruiting body was encountered inside the quadrants, first photos of the top and underside were taken. This provided an unaltered representation of the fungi before any possible damage occurred when the sample was removed from the substratum. The sample was given a sample number according to the quadrant and a brief description based upon fruiting body characteristics. The substratum was then observed. The wood was classified as alive or dead, whether it was on the trunk or branches, the bark intactness, level of decomposition, the diameter, and whether it was lying on the ground, upright, or suspended. The sample was then taken by cutting the fruiting body from the substratum with a pocketknife. The sample was then carefully wrapped in wax paper, keeping the characteristics intact, and then placed in a labeled paper bag. All samples were placed in a hard sample box for protection and organization.



Figure 5. *Oxyporus sp1.*

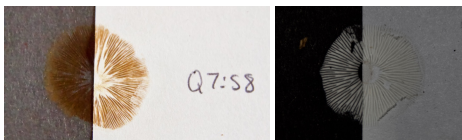
The samples were taken back to the station where they were organized, and the characteristics were described in detail. All of the fresh fruiting bodies were photographed with a white or black background and a penny for scale, as seen in Figure 5. For the wood-inhabiting fungi that had a cap or visible spores present, a spore print was attempted. The stalks of the capped mushrooms were cut off and placed equally on white

Table 1 Example sample taken. The sample number indicates that it is the third individual from Quadrant 8 (located from 1800-1815m). Later identified as *Oxyporus* sp1. Figure 5

Sample Number	Q8, S3
Description	Cantaloupe orange radiating disk polypore with spinach green stains on top face
Substrata	Dead tree
Position	Suspended
Bark Intactness	3
Level of Decomposition	1
Diameter (cm)	17.2
Growth Habit	Gregarious
Spore Dispersal	Porous

and black construction paper, as seen in Figure 6. The samples were left for 24 hours and then unveiled. The color of the spores was noted. The handheld microscope was also used to examine spores and describe the shape when possible.

Due to the lack of materials and success in previous studies, it was not attempted to dry the fungi by stovetop or other mechanical methods in the field²³. The larger fruiting bodies were placed in the sun to dry, if the weather allowed, and were then moved in the research station where open windows allowed for wind drying. The dry fungi were then placed in labeled envelopes and stored to take back to Quito.

**Figure 6.** Examples of successful spore prints.

After the 3-week collection period, the samples were taken to Quito in their paper envelopes and deposited in the National Herbarium of Ecuador, part of the National Institute of Biodiversity. Some samples were adequately dehydrated in a fungus dryer, it can be seen in the description (Table 1) and some characteristics taken in the field phase, were used for identification. Some fungi were identified to the species while others only to the family, therefore a morphospecies name were given to these samples. The dried samples were documented and donated to the Herbario Nacional de Ecuador.

To analyze the diversity of all the samples, diversity indices of Chao1, Chao1-bc, ACE-1, transformed Shannon entropy, and transformed Gini-Simpson were calculated for both the species and families. Each of these diversity indices compares the degree of similarity in species or family between two communities, in this case different altitudes. The species diversity by number of individuals, species coverage, and sample coverage

were presented for the species and families for a study as a whole. To compare the different altitudinal communities, each were given equal weight due to equal sample effort and similarity indices were calculated for each diversity order to ensure comparison from a rare and common point of view. For a diversity order of 0 the Sorensen overlap and Jaccard shared diversity were calculated. For a diversity order of 1 Shannon beta diversity and horn overlap were analyzed. Finally, for a diversity order of 2, Morisita-Horn overlap was used.

3 RESULTS

3.1 Sample Diversity

In the structured collection time of the 13 0.1-hectare plots, 152 samples were documented. In addition to the quadrants, 23 opportunistic samples were taken from trail sides, or plots from the sister study investigating terrestrial fungi, producing a total abundance of 175. 40 of the samples were identified to species, 117 were given morphospecies to the genus, and 18 were given morphospecies to the family.

The Chao1 biodiversity index is a species richness estimator which uses the number of singletons (F1) and doubletons (F2), due to missing species information being concentrated in the low frequency accounts²⁴. The coefficient of variation (CV) measures the heterogeneity of a sample, the higher the more heterogeneous²⁵. A CV of 1.059 and 1.46 shows that the detection probability was not equal for all species, indicating a highly heterogeneous community. For this reason, the Chao1 was treated as the estimation's lower bound rather than the corrected Chao1-bc which is more accurate for a homogenous community. The modified Abundance-based Coverage (ACE-1) estimator uses the information contained at higher frequencies (f_3 - $f_{cutt\ off}$) and was treated as the point estimate due to its sensitivity to heterogeneous communities²⁶. The lower bound (Chao1) was used to calculate the undetected number of species and

Table 2 Biodiversity indices of all plots, altitudes, and opportunistic samples according to species and families

	Species	Family
Richness	152	36
Abundance	175	175
Singletons (F1)	141	12
Doubletons (F2)	5	6
Chao1	1800.39	50.00
ACE-1	3059	52.41
CV	1.06	1.46
Undetected #	1648	14.00
Undetected %	90.78	28.00

families ($Chao1 - Richness = Undetected\ number$).

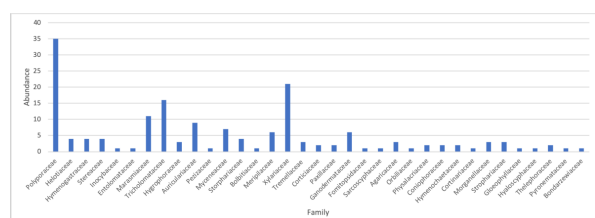


Figure 7. The abundances of each family present of all samples.

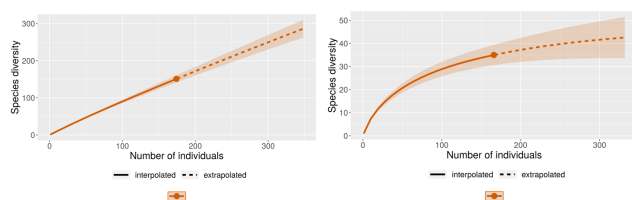


Figure 8. The sample-sized based rarefaction and extrapolation diversity curve of the species (left) and families (right) of all samples.

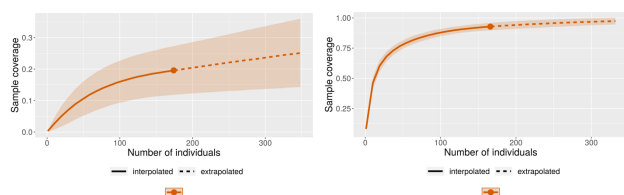


Figure 9. The sample-coverage based rarefaction and extrapolation sample coverage curve of the species (left) and families (right) of all samples.

3.2 Comparing Altitudes

The observed families were used explicitly to compare communities based upon altitude, because of the large number of species singletons throughout sampling. If species were used for comparison, all the communities, including quadrants of the same altitude, would be considered distinct. The samples from the six altitudes

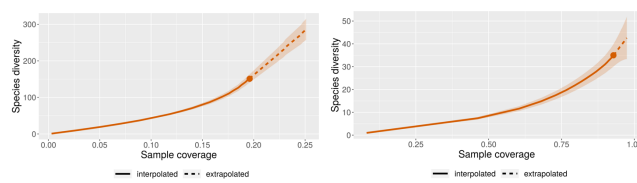


Figure 10. The coverage-based rarefaction and extrapolation diversity curve of species (left) and families (right) of all samples.

with two quadrants each were combined and used as communities for comparison. Shown in Table 2., the sample size of each altitude ranges from 16 to 31 while the number of observed families ranges from 10 to 13. Despite the variation in sample size throughout the altitudes, the number of observed families is consistent, and the sample effort was equal for each.

For the community comparison indices, the communities were all weighted equally. It is suggested that if the species, or family, frequencies, not the actual sizes of communities are the topic of interest, as in this case, equal weights should be used²⁷. To compare strictly family richness, with a diversity order (q) of 0, the Sorensen overlap and Jaccard shared diversity indices were used. These indices, as well as the Horn overlap ($q=1$) and Morisita-Horn ($q=2$) measure on a range of 0 to 1, 0 being identical and 1 being completely distinct. The Shannon Beta diversity exhibits how many distinct communities there are. The 1500/1700m comparison had the highest beta diversity, the most distinct, while the 1300/1500m comparison had the lowest beta diversity, the most similar.

4 DISCUSSION

4.1 Plot-based Study

The overall sampling of the study including all altitudes found an extremely diverse fungal community. Due to the extremely high number of singletons encountered, 141 of 152 samples, the Chao1 estimated a species richness of 1800.39. Therefore, the sampling encountered

Table 3 The sample size and the number of observed families for the two 0.1-hectare quadrants at each altitude.

	Sample Size	Number of Observed Families	Transformed Shannon Entropy	Transformed Gini-Simpson
1300 m	21	10	7.388	5.580
1500 m	31	13	10.833	9.330
1700 m	16	10	8.443	7.111
1800 m	21	13	11.029	9.383
1900 m	22	11	9.105	7.806
2000 m	19	12	10.790	9.757

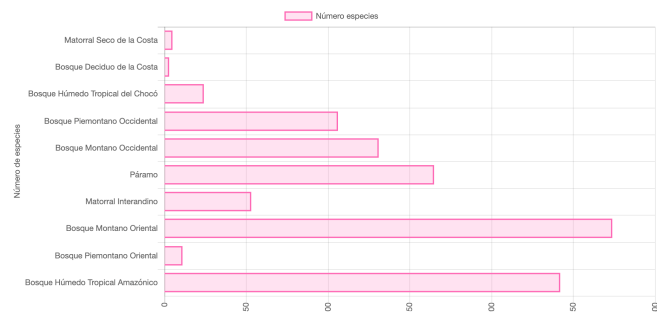
Table 4 Biodiversity indices to compare two altitudinal communities.

	C_{02} , Sorensen Overlap ($q=0$)	U_{02} , Jaccard Shared Diversity ($q=0$)	Shannon Beta Diversity ($q=1$)	$C_{12} = U_{12}$, Horn Overlap ($q=1$)	C_{22} , Morisita- Horn Overlap
1300 / 1500 m	0.5217	0.3529	1.282	0.6411	0.6438
1500 / 1700 m	0.5217	0.3529	1.5208	0.6771	0.7811
1700 / 1800 m	0.3478	0.2105	1.4034	0.5111	0.6742
1800 / 1900 m	0.5000	0.3333	1.4021	0.5124	0.4981
1900 / 2000 m	0.4348	0.2778	1.3968	0.5179	0.5602
1300 / 2000 m	0.4545	0.2941	1.4249	0.4891	0.4272

9.22% of the projected species in the community, based upon the lower bound. If the species richness point estimate was used (ACE-1), the study encountered only 4.97% of the species. Although the quantity of species encountered appears to only represent a small percentage of the community, this confirms the thinking in literature surrounding the extremely high fungal diversity in the tropics and specifically in the montane cloud forest³. Due to the high number of singletons when analyzing species richness and abundance, the diversity of fungal families was also investigated in order to draw further conclusions about the identity of the community.

A total family richness of 36 was found. The lower bound richness estimate was 50 with a point estimate of 52.41 indicating the study encountered 72% of the families present. This demonstrates that the study did effectively cover the sample region in regard to families. If the lower bound estimate of 50 families is correct, this expresses extremely high fungal diversity. The majority of the families had a low abundance of five individuals or less but *Polyporaceae*, *Xylariaceae*, and *Tricholomataceae* showed the highest abundance. The two most abundant, *Polyporaceae* and *Xylariaceae* are known for being common lignicolous, wood-inhabiting fungi in the tropics, consistent with the findings of this study²¹. Furthermore, *Xylariaceae* is the most diverse family in Ecuador with 120 species²⁸. Currently, there are 73 families of fungi on Earth and in a 1.3-hectare total sample area plus opportunistic sampling 49.32% were encountered and an estimated 68.49% were present. Even for

the tropics, this is high biodiversity. Compared to other regions of Ecuador, it has been shown that the eastern montane cloud forest has the highest fungal species diversity²¹.

**Figure 11.** A comparison of species richness to the different regions of Ecuador, from the FungiWebEcuador (Ordoñez, 2018).

First, analyzing the richness and abundance of species, at the species diversity versus the number of individuals it is clear that the study was far from reaching an asymptote noted by the straight line with a small error range on the left graph of Figure 8. This lack of a diversity plateau is consistent with investigations of a longer period of time such as a study focusing on the diversity of wood-inhabiting fungi along a rainfall gradient in Costa Rica⁹. This study lasted one year and concluded that the species ensemble was not completely sampled for any of their sample sites along the rainfall gradient⁹. Comparing this three-week study to that of one year exposes the time and resources necessary

to effectively sample a fungal population. The sample coverage graph (Figure 9) for species demonstrates a sample coverage of 19.73% with large error and small slope of extrapolation. This early plateau indicates high biodiversity and a much higher number of individuals would be necessary to have a complete sample coverage. The sample coverage-based diversity curve (Figure 10) shows that with only a sample coverage of 19.73% the species diversity is increasing rapidly and can be assumed that with a higher sample coverage the diversity will reach an asymptote and indicate extreme diversity.

Second, analyzing the richness and abundance of families, the diversity curve (Figure 8) shows the beginning of an asymptote. This implies that family diversity was well represented in this study and by doubling the sample size the family richness would only be extrapolated to approximately 41 families, a small increase compared to the species. The sample coverage curve (Figure 8) indicates a very high sample coverage and a clear asymptote. Lastly, the coverage-based diversity curve (Figure 10) accurately describes the diversity with the high sample coverage, needing only slight extrapolation. Overall, the fungi families were effectively sampled in this study justified by the high sample coverage and plateau of the family diversity. Compared to the families, the species were less effectively sampled due to the immense diversity present.

4.2 Comparing Altitudes

Each of the six altitudes, which received equal sample effort, had a similar number of observed families with varying abundances. The only two families that were present in all six altitudes, consistent with the most common families overall, were *Polyporaceae* and *Xylariaceae* with varying abundance. For example, at 1300m there were seven individuals of *Polyporaceae* while at 2000m there was one. This difference in abundance was quantitatively shown in the comparison of 1300/2000m with a lower value of 0.4272 for the Morisita-Horn overlap ($q=2$), which puts emphasis on common families. On the other hand, the comparison of 1500/1700m had a high Morisita-Horn overlap of 0.7811 due to the similarity in relative abundance of these two families. The presence of these families at each altitude basically indicates the adaptability of these families to the different humidity, precipitation, and forest structure associated with the altitudes.

None of the six community comparisons using similarity and overlap indices show quantitatively close to identical communities while neither do they show close to completely distinct communities. The communities that were the most distinct were 1500/1700m. They had the highest Shannon beta diversity of 1.5208, the highest Horn overlap ($q=1$) and Morisita-Horn overlap, combined with the largest difference in sample size and

observed number of families. That being said, the difference in these communities is definitely affected by the altitudinal difference, but other factors are involved. The 1500m quadrants were in secondary forest with more low vegetation while the 1700m quadrants were located in mature primary forest with larger trees and less ground cover. In a study comparing distribution of poroid fungi to different forest types found that the different forest types did not form distinct communities, but the areas did have different fungi best explained by the distance between the areas¹³. In this study, and that which compared forest types, the singular gradient focused on could not definitively separate the fungal communities on their own.

Due to the complexity of fungal communities, experts are still trying to formulate effective ways to represent distinctions in communities by gradients and abiotic factors. To effectively understand the communities many factors should be studied together. The problem with this is determining what factor is responsible for differences. For this reason, this study did not undertake both level of human disturbance and altitude, rather only considered the effect of altitude. An example of studying two factors is an investigation in Costa Rica looking at the effect of altitudinal and humidity gradients²⁹. Their main finding was the differences in the polypore communities according to levels of humidity. They also found significant difference according to altitude but the main difference in polypore fauna occurred at the same altitude²⁹. This conflicting community difference shows the difficulty of observing two gradients, or specifically altitude. Likewise, a study on the distribution of polypores in the Brazilian Amazonia found very little similarity among transects in the same primary forest³⁰.

These examples show the difficulty in formulating conclusions in fungal diversity according to traditional gradient measures. The most successful example of this is an investigation looking at species composition of Agaricomycetes according to a vegetational and elevational gradient³. The success of this study was mostly responsible to their defined sample areas. Three completely different altitudes with three completely different types of forest. They found the elevational gradient to have a strong influence on the fungal community, most likely due to the forest types changing the host plants, soil composition, and distribution of substratum³. This shows that a comprehensive approach is necessary when considering the effect of altitude on fungal communities.

5 CONCLUSION

This study successfully provided EcoMinga's Rio Zuñac reserve located in the eastern Ecuadorian montane cloud forest with a morphospecies list of 152 species of

wood-inhabiting fungi through the use of 0.1-hectare plots and opportunistic sampling. This region was found to be incredibly diverse in fungal species with an estimated number of 1800.39 species despite their only being 845 documented species in all of Ecuador²¹. When the diversity was compared on an altitudinal gradient it was neither quantitatively confirmed nor disproven that each 100 meters of elevation was comprised of a distinct fungal community. This study, combined with previous gradient fungal studies, brings about the question of the validity of current fungal study methods. Study of fungal communities is ecologically complicated and therefore requires more consideration to the many abiotic and biotic factors involved. The implications of the wood-inhabiting fungi in the tropics holds large importance in a comprehensive view of forest ecosystems and the carbon feedback cycle that affects climate. Future tropical fungal studies should look at multiple biotic and abiotic factors, such as prevalence and identity of substratum, precipitation, humidity, disturbance level, and botanical identity over a longer sampling period.

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7 EDITOR'S NOTES

This article was peer reviewed.

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