

Diversity and Distribution Pattern of Tree Rotting Fungi in Hardwood Forests in Lengkhar, Tashi Yangtse

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Abstract

The tree rotting fungi, scientifically referred to as xylophagus, are considered as the primary decomposer of trees in the forests as they produce enzymatic chemicals that degenerate the structural integrity and vital components of the trees. They grows on both standing and felled log woods. Studies and research in this field in Bhutan is limited. This study focused on polypores which grows on living, standing trees to provide a baseline dataset and guide to the diversity of the tree rotting fungi and their distribution through determining abundance and important value (IV) in Lengkhar and vicinity forest. For this, systematic line transects were established, and data were collected from plots laid systematically along these transects. The study documented 59 species, which was highly diverse ($H=3.24$). Among all, *Trametes versicolor* was the most abundant species ($IVI=58.08$), followed by *Mycena* spp. ($IVI=32.32$). The study recommends that related agencies consider mitigation measures to prevent the spread of these tree rotting fungi in the forests.

Keywords: Importance Value, Lengkhar, Polypores, Species, Tree Rotting Fungi

Introduction

There are about 144,000 known species of organisms under the kingdom fungi. Fungi are known to be eukaryotic organisms due to their specialized organelles and well-defined nuclei. Fungal deterioration of wood reduces structural integrity and increases porosity, making physical disruption easier and allowing chemicals and enzymes to penetrate deeper into the wood structure (Baker et al., 2017). Fungi are the primary decomposers of wood in nature. Fungi can produce enzymes that allow them to break down complex wood components including cellulose, hemicellulose, and lignin. White rot, brown rot, and

soft rot are the three types of fungal wood degradation (Piętko et al., 2019).

The principal biotic decomposers of wood are wood decay fungus. Living trees can be attacked by wood decay fungi, which can behave as genuine pathogens causing root rots and stem cankers, or as rotting agents for heartwood and sapwood. All wood-eating fungi are basidiomycetes, which are divided into four orders; Agaricales, Hymenochaetales, Polyporales, and Russulales (Gonthier & Nicolotti, 2007). Fungi are divided into three trophic levels; pathotrophs, who feed by injuring host cells, symbiotrophs, who feed by sharing nutrients with host cells, and saprotrophs, who feed by breaking down dead host cells (Burgess et al., 2016).

Many species are involved in the degradation of wood, however, fungi are the primary cause of a tree's diminished mechanical strength in terms of risk assessment (Terho et al., 2007). Therefore, this study evaluated the diversity of tree rotting fungi and their distribution in Lengkhar locality under Trashy Yangtse Dzongkhag.

Materials and methods

Study area

This study on tree rotting fungi diversity and their distribution pattern in hardwood forest was conducted in Lengkhar hardwood forest in Khamdang Gewog under Tashi Yangtse District in eastern Bhutan. The district covers a total area of 1437.9 Km² (555.2 sq miles) and consists of eight *gewogs*. The study area lies within elevations 1750 to 1880 masl with average annual precipitation of 34.86mm. The District falls within 27.°35' 0" N and 91°28' 0" E. The present study site, Lengkhar, falls under Khamdang Gewog which covers an area of 44.5 sq. km (Figure 3.1). The forest types in this study area include mix-hardwood forest, broadleaved forest, conifer forest, and cool-broadleaved forest.

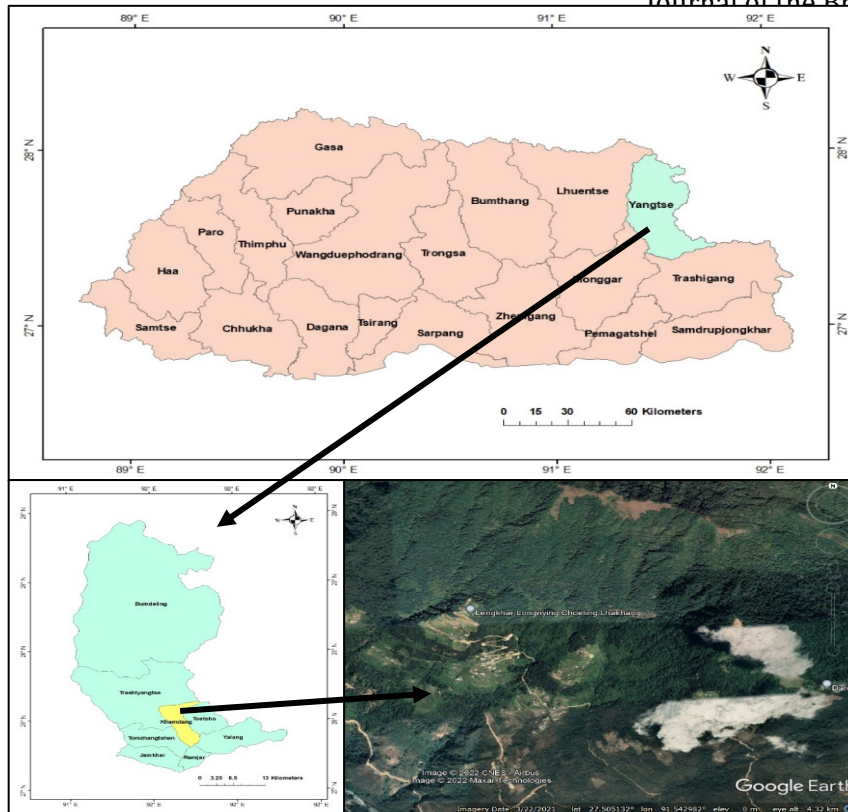


Figure 3.1 Map showing the study area

Research design and data collection

For monitoring the diversity of tree rotting fungi, area-based plot method was used to record individual counts of targeted species in the sampling plots. A transect belt was laid out within the area-based plots to assess the population diversity along altitudinal gradients. These methods are suggested as appropriate for the collection of macromycetes' fruiting bodies, and are often the quickest way to record new species in a research region (Ngansop et al., 2019; Schmit & Lodge, 2004).

Data collection was carried out in March 2022. This study followed a longitudinal research design, where data were collected from the transects repetitively. In total, 4 transects were laid, with the first transect being randomly placed and the rest systematically arranged across the gradients maintaining an interval of 50m. For each transect line, 15 sample plots of 50x50m and an interval of

33m distance was maintained. The identification of the samples collected were confirmed using the Fungi of Bhutan (Penjor, et al., 2010) book and by consulting experts.

Results and Discussion

Species composition and Importance Value

The study recorded a total of 59 species of tree rotting fungi falling in 2 Divisions, 12 Orders, and 15 families. The most dominant family recorded was Polyporaceae (n=17), followed by Fomitopsidaceae (n= 8) (Table 4.1). All species recorded were found responsible for rotting of trees. Moreover, the number of species sighting varied from plot to plot (Figure 4.2). From a total of 59 species enumerated, *Trametes versicolor* was the most dominant species (IVI=58.08), followed by *Mycena* spp. (IVI=32.32), and *Nectria* spp. (IVI=14.65). Of all, *Suillus* spp. was the least dominant species.

Table 4.1 Taxonomic classification of tree rotting fungi

Name of species	Family	Genus	Species
<i>Auricularia auricularies</i>	Auriculariaceae	<i>Auricularia</i>	<i>Auricularies</i>
<i>Fomitopsis ochracea</i>	Formitopsidaceae	<i>Fomitopsis</i>	<i>Ochracea</i>
<i>Laetiporus sulphureus</i>	Formitopsidaceae	<i>Laetiporus</i>	<i>Sulphureous</i>
<i>Trametes versicolor</i>	Polyporaceae	<i>Trametes</i>	<i>Versicolor</i>
<i>Spongipellis pachyodon</i>	Polyporaceae	<i>Spongipellis</i>	<i>Pachyodon</i>
<i>Ganoderma applanatum</i>	Ganodermataceae	<i>Ganoderma</i>	<i>Applanatum</i>
<i>Phellinus pini</i>	Hymenochaetaceae	<i>Phellinus</i>	<i>Pini</i>
<i>Ganoderma polychromum</i>	Ganodermataceae	<i>Ganoderma</i>	<i>Polychromum</i>
<i>Armillaria mellea</i>	Physalacriaceae	<i>Armillaria</i>	<i>Mellea</i>
<i>Oxyporus populinus</i>	Schizoporaceae	<i>Oxyporus</i>	<i>Populinus</i>
<i>Polyporus squamosus</i>	Polyparaceae	<i>Polyporus</i>	<i>Squamosus</i>
<i>Perenniporia fraxinophila</i>	Polyparaceae	<i>perenniporia</i>	<i>Fraxinophila</i>
<i>Trametes ochracea</i>	Polyporaceae	<i>Trametes</i>	<i>Ochracea</i>
<i>Pleurotus ostreatus</i>	Pleurotaceae	<i>Pleurotus</i>	<i>Ostreatus</i>
<i>Fomitopsis pinicola</i>	Formitopsidaceae	<i>Fomitopsis</i>	<i>Pinicola</i>
<i>Pholiota</i> spp.	Strophariaceae	<i>Pholiota</i>	Spp
<i>Sparassis</i> spp.	Sparassidaceae	<i>Sparassis</i>	Spp
<i>Omphalotus</i> spp.	Marasmiaceae	<i>Imphalotus</i>	Spp
<i>Trametes</i> spp.	Polyporaceae	<i>Trametes</i>	Spp
<i>Apioperdon pyriforme</i>	lycoperdaceae	<i>Apioperdon</i>	<i>pyriforme</i>
<i>Perenniporia</i> spp.	polyparaceae	<i>perenniporia</i>	spp.
<i>Piptoporus betulina</i>	Formitopsidaceae	<i>Piptoporus</i>	<i>Betulina</i>
<i>Polyporus</i> spp.	Polyporaceae	<i>Polyporus</i>	spp.
<i>Armalaria</i> spp.	Physalacriaceae	<i>Armalia</i>	spp.
<i>Trametes hirsute</i>	Polyporaceae	<i>Trametes</i>	<i>Hirsute</i>
<i>Fomes</i> spp.	Polyporaceae	<i>Fomes</i>	spp.
<i>Mycena</i> spp.	Mycenaceae	<i>Mycena</i>	spp.
<i>Polyporous cf. badius</i>	Polyporaceae	<i>Polyporous</i>	spp.
<i>Trichaptum cf fuscoviolaceum</i>	Incertae sedis	<i>Trichaptum</i>	spp.
<i>Pholiota cf. microspore</i>	Strophariaceae	<i>Pholiota</i>	spp.
<i>Aff. Melanoporia castanea</i>			
<i>Aff. Coriolopsis glabrorigens</i>	Polyporaceae	<i>Coriolopsis</i>	<i>Glabrorigens</i>
<i>Aff. Nigroporus vinosus</i>	Steccherinaceae	<i>Nigroporus</i>	<i>Vinosus</i>
<i>Mycena cf. haematopoda</i>	Mycenaceae	<i>Mycena</i>	<i>Haematopoda</i>
<i>Fomes fomentarius</i>	Polyporaceae	<i>Fomes</i>	<i>Fomentaris</i>
<i>Laetiporus</i> spp.	Fomitopsidaceae	<i>Laetiporus</i>	spp.
<i>Schizophyllum commune</i>	Schizophyllaceae	<i>schizophyllum</i>	<i>Commune</i>
<i>Trichaptum abietinum</i>	incertae sedis	<i>Trichaptum</i>	<i>Abietinum</i>

<i>Fomes fomentarius</i>	Polyporaceae	<i>Fomes</i>	<i>Fomentarius</i>
<i>Corioloopsis</i> spp.	Polyporaceae	<i>Corioloopsis</i>	
<i>Microporus affinis</i>	Polyporaceae	<i>Microporus</i>	<i>Affinis</i>
<i>Lichennomphalia</i> spp.	Hygrophoraceae	<i>Lichennomphalia</i>	
<i>Calocera</i> spp.	Dacrymycetaceae	<i>Calocera</i>	
<i>Cyptotrama</i> spp.	Physalacriaceae	<i>Cyptotrama</i>	
<i>Gloeophyllum</i> spp.	Gloeophyllaceae	<i>Gloeophyllum</i>	
<i>Pycnoporus</i> spp.	Polyporaceae	<i>Pycnoporus</i>	
<i>Lachnellula</i> spp.	Lachnaceae	<i>Lachnellula</i>	
<i>Hypoxylon</i> spp.	Hypoxylaceae	<i>Hypoxylon</i>	
<i>Diatrype disciformis</i>	Diatrypaceae	<i>Diatrype</i>	<i>Disciformis</i>
<i>Nectria</i> spp.	Nectriaceae	<i>Nectria</i>	
<i>Biscogniauxia</i> spp.	Xylariaceae	<i>Biscogniauxia</i>	
<i>Phlebia</i> spp.	Meruliaceae	<i>Phlebia</i>	
<i>Antrodia</i> spp.	Fomitopsidaceae	<i>Antrodia</i>	
<i>Daedalea</i> spp.	Fomitopsidaceae	<i>Daedalea</i>	
<i>Hymenochaete</i> spp.	Hymenochaetaceae	<i>Hymenochaete</i>	
<i>Inonotus</i> spp.	Hymenochaetaceae	<i>Inonotus</i>	
<i>Pseudomerulius</i> spp.	Tapinellaceae	<i>Pseudomerulius</i>	
<i>Stereum</i> spp.	Stereaceae	<i>Stereum</i>	

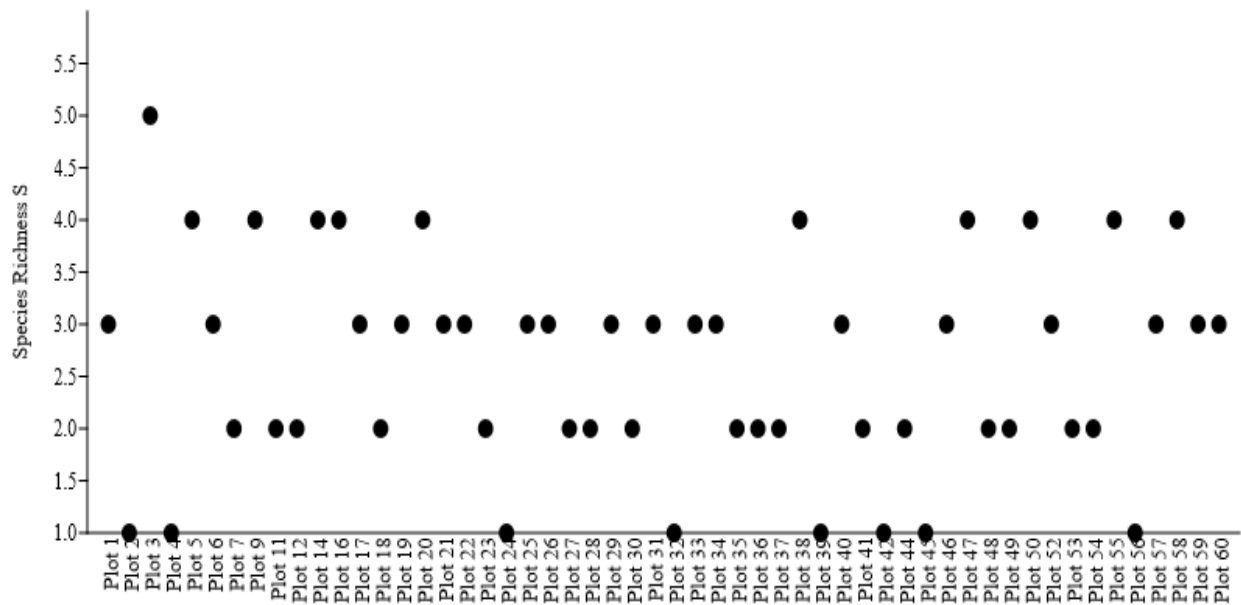


Figure 4.1 Species richness of tree rotting fungi

Shannon diversity index (H)

The value of Shannon diversity index for the 59 species of tree rotting fungi was 3.24 (Table 4.1), depicting a higher diversity of tree rotting fungi in the study area. The Shannon diversity index of other species ranged from 1.5 to 3.5 (Annexure 2). Moreover, the study found that the species were not evenly distributed among the plots. Of all, plot no. 3 had the highest species count and diversity

($H'=1.35$). The high diversity in this particular plot may be due to suitability of area with environmental factors such as temperature, humidity, precipitation, and evapotranspiration rate being moderate and having physical factors such as more suitable aspect and canopy cover. According to Aghajani et al., 2017; as cited in Robledo and Renison, the types of forest structure and its variables affect the existence of the polypores or tree rotting fungi.

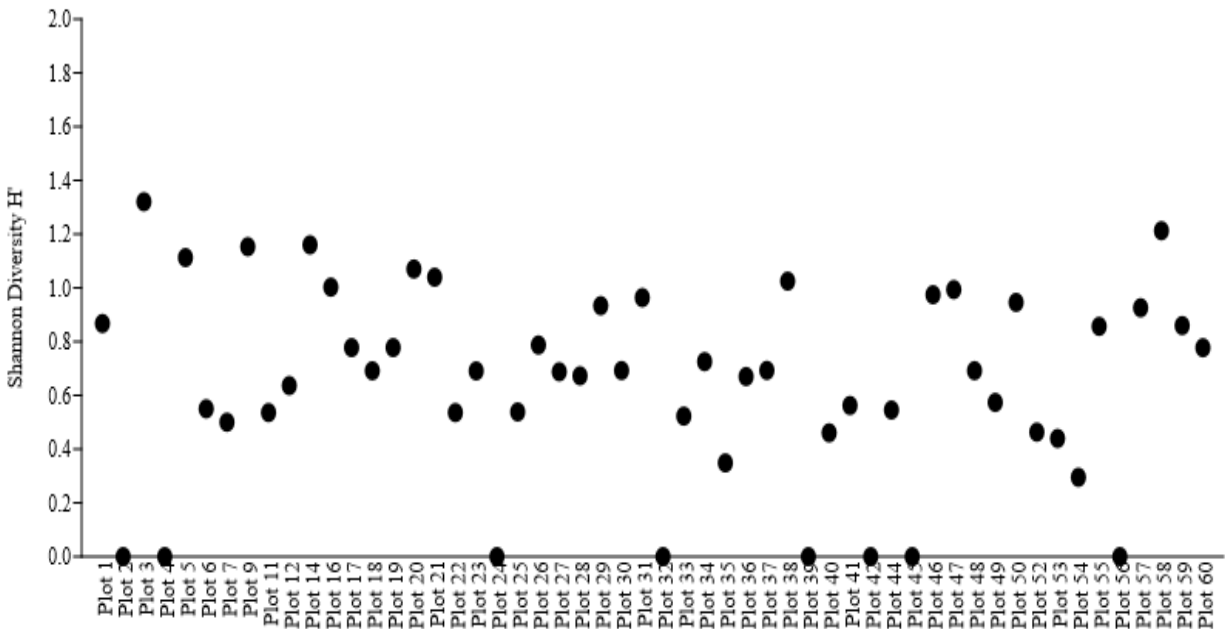


Figure 4.2 Shannon Diversity Index for all the plots

Relationship between the individual counts and slope percentage

There was a negative, medium, and significant correlation between the slope and the individual count of the species in the study area ($r = -.51, p =$

$.04$) (Table 4.3). There was a higher number of individuals in areas of gentler slope which was similar to what Xu et al. (2020) also reported. The pattern of colonization decreases with the increase in slope.

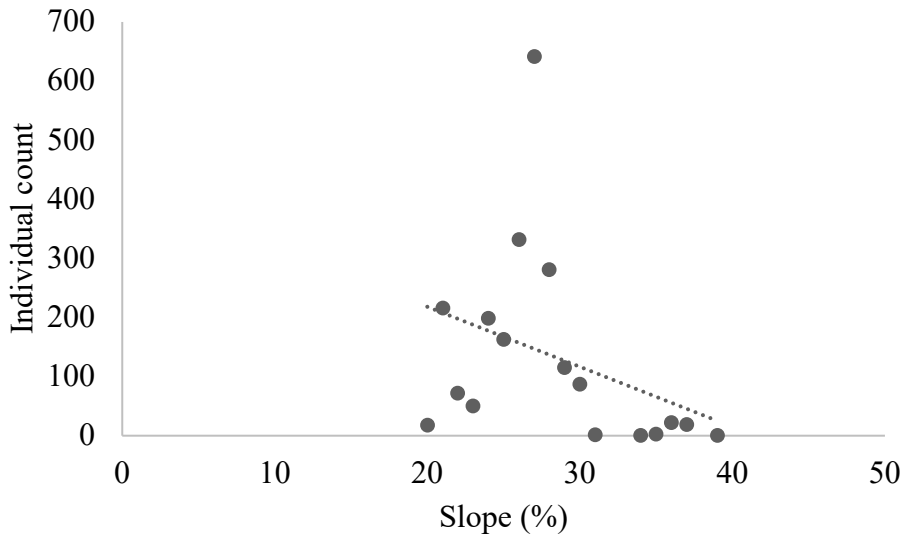


Figure 4.3 Number of individuals against Slope (%)

Conclusion and recommendations

A total of 59 species of tree rotting fungi were found in the study area which falls within the cool broadleaved forest range of the country. The 59 species of tree rotting fungi sampled from 60 plots, covering an area of 15 hectares, show clearly that tree rotting fungi thrive and are highly diverse in the current study area. In the field, most of the host trees were observed degraded and weakened as compared to the trees found in further from the study site.

Trametes versicolor was found growing in large troops in almost all the plots that were sampled, and was the most dominant species. The study also

found that diversity of tree rotting fungi was not totally determined by landscape parameters such as slope percentage but determined also by the presence of suitable host tree species.

Important tree species in the study area such as *Quercus grifithii*, *Betula alnoides*, *Quercus glauca*, and *Acer cambelli* were found degraded both in girth development and apical growth with the fungi degenerating the integral structures of the trees such as lignin and cellulose. A proper survey and more studies must be conducted to eliminate the conks in the hardwood forests of Bhutan to help protect and sustain these tree species.

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