

## Article

# Fungal Diversity and Distribution in the Biodiversity Hotspots of the Western Himalayas

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**Abstract:** The western Himalayan region is a biodiversity hotspot. Although much of the flora and fauna has been documented, there are very few studies on fungal diversity. We present the statistical analyses of the sample collections from the last 150 years of data in the fungarium of the Forest Research Institute. We found that the host tree species—pine, oak, deodar, and spruce, had very high Shannon diversity (SD) and species richness (SR), while Dalbergia and Rhododendron had moderate to low SD and SR values; although sal occurs at lower altitudes, it has high SD and SR values. Among fungal families, the highest SD and SR value was found in Polyporaceae. Hymenochaetaceae, Peniophoraceae, Coleosporiaceae, and Stereaceae also showed SD with moderate SR. Fomitopsidaceae, Cronartiaceae, Ganodermataceae, and Thelephoraceae have low biodiversity and species. Thelephoraceae are distributed above 2000 m altitude, and Ganodermataceae and Hymenochaetaceae have wider distribution ranges, namely, 0–3500 m and 0–5000 m, respectively. The Polyporaceae show diverse variations in species distribution and occur between 0 and 4500 m; Coleosporiaceae and Cronartiaceae around 2000 m; Stereaceae, Meruliaceae, Peniophoraceae, and Fomitopsidaceae occur between 1700 and 1800 m, with all Stereaceae and Fomitopsidaceae having different distribution ranges of up to 5000 m. We found that areas with relatively low rainfall had lower species richness, and vice versa, and that high solar radiation negatively affected fungal density and SR, as observed in the distribution of Thelephoraceae. While families with high SD and SR values such as Polyporaceae were found under relatively high rainfall, moderate solar radiation, and high temperatures. Similar studies need to be undertaken in other parts of the Himalayas and the importance of fungi in ethnobotany needs to be understood to ensure sustainable use.

**Keywords:** fungi; fungal diversity; western Himalayan region; PCA; ANOVA



**Citation:** Yadav, N.; Rakholia, S.; Ali, N.; Yosef, R. Fungal Diversity and Distribution in the Biodiversity Hotspots of the Western Himalayas. *Diversity* **2023**, *15*, 1106. <https://doi.org/10.3390/d15111106>

Academic Editor: Ipek Kurtboke

Received: 16 September 2023

Revised: 16 October 2023

Accepted: 23 October 2023

Published: 24 October 2023



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## 1. Introduction

The Eocene Tibeto-Himalayan mountain ranges, also known as the ‘third pole,’ play an essential role in global climate dynamics [1] and display a complex and high biodiversity [2]. The Himalayan ecosystems are among the most sensitive, especially in the climate change scenario, and among the most vulnerable global biodiversity hotspots [3,4]. Unfortunately, the flora and fauna of the Himalayan regions are among the least studied [5], and the paucity of data on several regions or even groups of organisms is worrying, especially on fungi and their hosts [2].

Kumar et al. [6] noted that fungal studies in India are generally limited and that only 7–8% of the total diversity has been reported to date. They also found that the fungus-to-plant ratio was 10.6:1. They highlighted the urgent need for long-term numerical studies of fungi from the different regions of India, particularly because many contain medicinal chemicals important to human well-being. They pointed out that data for the northwest Himalayas need to be improved and that it is important to collect baseline data because forests are being rapidly deforested even though most regions are protected areas.

There are few studies examining or assessing the biodiversity in the western Indian Himalayan region [1,7], with most studies conducted in the central region of Nepal [2]. The western Himalayan region provides an important habitat for various ectomycorrhizal fungi, and fungal diversity is assessed by collecting sporocarps associated with host roots and often with pine trees [8]. Fungal biodiversity in the Himalayan region is crucial for ecosystem services such as Ganodermataceae, which provide many ecosystem services to local human communities through food and medicinal applications [9].

Families such as the Ganodermataceae also provide diverse ecosystem services. They can significantly influence soil microbial composition, soil properties, tree growth, and medicinal values such as antitumor, anti-inflammatory, and detoxifying [10]. On the other hand, other species of fungal families, such as Polyporaceae and Hymenochaetaceae, are common in this region and regulate ecosystem services such as nutrient cycling by decomposing dead and decaying wood, i.e., they are saprotrophic [11].

In the western Himalayas, in forests of Sarkaghat region of Mandi, Himachal Pradesh, ectomycorrhizal fungi were recently reported to have several families including Fomitopsidaceae, Ganodermataceae, Hymenochaetaceae, Polyporaceae, and Schizophyllaceae. However, the study also noted that more data on their geographical distribution are needed [12]. In central Europe, wood-dwelling fungal communities occur in the Fagus (Beech) and Picea (Spruce) tree communities, in which saprotrophic fungal families (namely, Polyporaceae, Peniophoraceae, Fomitopsidaceae, Hymenochaetaceae) of the division Basidiomycetes are typical in the various stages of wood decay [13]. However, studies in southern Europe have not examined wood-dwelling fungi in detail. A recent study shows that higher rainfall has a positive effect on fungal diversity. In contrast, higher temperatures have a negative influence, and tree species richness with structural and ecological heterogeneity has a greater influence on fungal diversity [14].

It is also important to understand the range of species distribution depending on topography. Some species of Ganodermataceae occur in central Europe at medium altitudes of 500 m but can also reach altitudes of up to 1500 m, and are usually found in mixed forests as well as in beech and coniferous forests; therefore, altitude and forest types are important distribution variables [15]. Families of the order Polyporales, including Fomitopsidaceae and Polyporaceae, were found at 1800–2100 m altitude with a temperature range between 18 °C and 23 °C and a relative humidity of 60–70%. These species are found on leaf litter and wood substrates [16]. Forest regions characterized by drier, less disturbed, and warmer forest zones, including tropical and subtropical zones, are dominated by porous macro fungi, such as the Polyporales group [17]. Fungal diversity is also significantly related to the type of host tree species, as the tree species also influence the rhizosphere. For example, the Banj Oak (*Quercus leucotrichophora*) is associated with moisture- and nutrient-rich soil, while the Chir Pine (*Pinus roxburghii*) is associated with nutrient- and moisture-poor soils [18]. Since Banj Oak is a late successional tree host, Chir Pine is an early successional tree in a forest ecosystem [19]. In addition, soil nutrients and altitude play a crucial role in fungal diversity as tree hosts also influence soil microbial biomass, such as mixed oak–pine forests in temperate climates, which have high microbial biomass, i.e., carbon (C) and nitrogen (N) and C:N ratios above 5 indicate that fungal communities dominate the soil compared to bacterial communities [20]. Therefore, we analyzed the richness, diversity, and distribution of fungal species and fungal host tree species in the western Himalayan region.

Although previous studies have shown the mycorrhizal fungal association of about 15 fungal genera with Himalayan tree species such as western Himalayan Fir (*Abies pindrow*), Deodar Cedar (*Cedrus deodara*), Himalayan Spruce (*Picea smithiana*), Chir Pine, Bhutan Pine (*Pinus wallichiana*), Tree Rhododendron (*Rhododendron arboreum*), White Oak (*Quercus incana*), and Brown Oak (*Quercus semicarpifolia*) [21], their comparative analysis in terms of Shannon diversity and species richness has not been comprehensively analyzed.

## 2. Materials and Methods

### 2.1. Data Collection

The dataset used for this study included samples from the Forest Research Institute (FRI) fungarium, Dehradun, India (Figure 1). The FRI fungarium was founded in 1906 and the oldest Indian specimens date back to 1878, making it one of the oldest and largest in India. Over 12,000 fungal samples, including mushrooms, molds, and yeasts, are stored. The specimens were collected mainly from the western Himalayan region, the central highlands, and the Karakoram mountains in the Kashmir region. Fungarium sample data are publicly available online at: <https://frifungarium.bicfri.in/>, accessed on 13 August 2023. The FRI Fungarium follows the traditional scientific taxonomic classification system, i.e., Linnaeus system as it has the first connection in history to the Austro-Hungarica herbarium.



**Figure 1.** Representative fungarium samples from each fungal family analyzed in this study. The numbered labels show: (1) Coleosporiaceae, (2) Cronartiaceae, (3) Fomitopsidaceae, (4) Peniophoraceae, (5) Stereaceae, (6) Hymenochaetaceae, (7) Ganodermataceae, (8) Meruliaceae, (9) Thelephoraceae, (10) Polyporaceae.

A large sample size was selected ( $N = 2066$ ) based on the tree species of interest as well as confirmed geolocations and taxonomic details. Based on abundance in the datasets, the top ten fungal families were selected for analysis to limit bias in comparison to diversity and richness across host trees and fungal families. The host tree species analyzed are native to the Himalayan region. These include Fig (*Abies*), Deodar (*C. deodara*), *Dalbergia*, Sal (*Shorea*), Spruce (*Picea*), *Rhododendron*, Pine (*Pinus*), and Oak (*Quercus*).

### 2.2. Topographic and Climatic Variables

For the analysis of fungal families, we selected four types of variables. We used Worldclim version 2.1 historical climate datasets based on geolocations, including the SRTM 30 arc seconds altitude dataset. In addition, we used the mean temperature, precipitation, and solar radiation with a resolution of 30 arc seconds each, which have a temporal time range of 30 years, i.e., from 1970 to 2000 [22].

As far as rainfall is concerned, the average precipitation in July was considered the primary rainy season in India, known as monsoon. It is essential to understand the significant impact of monsoon onset on phenology, especially with regard to the peak growth rate of many species in coniferous forests in the Himalayan region [23].

### 2.3. Statistical Analysis

We performed the statistical analysis in the R version 4.3.0 statistical environment. First, we performed PCA (principal component analysis) with ANOVA (analysis of variance) to understand the variations and distribution of fungal families in relation to climatic and environmental conditions. It is crucial to understand the phenological and ecological characteristics of the fungal families using violin plots showing density distributions to gain more knowledge about these dominant fungal families. PCA–ANOVA is used to derive F-statistics with variances, and 6.63 is the threshold at a significance level of 0.01, i.e., F-values above 6.63 indicate significant differences between fungal families. The PCA–ANOVA combination is used in order to understand the environmental variables that characterize the fungal families, as applied in a similar study on oak forests with different topography and climatic conditions [24]. Furthermore, the F-statistics indicate the significant differences between the fungal families, and similarly, the  $p$ -values represent the probability that the observed differences between the fungal families occurred by chance between groups. While variance ( $\sigma^2$ ) only shows the overall observed variation in the values of environmental variables to understand the contribution of these variables to the distribution of fungal families. These statistics are crucial for understanding how environmental and climatic variables are related to the distribution of fungal families and their ecological preferences.

In addition, the Shannon diversity index ( $H$ ) was used to measure diversity for both fungal families and host tree species. Additionally, species richness was calculated and plotted against the Shannon diversity index to compare richness and diversity. Where ‘ $n$ ’ is the Shannon index, ‘ $p$ ’ is the ratio of individuals of a particular species, and ‘ $N$ ’ is the total number of individuals observed. The ‘ $\ln$ ’ denotes the natural logarithm, ‘ $\Sigma$ ’ signifies the sum of these calculations, and ‘ $s$ ’ denotes the number of different species [25].

We also included species richness, which provides a primary count of the number of different species in a given area without taking into account the abundance of each species or the distribution of their relative abundance. All these statistical analyses were performed in R statistical software (R version 4.3.0). R packages including FactoMineR and Vegan were used to perform the PCA–ANOVA and diversity analysis, respectively.

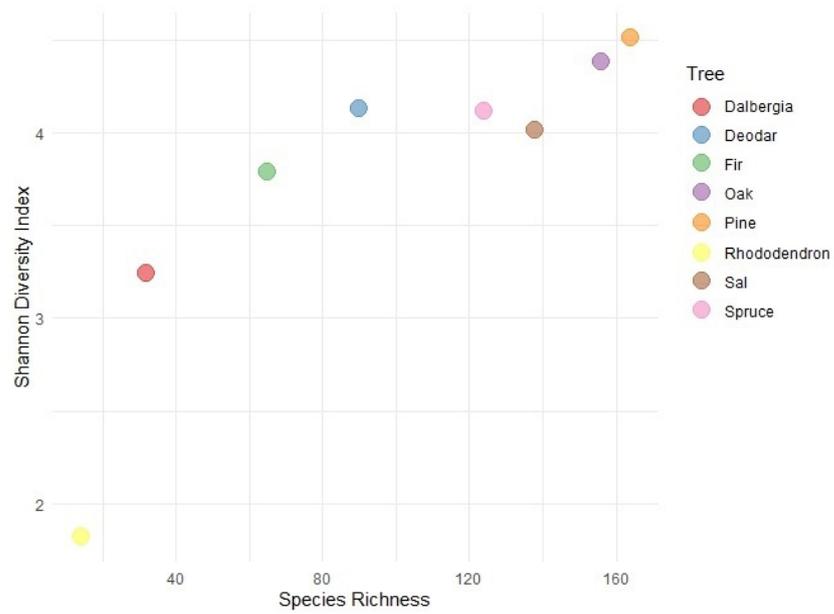
## 3. Results

### 3.1. Host Tree—Fungal Species Diversity and Richness

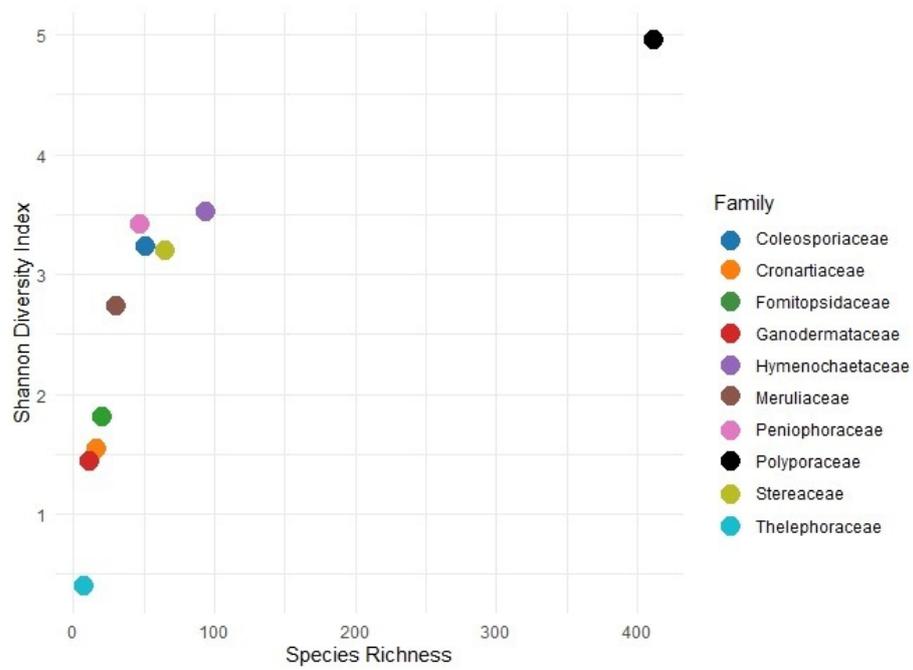
Separate analysis was performed for host tree species and fungal families to determine fungal species diversity and richness. Among the host tree species, pine ( $H' = 4.5$ ; ssp. 165) and oak ( $H' = 4.38$ ; ssp. 156) recorded a very high diversity and species richness. In addition, Deodar ( $H' = 4.13$ ; ssp. 90) and Spruce ( $H' = 4.11$ ; ssp. 124) recorded very high diversity and relatively moderate species richness. *Dalbergia* ( $H = 3.2$ ; ssp. 32) and *Rhododendron* ( $H = 1.81$ ; ssp. 14) showed moderate to low species biodiversity and very low richness. However, due to the small sample size, bias can also occur with *Rhododendrons*. Furthermore, *Shorea*, which occurs at relatively lower elevations than conifer species, exhibits high diversity ( $H' = 4.01$ ; ssp. 138) and species richness (Figure 2).

### 3.2. Fungal Family—PCA–ANOVA, Species Diversity, and Richness

Polyporaceae had the highest diversity and species richness among all fungal families ( $H' = 4.95$ ; ssp. 412). Hymenochaetaeaceae, Peniophoraceae, Coleosporiaceae, and Stereaceae also showed high diversity, i.e.,  $H' = 3.52$ ,  $H' = 3.41$ ,  $H' = 3.23$ , and  $H' = 3.19$ , respectively, with moderate species richness (ssp. > 40). Other families, including Fomitopsidaceae, Cronartiaceae, Ganodermataceae, and Thelephoraceae, have low species diversity, i.e.,  $H' = 1.81$ ,  $H' = 1.53$ ,  $H' = 1.43$ , and  $H' = 0.39$ , respectively. In addition, species richness is low (ssp. < 25) (Figure 3, Table 1).



**Figure 2.** Shannon diversity index vs. species richness graph for fungal diversity on host tree species.

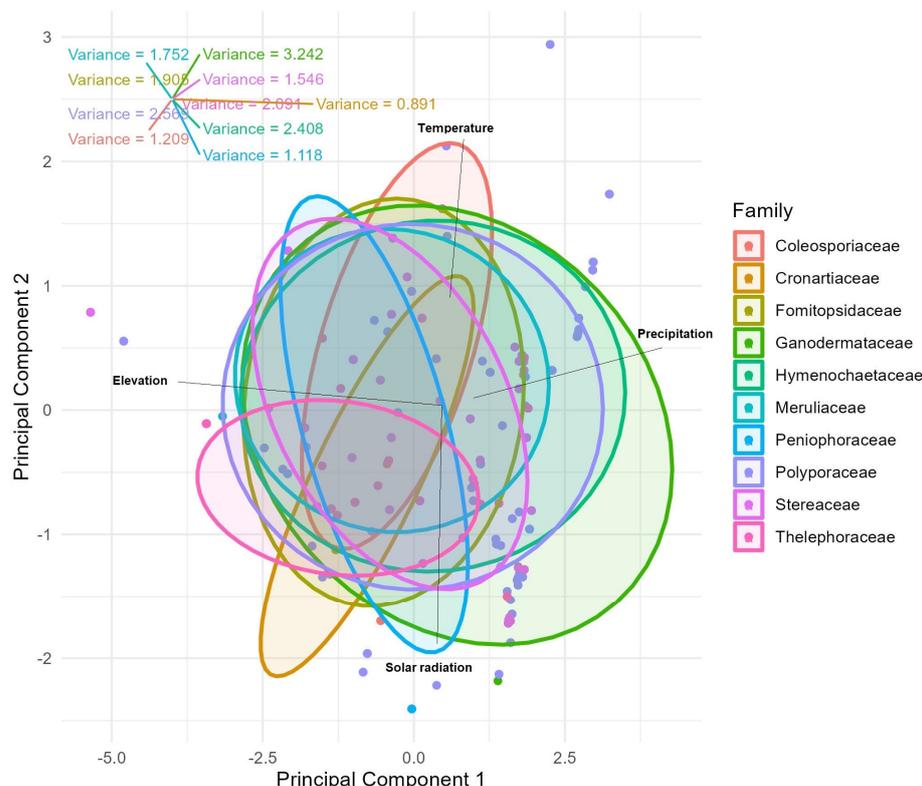


**Figure 3.** Shannon diversity index vs. species richness graph for fungal diversity of fungal families.

**Table 1.** Shannon diversity (SD) and species richness (SR) for each fungal family.

Family	Shannon Diversity (SD)	Species Richness (SR)
Coleosporiaceae	3.23	51
Cronartiaceae	1.53	17
Fomitopsidaceae	1.81	21
Ganodermataceae	1.43	12
Hymenochaetaceae	3.52	94
Meruliaceae	2.73	30
Peniophoraceae	3.41	47
Polyporaceae	4.95	412
Stereaceae	3.19	65
Thelephoraceae	0.39	8

The *p*-values for the fungal families that show significant differences between the fungal families include Hymenochaetaceae ( $\sigma^2 = 2.4$ ,  $F = 11.6$ ,  $p < 0.01$ ), Stereaceae ( $\sigma^2 = 1.5$ ,  $F = 10.5$ ,  $p < 0.01$ ), Thelephoraceae ( $\sigma^2 = 2.09$ ,  $F = 28.4$ ,  $p < 0.01$ ), Peniophoraceae ( $\sigma^2 = 1.1$ ,  $F = 20.7$ ,  $p < 0.01$ ), and Cronartiaceae ( $\sigma^2 = 0.89$ ,  $F = 14.5$ ,  $p < 0.01$ ). The variances also indicate the within-family variability found in the PCA–ANOVA, with Ganodermataceae ( $\sigma^2 = 3.24$ ,  $F = 2.09$ ) and Polyporaceae ( $\sigma^2 = 2.56$ ,  $F = 3.72$ ) having higher variances (Figure 4, Table 2).



**Figure 4.** PCA—ANOVA shows the differentiation between fungal families as well as variances for temperature, precipitation, altitude, and solar radiation.

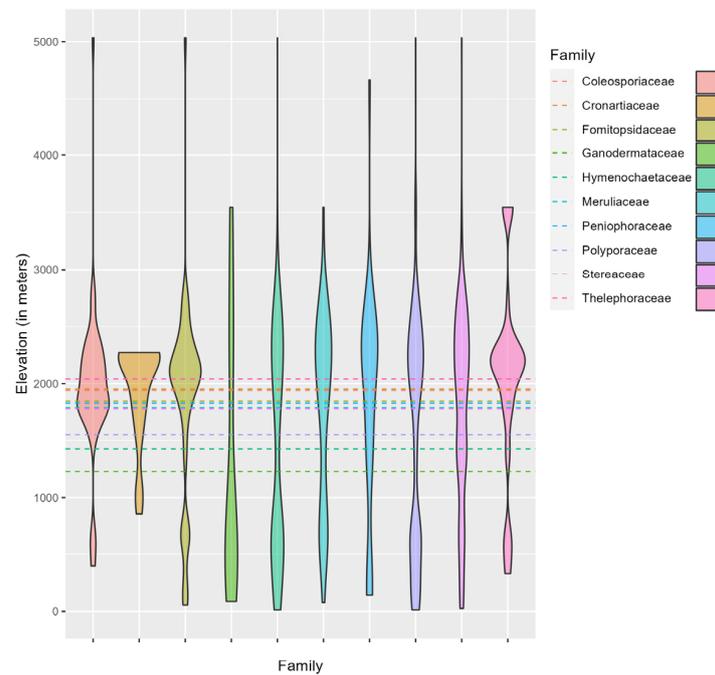
**Table 2.** Shannon diversity (SD) and species richness (SR) for the respective tree (genus/species).

Tree	Shannon Diversity (SD)	Species Richness (SR)
Fig ( <i>Abies</i> )	3.78	65
Deodar ( <i>C. deodara</i> )	4.13	90
<i>Dalbergia</i>	3.24	32
Spruce ( <i>Picea</i> )	4.11	124
<i>Rhododendron</i>	1.81	14
Pine ( <i>Pinus</i> )	4.5	164
Sal ( <i>Shorea</i> )	4.01	138
Oak ( <i>Quercus</i> )	4.38	156

### 3.3. Spatio-Climatic Distribution of Fungal Families

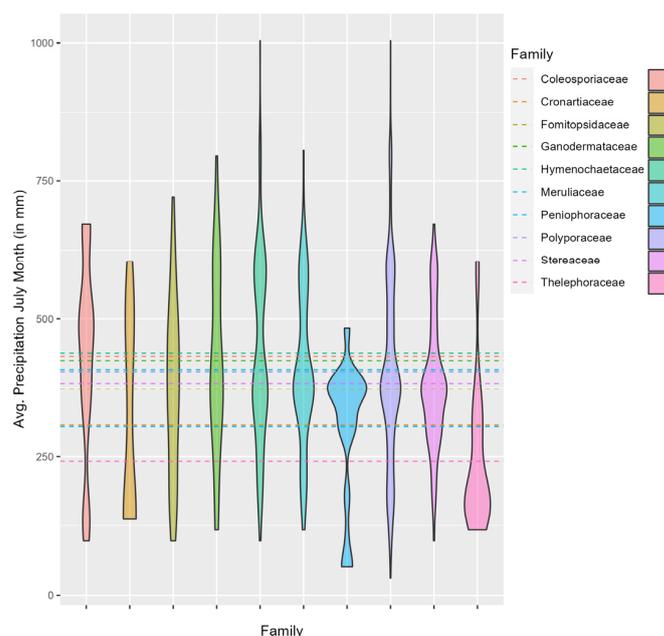
The family Thelephoraceae is one of the families distributed above 2000 m mean altitude, in contrast to families such as Ganodermataceae and Hymenochaetaceae, which, although distributed below 1000 m mean altitude, have more extensive distribution ranges between 0–3500 m and 0–5000 m, respectively. The family Polyporaceae shows diverse variations in species distribution with respect to altitude ranges and occurs between 0 and 4500 m, with the mean altitude being slightly above 1500 m. Coleosporiaceae and Cronartiaceae have a mean altitude of just under 2000 m with slight variation. The distribution is usually around 2000 m. In addition, the four families, Stereaceae, Meruliaceae, Peniophoraceae, and Fomitopsidaceae,

occur between 1700 and 1800 m mean altitude, with all Stereaceae and Fomitopsidaceae having different altitude distribution ranges of up to 5000 m (Figure 5).



**Figure 5.** Violin plot showing the data distribution of the fungal family with respect to elevation. Dashed lines show the average of the altitude values recorded for several points of the respective fungal family.

Furthermore, Hymenochaetaceae, Coleosporiaceae, and Ganodermataceae have some of the highest mean precipitation, namely, 438 mm, 432 mm, and 424 mm, respectively. In comparison, Thelephoraceae are among the family with the lowest average rainfall at 242 mm, along with others such as Peniophoraceae and Cronartiaceae at 304 mm and 307 mm, respectively (Figure 6, Table 3).

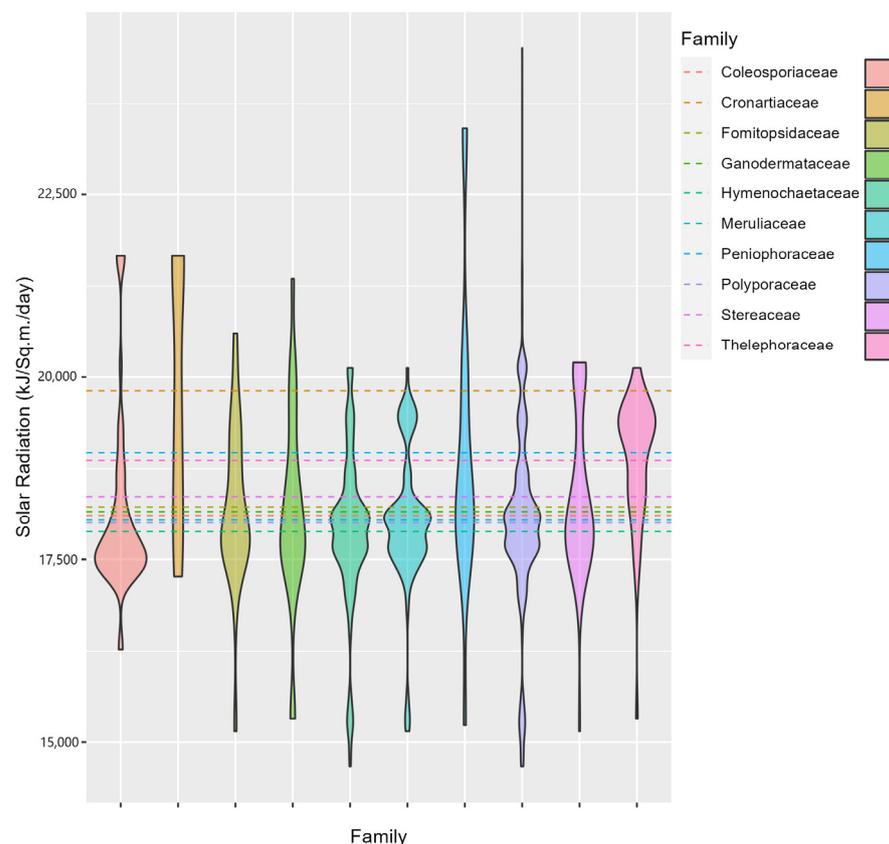


**Figure 6.** Violin plot showing the data distribution of fungal families relative to rainfall. Dashed lines show the mean precipitation values (July) recorded for several points for each fungal family.

**Table 3.** Mean values of the spatio-climatic variables used in the study for the distribution of the fungal families.

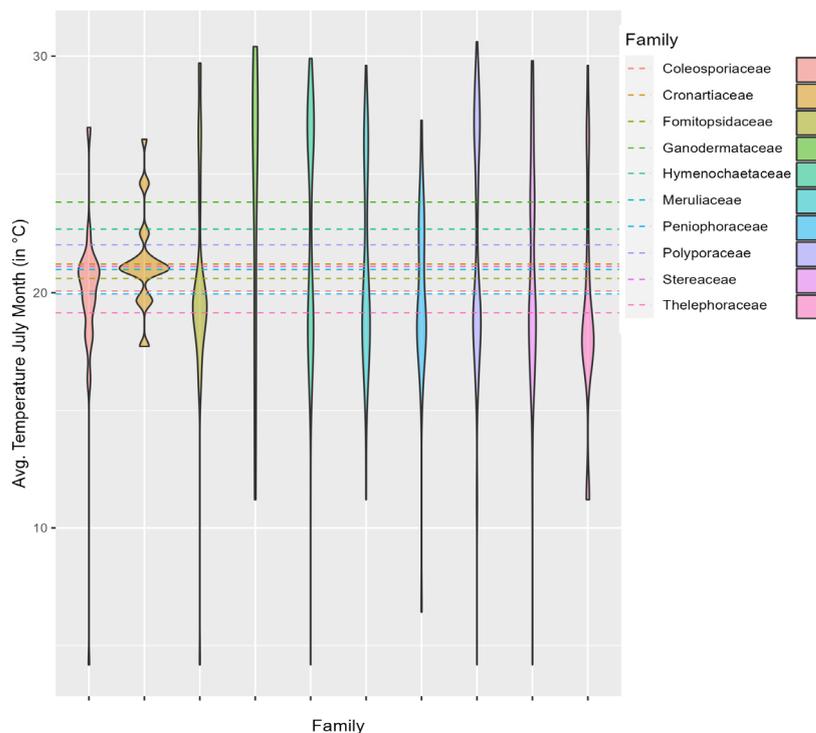
Family	Solar Radiation ( $\text{kJ m}^{-2} \text{ day}^{-1}$ )	Precipitation (mm)	Altitude (m)	Temperature ( $^{\circ}\text{C}$ )
Coleosporiaceae	18,109	432	1943	20.07
Cronartiaceae	19,811	307	1955	21.21
Fomitopsidaceae	18,225	373	1849	20.60
Ganodermataceae	18,161	424	1228	23.82
Hymenochaetaceae	17,880	438	1424	22.68
Meruliaceae	18,040	408	1792	20.98
Peniophoraceae	18,968	304	1831	19.95
Polyporaceae	18,004	405	1547	22.02
Stereaceae	18,366	383	1781	21.11
Thelephoraceae	18,864	242	2041	19.12

In contrast, the three species, Thelephoraceae, Peniophoraceae, and Cronartiaceae, have relatively higher mean solar radiation of 18,864, 18,968, and 19,811  $\text{kJ m}^{-2} \text{ day}^{-1}$ , respectively (Figure 7, Table 3). Furthermore, Hymenochaetaceae had the lowest mean solar radiation of 17,880  $\text{kJ m}^{-2} \text{ day}^{-1}$ .

**Figure 7.** Violin plot showing the data distribution of the fungal family in relation to solar radiation. Dashed lines show the average of the solar radiation values recorded for several points for the respective fungal family.

Regarding the temperature distribution, Thelephoraceae and Peniophoraceae were found to have a mean temperature of less than 20  $^{\circ}\text{C}$ , while Thelephoraceae has a tendency towards temperatures lower than 20  $^{\circ}\text{C}$ . In contrast, Ganodermataceae has a temperature range from 10 to 30  $^{\circ}\text{C}$  with an average temperature of 23.8  $^{\circ}\text{C}$  ( $\pm 6$ ), which is the highest among the families, followed by Hymenochaetaceae and Polyporaceae with 22.6  $^{\circ}\text{C}$  ( $\pm 4.7$ ).

and 22 °C (±4.9). However, they have a wider temperature distribution range from 0 to 30 °C. In addition, Coleosporiaceae has a relatively lower average temperature, namely, 20 °C (±3.1), with a temperature range of 0–25 °C. Cronartiaceae has a mean temperature of about 21.2 °C (±1.9) with a minimum temperature range of 18–26 °C (Figure 8, Table 3).



**Figure 8.** Violin plot showing the data distribution of fungal families relative to temperature. Dashed lines show the mean of temperature values (July) recorded for multiple points for each fungal family.

Furthermore, a total of eight genera containing ectomycorrhizal fungal species were identified, with five genera belonging to the Polyporaceae and three belonging to the Thelephoraceae. In addition, four genera of the family Coleosporiaceae are identified as rust fungi, while one genus of rust fungi is Cronartiaceae. In the remaining fungal families, about 35 genera were identified as wood-decaying fungi (Table 4).

**Table 4.** Table showing genera of the respective fungal families.

Fungal Family	Genera	Category
Coleosporiaceae	<i>Coleosporium, Chrysomyxa, Schroeteriaster, Caeoma</i>	Parasitic (Rust)
Cronartiaceae	<i>Cronartium</i>	Parasitic (Rust)
Fomitopsidaceae	<i>Daedalea, Fomitopsis, Pycnoporellus</i>	Saprotrophic (Wood decay)
Ganodermataceae	<i>Amauroderma, Ganoderma</i>	Saprotrophic (Wood decay)
Hymenochaetaceae	<i>Hymenochaete, Inonotus, Polystictus, Phellinus, Coltricia, Cyclomyces</i>	Saprotrophic (Wood decay)
Meruliaceae	<i>Irpex, Merulius, Phlebia, Cerocorticium, Hyphoderma, Steccherinum</i>	Saprotrophic (Wood decay)
Peniophoraceae	<i>Duportella, Peniophora</i>	Saprotrophic (Wood decay)
Polyporaceae	<i>Lenzites, Polyporus *, Trametes *, Favolus, Fomes, Hexagonia,</i>	Saprotrophic (Wood decay)
	<i>Grammothele, Hirschioporus, Lentinus *, Leptoporus, Lopharia *,</i>	Symbiotic (Ectomycorrhizal)
	<i>Microporus *, Panus, Nigroporus, Poria, Tyromyces, Epithele, Coriolopsis,</i>	
	<i>Pyrofomes, Loweporus, Pycnoporus, Coriolus</i>	
Stereaceae	<i>Aleurodiscus, Stereum</i>	Saprotrophic (Wood decay)
Thelephoraceae	<i>Thelephora *, Tomentella *, Caldesiella *</i>	Symbiotic (Ectomycorrhizal)

\* Indicates genera having ectomycorrhizal species.

#### 4. Discussion

Our study shows that high diversity and species richness occur in oak-dominated forests, including mainly wood-decaying fungi species from families such as Polyporaceae, Hymenochaetaceae, Peniophoraceae, Ganodermataceae, and Thelephoraceae, in the western Himalayas which are similar to the study focusing on Polyporaceae diversity in the eastern Himalayan diversity in southwest China [26]. This is consistent with other studies [27], including one in which 24 fungal species were identified as host specific and associated only with oaks [28]. One study also found ectomycorrhizal hotspots in oak forests worldwide, with southwestern Mexico being a hotspot for oak forest ectomycorrhizal diversity [29].

Another important finding of the study is that host tree species such as Spruce, Deodar, and Shorea have a high fungal diversity. Shorea, a woody species used for timber production, exhibits high species richness as well as ectomycorrhizal and endomycorrhizal fungal associations previously reported only from the eastern Himalayas [30]. Therefore, continued removal of Shorea for the timber industry may impact the fungal species found there.

As obligatory dependents on plants, plant diversity determines fungal diversity and populations [6]. Therefore, although the sample sizes of Rhododendrons are small, the threat to the species in the study region [31] and the phenological changes documented in recent years [4,32], may impact future diversity. Similarly, conifers, especially Pines, host many species of fungi. Many of these are endemic to the Himalayan hotspots arc, and there is a need for sustainable conservation strategies for these species at the national level [33]. Our results highlight the need for species specific studies, particularly those understudied before it is quite late.

Similarly, Cronartiaceae, Peniophoraceae, and Thelephoraceae are located in areas with relatively low rainfall and have lower species richness compared to all other families. In contrast, Hymenochaetaceae and Polyporaceae, which occur in environments with higher rainfall, recorded a high species richness, which is also confirmed by a study of oak forests in the Mediterranean region that showed a positive association between higher precipitation and species richness, especially in the dry season [34].

Furthermore, fungal families such as Polyporaceae and Hymenochaetaceae occur at altitudes of around 1500 m and have very high species richness in this Himalayan region. This result concurs with a study focusing on the mid-domain effect (MDE) for ectomycorrhizal fungi. It conforms to Miyamoto et al. [35] as MDEs have the highest species richness in central geographical locations [36].

Also, the families Cronartiaceae and Thelephoraceae, which occur in high solar radiation environments, have lower diversity and species richness, with the exception of Peniophoraceae, which have high diversity and moderate species richness. However, the variation is higher in Peniophoraceae compared to these two families, indicating an adaptation to higher solar radiation, as fungal communities are known to tolerate higher solar radiation and extreme desiccation and require adaptations such as melanin accumulation [37,38].

Nevertheless, the abundance of parasitic Fomitopsidaceae is significant in this study as they are classified in the order Polyporales, with most of its species having a parasitic affinity for woody plants and a propensity to cause brown rot [39]. Species from the Cronartiaceae and Coleosporaceae families are also known to cause rust diseases on conifers, and are therefore parasitic in nature [40].

Due to the accelerating climate change and the unprecedented impact of anthropogenic activities, the world is facing climatic and other environmental challenges. Mapping biodiversity at all levels is challenging in extreme geophysical habitats such as the Tibeto-Himalayan mountains. Although the more easily studied species, like vertebrates and plants, have been documented [1,4,34,41], the less prominent species like fungi are neglected. Kumar et al. [6] stated that there are no current records of the number of macro-wood-decaying fungi in India. The significance of our study lies in the analysis of the long-term collection in the national fungarium and host plants. The continued exploitation

of these under-studied species, which play an essential ecological role in the forest health, can have detrimental impacts for all involved [32].

Our study in the western Indian Himalayan region highlights the importance of conducting similar studies in the central and eastern parts of the range. Mehta et al. [5] reported that the plant species diversity was highest in the east. Nevertheless, more information about the ecology of the relevant fungal populations needs to be available. Devi et al. [42] also reported the degradation of agro-forestry systems in the Himalayas, with pressure from human populations threatening countless ecosystem services.

We conclude that there is a high diversity and species richness of fungi in oak, spruce, deodar, and sal dominated forests in the western Himalayas. We also found that areas with relatively low rainfall had lower species richness and vice versa. The high level of solar radiation also had a negative impact on the fungal diversity and species richness.

Additionally, this study addresses the data deficit in the Indian Himalayas related to fungal biodiversity. Our study has significant implications as various fungal family genera with different ecological functions such as wood decay, symbiotic ectomycorrhiza, and rust fungi have been identified and analyzed, which will serve as a guide to support sustainable ethnobotanical practices as well as conservation policy will focus on the medicinal, edible, or disease-related properties of these fungi. Since this study also links inferences about diversity and species richness with host tree species, forestry plantations can incorporate these findings to improve desirable fungal, floral, and faunal biodiversity.

Similar studies need to be conducted in other parts of the Himalayas and the importance of fungi in ethno-botanical culture needs to be understood to mitigate the sustainable use of host plants by local communities. Also, the authorities must include fungi in the region's RED lists accordingly.

**Author Contributions:** Conceptualization, N.Y., S.R. and R.Y.; methodology, S.R.; software, S.R. and N.A.; validation, N.Y., N.A. and S.R.; formal analysis, S.R.; investigation, S.R. and R.Y.; resources, N.Y.; data curation, N.Y., S.R. and N.A.; writing—original draft preparation, S.R.; writing—review and editing, S.R. and R.Y.; visualization, S.R.; supervision, R.Y.; project administration, S.R.; funding acquisition, N.Y. All authors have read and agreed to the published version of the manuscript.

**Funding:** This research received no external funding.

**Institutional Review Board Statement:** Not applicable.

**Data Availability Statement:** Data available from authors at reasonable request.

**Conflicts of Interest:** The authors declare no conflict of interest.

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