



# Spatial Distribution of Wood-Decaying Fungi in an Old-Growth Temperate Forest

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## ABSTRACT

Wood-decaying fungi play key roles in forest ecosystems; however, their spatial distribution in old-growth temperate forests has been poorly studied. In this study, we recorded wood-decaying fungi (polyporoid and corticioid) in a rectangular plot (260 m × 500 m) on Changbai Mountain, Northeastern China, over 2010. The total number of individual fruiting bodies recorded in the plot was 1741, comprising 170 species. We used nested quadrats from four starting points in order to examine species richness. The relationship between the number of species and quadrat size was then analyzed, and three models commonly used to describe species–area relationships were fitted to the data. We found that the logistic model satisfactorily described the species richness–area curves irrespective of where in the plot we started sampling. The results indicated that, when the sampling area increases, species richness increases quickly at first and then the increase slows, becoming asymptotic. Using Coleman rarefaction curves to examine the main factors influencing the distribution of wood-decaying fungi in the forest, we found that there was a positive relationship between dead wood fragment diameter and the number of fungal species fruiting.

**Keywords:** broadleaved korean pine mixed forest, northeastern china, rarefaction curve, species-area relationship

## 1. INTRODUCTION

Decomposition of dead wood is a vital aspect of nutrient cycling, soil formation and the carbon budget of forest ecosystems. Dead wood also acts as an important functional component for biodiversity in boreal forest ecosystems, because thousands of species are dependent on decaying trees for habitat and substrate [1]. Wood-decaying fungi are one such group. They are ubiquitous and crucial components of

natural forests, delivering many important ecological functions, including influencing the general nutrient- and carbon-cycling of forests, providing habitats and food for many other organisms and enabling the regeneration of forests. Several species are important agents of disturbance in forests [2-5] and some are precursors to or facilitators for other fungal species or insects [6-7].

Wood-decaying fungi are important components of the whole forest ecosystem, as well as being part of the biodiversity within forests. Thus it is important to conserve these fungi for the well-being of other organisms. The species diversity of wood-decaying fungi tends to be positively correlated with the amount of substrate [8-12]. Unsustainable forestry has drastically reduced the abundance and diversity of dead wood and associated wood-decaying organisms [13]. A positive relationship between the size of fragments of dead wood and the number of fruiting fungal species has also been reported [14-16]. But some questions remain. What area of habitat is required in a given system to support all the wood-decaying fungi in that region? Is it possible to define the relationship between the number of species and the amount of dead wood? Is the spatial distribution of wood-decaying fungi affected by increasing amounts of available substrate?

The species-area relationship (SAR) could be a valuable tool for examining these questions; indeed, it has been considered "one of community ecology's few genuine laws" [17]. Species-area relationships are often used to guide practical conservation planning and have also been recognized as important tools for predicting the effects of habitat loss [13, 18-20]. A large number of natural communities have been investigated, especially by plant ecologists. They found that different communities may exhibit different types of species-area relations. Among them, three expressions are most widely used: exponential model, power model and logistic model [21].

Changbaishan Nature Reserve, in Northeastern China, established in 1960, which became part of the UNESCO Man and the Biosphere (MAB) program in 1980,

is a MAB Biosphere Reserve (<http://www.unesco.org/mabdb/br/brdir/directory/biores.asp?mode=all&code=CPR+01>). The reserve contains an old-growth temperate forest, covering 42,334 ha [22]. Due to its remote location and protection policy, the forest is well conserved and there is low species-limited human disturbance. There is a high diversity of wood-decaying fungi here and many new ones have been reported from this region recently [23-28]. The size and decay stage of dead wood are known to influence fungal diversity [14,29].

In this study we examined the species-area relationship for wood-decaying fungi in old-growth temperate forest to determine exactly how fungal diversity changed with increasing forest area. In addition, the main characteristics of dead wood that influence the distribution of wood-decaying fungi were investigated, with a view to enhancing conservation of these species.

## 2. MATERIALS AND METHODS

### 2.1 Study Area

The study site is in the Changbaishan Nature Reserve, located along the border of China and North Korea, extending from 127°42' to 128°17'E and 41°43' to 42°26'N (Figure 1a). The reserve is approximately 200,000 ha, with elevations ranging from 740 m to 2,691 m at the summit of Changbai Mountain, the highest mountain in northeastern China. The northern slope is relatively gentle (average gradient <3%), whereas the other slopes are quite steep (average gradient 10%). The area has a temperate continental climate, with long, cold winters and short, warm summers. The vegetation on the northern slope has a distinct zonal distribution. The forests between 750 m and 1,100 m are temperate, containing *Pinus koraiensis* Sieb. Et Zucc.

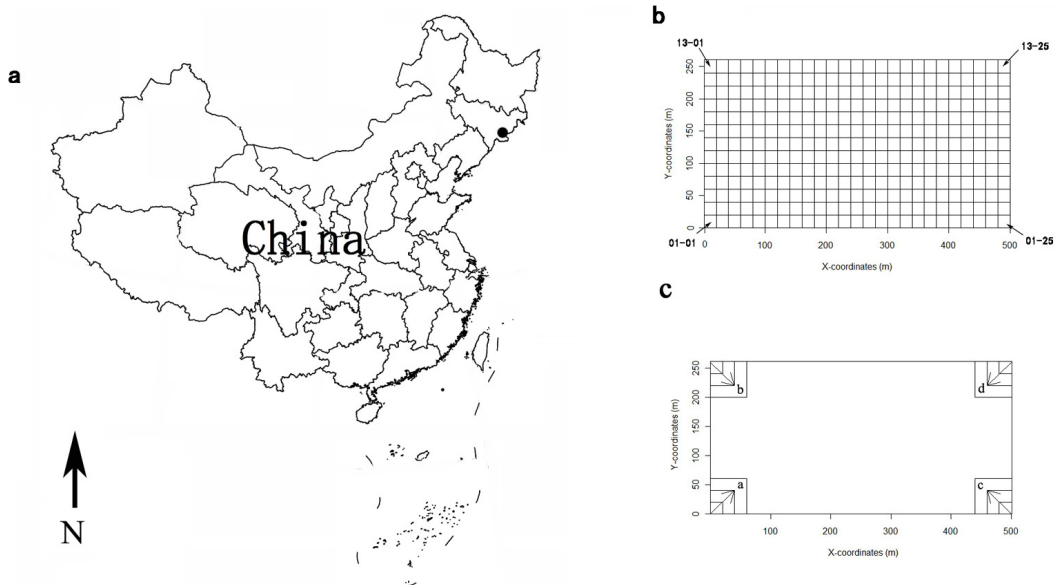
and broadleaved trees, including *Populus ussuriensis* Kom., *Betula platyphylla* Suk., *Tilia amurensis* Rupr., *Quercus mongolica* Fisch. Ex Ledeb., *Acer mono* Maxim. and *Fraxinus mandshurica* Rupr. Between 1,100 m and 1,700 m the vegetation becomes an evergreen coniferous forest dominated by *Abies holophylla* Maxim., *A. nephrolepis* (Trautv.) Maxim., and *Picea jezoensis* Carr. From 1,700 m to 2,000 m there is sub-alpine forest dominated by *B. ermanii* Cham. and *Larix olgensis* A. Henry; above 2,000 m there is bare rock and a volcanic lake.

In 2010, we chose a 13 ha area of broadleaved Korean pine mixed forest measuring 260 m × 500 m as the study plot, located in the interior of the Changbaishan Nature Reserve. This plot was subdivided into 325 contiguous 20 m × 20 m square subplots, and 1-25 in each numbered row of plots, starting in the southwest corner' or whatever is appropriate (Figure 1b). The elevation of the area ranges from 791.8 m to 809.5 m and the mean elevation is

801.5 m.

Because the basidiocarps of most wood-decaying fungi only appear briefly and at specific times of the year, we surveyed the plot twice: in early July and early September of 2010. Each survey lasted about 7 days. Species were only recorded if basidiocarps were found; we did not include non-fruiting mycelia, which may be present in trunks or wood, because these mycelia are very hard to identify. This approach has been widely used [30,31].

All of the subplots were examined and, within each, all of the polypores and corticoids (*Aphylllophorales*) growing on all dead wood with a diameter ≥ 1 cm were recorded. The stage of wood decay, adapted and modified from Edman and Jonsson [32], was classified as: 1= fallen trunks or branches with wood hard and bark intact; 2= fallen trunks and other dead wood with wood hard and bark broken up into patches but > 50% remaining; 3= all dead wood with wood hard to slightly soft, <50%



**Figure 1.** a. The study site located in the Changbaishan Nature Reserve, northeastern China. b. The 325 numbered square subplots (20 m × 20 m) located in the large 500 m × 260 m rectangular plot. c. The four locations of the starting points for the nested quadrats.

bark left, texture smooth; 4= all dead wood with wood soft with small to large pieces of wood lost; trunk outline intact to deformed. The living tree also has been included for some species growing on them.

The coordinates of each fungal record within the subplots were determined by measuring the vertical distance between the fungi to the edge of the subplot; the southwest corner was defined as the origin. These coordinates could also be transformed into the whole plot coordinates. The origin of the whole plot was located by GPS. If a fallen trunk was lying across two subplots, A and B, and a fungus growing on it was located in subplot A, the location of this fungus was recorded as being in subplot A. When the same fungal species were found on an individual host, multiple fruiting bodies of the same species were counted as only a single individual. At a single location, if the same fungus was present during the both surveys, it was counted as one individual during the year. The fungi were identified in situ or collected for microscopic identification. The host of each fungal individual was identified to the species level by local forestry experts.

## 2.2 Data Analyses

In this study, species richness is defined as the number of species in the study area and abundance as the number of all of the individuals. Density is defined as the number of individuals/unit area.

The statistical analyses of the fungal data for each plot were based on nested quadrats, from the first small plot (20 m × 20 m), increasing to cover the entire 260 m × 500 m plot, with the four different starting points as shown in Figure 1c. Data was cumulative, so the large quadrats always included data from the small quadrats that

they contained.

The species–area relationships were examined in relation to three models: the power model, the exponential model and the logistic model. The goodness-of-fit of the curves to the models was determined using the sum of squares of the residuals. The simplest way to test whether models are significantly different is to check the 95% confidence intervals of the model parameters [33]. If the confidence intervals for corresponding parameters do not overlap, then we conclude they are significantly different. All the statistical tests of significance and confidence intervals in this paper were calculated for the  $p=0.05$  level. Four factors were selected: the species and number of dead wood fragments, the species and number of living trees in the plot. The results of a simple regression analysis were used to determine which factors were most influential. The statistical analysis was conducted using R version 2.13.0.

The distribution and diversity of wood-decaying fungi on various sizes of dead wood fragments and the decay stage were investigated by comparison with Coleman rarefaction curves [34].

## 3. RESULTS

### 3.1 Collection Results

In 2010, 1741 individual fungi were recorded, comprising 170 species (Table 1).

The dominant species in the wood-decaying fungal community in the plot included eight species each with more than 40 individuals, accounting for 46.1% of all of the records: *Ganoderma lipsiense*, *Hyphodontia flavipora*, *Irpex lacteus*, *Oxyporus populinus*, *Stereum subtomentosum* and *Trametes versicolor*.

These data were examined in relation to the nested quadrats originating from the

four different points shown in Figure 1c.

### 3.2 Species–area Relationship

The species–area relationship took the form of a curve with a progressively more gentle gradient. When the sampling area was 4 ha (31% of the entire plot), there were 103 species on average, approximately 60% of the total number of species in the plot. As the size of the sampling area increased, the rate of species increase declined (Figure 2). Of the three models considered, the Logistic best described the species–area curves, with the lowest sums of residuals. The Exponential model provided the

poorest fit for the data. The Power model provided a better description of the figures than the Exponential model (Table 2). In addition, the location of the first sampling point had no effect on the model parameters. For example, the limits of the 95% confidence intervals for parameter  $\beta$  in the logistic model for sample designs a and b were 52.71 to 57.01 and 55.49 to 59.37, respectively (Table 2), and thus have a large overlap. Therefore, the Logistic model best described the wood-decaying fungi species–area relationship in the old-growth temperate forest of Changbai Mountain.

**Table 1.** The species and number of individuals of wood-decaying fungi in the temperate forest plot.

Species	No. of occurrences
<i>Antrodia xantha</i> (Fr.) Ryvarden	1
<i>Antrodia albida</i> (Fr.) Donk	14
<i>Antrodia heteromorpha</i> (Fr.) Donk	1
<i>Antrodia hingganensis</i> Y.C. Dai & Penttilä	1
<i>Antrodia macrospora</i> Bernic. & De Dom.	1
<i>Antrodia malicola</i> (Berk. & M.A. Curtis) Donk	5
<i>Antrodia serialis</i> (Fr.) Donk	1
<i>Antrodiella albocinnamomea</i> Y.C. Dai & Niemelä	13
<i>Antrodiella brunneimontana</i> (Corner) T. Hatt.	2
<i>Antrodiella gypsea</i> (Yasuda) T. Hatt. & Ryvarden	3
<i>Antrodiella semisupina</i> (Berk. & M.A. Curtis) Ryvarden s. l.	1
<i>Auricularia auricula-judae</i> (Bull.) Quél.	1
<i>Bjerkandera adusta</i> (Willd.) P. Karst.	70
<i>Bjerkandera fumosa</i> (Pers.) P. Karst.	1
<i>Castanoporus castaneus</i> (Lloyd) Ryvarden	4
<i>Ceriporia purpurea</i> (Fr.) Donk	1
<i>Ceriporiopsis aneirina</i> (Sommerf.) Domański	1
<i>Ceriporiopsis balaenae</i> Niemelä	1
<i>Ceriporiopsis gilvescens</i> (Bres.) Domański	3
<i>Cinereomyces lenis</i> (P. Karst.) Spirin	1
<i>Cinereomyces vulgaris</i> (Fr.) Spirin	2
<i>Climacocystis borealis</i> (Fr.) Kotl. & Pouzar	1
<i>Climacodon pulcherrimus</i> (Berk. & M.A. Curtis) Nikol.	1
<i>Coltricia perennis</i> (L.) Murrill	1
<i>Corticium roseocarneum</i> (Schwein.) Hjortstam	1

Species	No. of occurrences
<i>Cyclomyces xeranticus</i> (Berk.) Y.C. Dai & Niemelä	9
<i>Cylindrobasidium evolvens</i> (Fr.) Jülich	1
<i>Daedalea dickinsii</i> Yasuda	32
<i>Daedalea incana</i> (P. Karst.) Sacc. & D. Sacc.	1
<i>Daedaleopsis confragosa</i> (Bolton) J. Schröt.	3
<i>Daedaleopsis sinensis</i> (Lloyd) Y.C. Dai	1
<i>Daedaleopsis tricolor</i> (Bull.) Bondartsev & Singer	24
<i>Datronia mollis</i> (Sommerf.) Donk	2
<i>Datronia stereoides</i> (Fr.) Ryvarden	6
<i>Dentipellis fragilis</i> (Pers.) Donk	7
<i>Dentipellis leptodon</i> (Mont.) Maas Geest.	1
<i>Diplomitoporus flavescens</i> (Bres.) Domański	1
<i>Elmerina</i> cf. <i>hexagonoides</i> (A. David & Jaq.) Núñez	1
<i>Elmerina cladophora</i> (Berk.) Bres.	7
<i>Elmerina holophaea</i> (Pat.) Parmasto	11
<i>Fomes fomentarius</i> (L.) Fr.	30
<i>Fomitiporia punctata</i> (P. Karst.) Murrill	11
<i>Fomitopsis cajanderi</i> (P. Karst.) Kotl. & Pouzar	4
<i>Fomitopsis niveomarginata</i> L.W. Zhou & Y.L. Wei	4
<i>Fomitopsis pinicola</i> (Sw.) P. Karst.	14
<i>Funalia trogii</i> (Berk.) Bondartsev & Singer	3
<i>Ganoderma lipsiense</i> (Batsch) G.F. Atk.	42
<i>Ganoderma lingzhi</i> Sheng H.Wu, Y.C. Dai & Y. Cao	1
<i>Gelatoporia pannocincta</i> (Romell) Niemelä	1
<i>Gelatoporia subvermispora</i> (Pilát) Niemelä	1

Table 1. Continued.

Species	No. of occurrences	Species	No. of occurrences
<i>Gloeocystidiellum clavuligerum</i> (Höhn. & Litsch.) Nakasone	8	<i>Perenniporia maackiae</i> (Bondartsev & Ljub.) Parmasto	16
<i>Gloeophyllum sepiarium</i> (Wulfen) P. Karst.	2	<i>Perenniporia medulla-panis</i> (Jacq.) Donk	1
<i>Gloeoporus dichrous</i> (Fr.) Bres.	4	<i>Perenniporia subacida</i> (Peck) Donk	2
<i>Haploporus odoros</i> (Sommerf.) Bondartsev & Singer	1	<i>Perenniporia tenuis</i> (Schw.) Ryvardeen	1
<i>Haploporus</i> sp.	3	<i>Phaeolus schweinitzii</i> (Fr.) Pat.	1
<i>Hericium coralloides</i> (Scop.) Pers.	5	<i>Phanerochaete chrysorbiza</i> (Torr.) Budington & Gilb.	2
<i>Hericium erinaceus</i> (Rull ex F.) Pers.	12	<i>Phanerochaete filamentosa</i> (Berk. & M.A. Curtis.) Burds.	3
<i>Hydnum</i> sp.	4	<i>Phellinidium fragrans</i> (M.J. Larsen & Lombard) Nuss	2
<i>Hymenochaete corrugata</i> (Fr.) Lév.	2	<i>Phellinus baumii</i> Piltt	8
<i>Hymenochaete intricata</i> (Lloyd) S. Ito	20	<i>Phellinus ferreus</i> (Pers.) Bourdot & Galzin	1
<i>Hymenochaete tabacina</i> (Sowerby) Lév.	16	<i>Phellinus ferruginosus</i> (Schrad.) Pat.	3
<i>Hyphodontia flavipora</i> (Cooke) Sheng H. Wu	67	<i>Phellinus gilvus</i> (Schwein.) Pat.	13
<i>Hyphodontia latitans</i> (Bourdot & Galzin) Ginns & M.N.L. Lefebvre	1	<i>Phellinus laevigatus</i> (Fr.) Bourdot & Galzin	2
<i>Hyphodontia paradoxa</i> (Schrad.) Langer & Vesterh.	2	<i>Phellinus lundellii</i> Niemelä	1
<i>Inonotus hispidus</i> (Bull.) P. Karst.	3	<i>Phellinus pini</i> (Brot.) A. Ames	14
<i>Inonotus obliquus</i> (Ach. ex Pers.) Pilát	1	<i>Phelebia chrysocreas</i> (Berk. & M.A. Curtis) Burds.	1
<i>Inonotus radiatus</i> (Sowerby) P. Karst.	1	<i>Phelebia radiata</i> Fr.	11
<i>Irpex hydroides</i> Y.W. Lim & H.S. Jung	8	<i>Phelebia rufa</i> (Pers.) M.P. Christ.	1
<i>Irpex lacteus</i> (Fr.) Fr. s. l.	197	<i>Phelebia tremellosa</i> (Schrad.) Nakasone & Burds.	33
<i>Ischnoderma benzoinum</i> (Wahlenb.) P. Karst.	6	<i>Phelebiopsis gigantea</i> (Fr.) Jülich	1
<i>Junghubnia luteoalba</i> (P. Karst.) Ryvardeen	2	<i>Plicatura crispa</i> (Pers.) Rea	10
<i>Junghubnia nitida</i> (Pers.) Ryvardeen	15	<i>Polyporus alveolaris</i> (DC.) Bondartsev & Singer	1
<i>Junghubnia semisupiniformis</i> (Murrill) Ryvardeen	1	<i>Polyporus badius</i> (Pers.) Schwein.	13
<i>Laetiporus sulphureus</i> (Bull.) Murrill	4	<i>Polyporus ciliatus</i> Fr.	1
<i>Lenzites betulina</i> (L.) Fr.	7	<i>Polyporus hemicapnodes</i> Berk. & Broome	19
<i>Leucopbellinus irpicoides</i> (Pilát) Bondartsev & Singer	17	<i>Polyporus mori</i> (Pollini) Fr.	1
<i>Lopharia cinerascens</i> (Schwein.) G. Cunn.	1	<i>Polyporus umbellatus</i> (Pers.) Fr.	1
<i>Lopharia mirabilis</i> (Berk. & Broome) Pat.	11	<i>Polyporus varius</i> (Pers.) Fr.	1
<i>Melanoporia castanea</i> (Imazeki) T. Hat. & Ryvardeen	9	<i>Postia alni</i> Niemelä & Vampola	8
<i>Merulius tremellosus</i> Schrad.	6	<i>Postia caesia</i> (Schrad.) P. Karst.	1
<i>Mycorrhaphium adustum</i> (Schwein.) Maas Geest.	22	<i>Postia fragilis</i> (Fr.) Jülich	7
<i>Oligoporus obductus</i> (Berk.) Gilb. & Ryvardeen	3	<i>Postia guttulata</i> (Peck) Jülich	1
<i>Oligoporus seiceomollis</i> (Romell) Bondartseva	12	<i>Postia hibernica</i> (Berk. & Broome) Jülich	1
<i>Omnia tomentosa</i> (Fr.) P. Karst.	2	<i>Postia lactea</i> (Fr.) P. Karst.	1
<i>Oxyporus corticola</i> (Fr.) Ryvardeen	5	<i>Postia leucomallella</i> (Murrill) Jülich	1
<i>Oxyporus latemarginatus</i> (Durieu & Mont.) Donk	1	<i>Postia pileata</i> (Parmasto) Y.C. Dai & Renvall	6
<i>Oxyporus obducens</i> (Pers.) Donk	1	<i>Postia stiptica</i> (Pers.) Jülich	3
<i>Oxyporus populinus</i> (Schumach.) Donk	92	<i>Protomerulius caryae</i> (Schwein.) Ryvardeen	1
<i>Oxyporus sinensis</i> X.L. Zeng	1	<i>Pycnoporellus fulgens</i> (Fr.) Donk	2
<i>Parmastomyces mollissimus</i> (Maire) Pouzar	1	<i>Pyrrhoderma scaura</i> (Lloyd) Ryvardeen	4
<i>Peniophorella odontiformis</i> (Boidin & Berthier) K.H. Larss.	3	<i>Radulomyces copelandii</i> (Pat.) Hjortstam & Spooner	1
		<i>Ramaria flaccida</i> (Fr.) Bourdot	11
		<i>Resupinatus</i> sp.	1
		<i>Rigidoporus crocatus</i> (Pat.) Ryvardeen	1

**Table 1.** Continued.

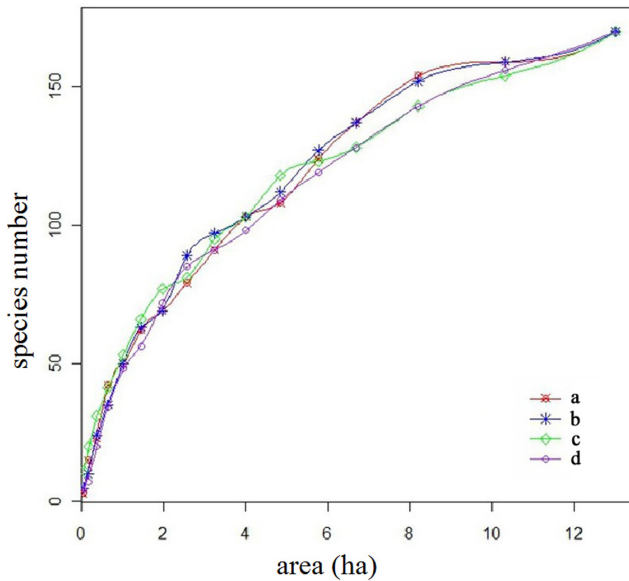
Species	No. of occurrences	Species	No. of occurrences
<i>Rigidoporus eminens</i> Y.C. Dai	2	<i>Trametes gibbosa</i> (Pers.) Fr.	8
<i>Rigidoporus microporus</i> (Sw.) Overeem	3	<i>Trametes hirsuta</i> (Wulfen) Pilát	11
<i>Schizophyllum commune</i> Fr.	11	<i>Trametes ochracea</i> (Pers.) Gilb. & Ryvarden	9
<i>Schizopora cystidiata</i> A.D. David & Rajchenb.	2	<i>Trametes orientalis</i> (Yasuda) Imazeki	1
<i>Serpula himantoides</i> (Fr.) P. Karst.	1	<i>Trametes pubescens</i> (Schumach.) Pilát	10
<i>Serpula lacrymans</i> (Wulfen) J. Schröt.	1	<i>Trametes</i> sp.	1
<i>Skeletocutis nivea</i> (Jungh.) Jean Keller	32	<i>Trametes velutina</i> (Pers.) G. Cunn.	19
<i>Skeletocutis ochroalba</i> Niemelä	3	<i>Trametes versicolor</i> (L.) Lloyd	96
<i>Spongipellis spumeus</i> (Sowerby) Pat.	29	<i>Trametopsis cervina</i> (Schwein.) Tomšovský	5
<i>Steccherinum laeticolor</i> (Berk. & M.A. Curtis.) Banker	1	<i>Trichaptum abietinum</i> (Pers.) Ryvarden	59
<i>Steccherinum ochraceum</i> (Pers. Ex J.F. Gmelin) Gray	37	<i>Trichaptum pargamenum</i> (Fr.) G. Cunn.	21
<i>Stereum gausapatum</i> (Fr.) Fr.	9	<i>Trichaptum polycystidiatum</i> (Pilát) Y.C. Dai	1
<i>Stereum hirsutum</i> (Willd.) Pers.	35	<i>Tyromyces canadensis</i> Overh. ex J. Lowe	3
<i>Stereum subtomentosum</i> Pouzar	179	<i>Tyromyces chioneus</i> (Fr.) P. Karst.	2
<i>Thelephora anthocephala</i> (Bull.) Fr.	1	<i>Tyromyces kmetii</i> (Bres.) Bondartsev & Singer	1
<i>Tomentella crinalis</i> (Fr.) M.J. Larsen	2	<i>Xylobolus frustulatus</i> (Pers.) Boidin	27
<i>Trametes conchifer</i> (Schwein.) Pilát	3	<i>Xylobolus</i> sp.	4
		<i>Xylobolus spectabilis</i> (Klotzsch) Boidin	20

**Table 2.** Comparison of Logistic, Exponential and Power models with respect to the wood-decaying fungi of according to a, b, c and d design separately.

Design	Logistic model $S = \alpha / \beta \pm \exp(-\gamma \ln(A))$		Exponential model $S = \alpha \pm \beta \ln(A)$		Power model $S = \alpha A^\beta$	
	Parameters $\pm$ conf.	Residual	Parameters $\pm$ conf.	Residual	Parameters $\pm$ conf.	Residual
a	$\alpha = 54.86 \pm 2.15$ $\beta = 0.14 \pm 0.03$ $\gamma = 0.69 \pm 0.06$	14.50	$\alpha = 66.93 \pm 4.9$ $\beta = 31.03 \pm 2.9$	67.79	$\alpha = 50.23 \pm 1.85$ $\beta = 0.5 \pm 0.02$	20.31
b	$\alpha = 57.43 \pm 1.94$ $\beta = 0.2 \pm 0.02$ $\gamma = 0.79 \pm 0.05$	12.11	$\alpha = 67.48 \pm 4.83$ $\beta = 31.64 \pm 2.86$	66.81	$\alpha = 51.3 \pm 2.23$ $\beta = 0.49 \pm 0.02$	24.48
c	$\alpha = 59.99 \pm 1.51$ $\beta = 0.12 \pm 0.03$ $\gamma = 0.57 \pm 0.03$	7.75	$\alpha = 69.91 \pm 4.41$ $\beta = 28.93 \pm 2.62$	61.04	$\alpha = 54.49 \pm 1.09$ $\beta = 0.45 \pm 0.01$	11.82
d	$\alpha = 52.67 \pm 1.62$ $\beta = 0.17 \pm 0.02$ $\gamma = 0.76 \pm 0.05$	10.89	$\alpha = 63.94 \pm 4.75$ $\beta = 30.82 \pm 2.82$	65.71	$\alpha = 47.8 \pm 1.86$ $\beta = 0.51 \pm 0.02$	20.51

Taking starting point a as an example, the fitted equations were as follows: Logistic model,  $S = 54.86 / (0.14 + \exp(-0.69 \ln(A)))$  i.e.  $S = 54.86 / (0.14 + A^{-0.69})$ ; Exponential model,  $S = 66.93 + 31.03 \ln(A)$ ; and Power model,  $S = 50.23 A^{0.5}$ . Using the

three fitted models, the estimated numbers of species in the different areas are presented in Figure 3. The predictions of the logistic model are closer to the observed numbers in the plots.



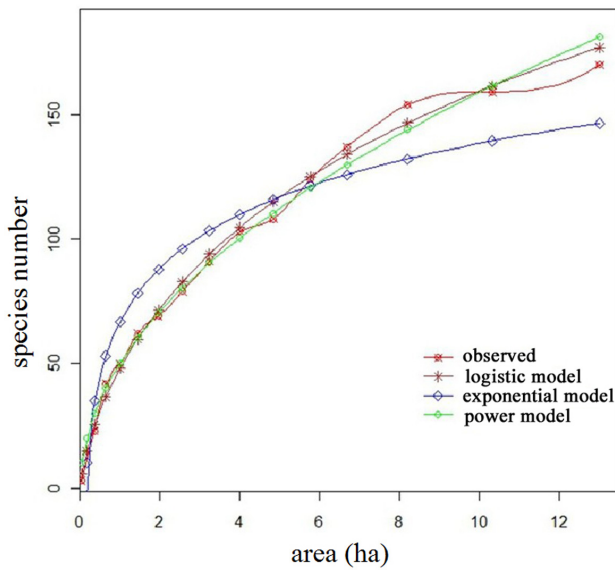
**Figure 2.** Species-area curves for the different starting points (a, b, c and d) shown in Figure 1c.

For the small sampling areas (0.04 ha), the Exponential model consistently produces large deviations from the observed data, and the Power model triples the value of the observed data (Table 3). Generally

speaking, the Power model provides a better fit for the observations than the exponential model. The predicted values based on the Logistic model are closer to the observed numbers for the plots (Figure 3).

**Table 3.** The predictions of species for the old-growth forest using the Logistic, Exponential and Power models according to a design.

Area (ha)	No. of observed species	Prediction using the following models		
		Logistic	Exponential	Power
0.04	3	5.9	—	10.0
0.16	15	14.9	10.1	20.1
0.36	23	25.4	35.2	30.1
0.64	42	36.6	53.1	40.2
1	50	48.1	66.9	50.2
1.44	62	59.8	78.2	60.3
1.96	69	71.4	87.8	70.3
2.56	79	82.8	96.1	80.4
3.24	91	93.9	103.4	90.4
4	103	104.7	109.9	100.5
4.84	108	115.0	115.9	110.5
5.76	124	125.0	121.3	120.6
6.68	137	133.9	125.9	129.8
8.2	154	146.6	132.2	143.8
10.32	159	161.5	139.4	161.4
13	170	176.8	146.5	181.1

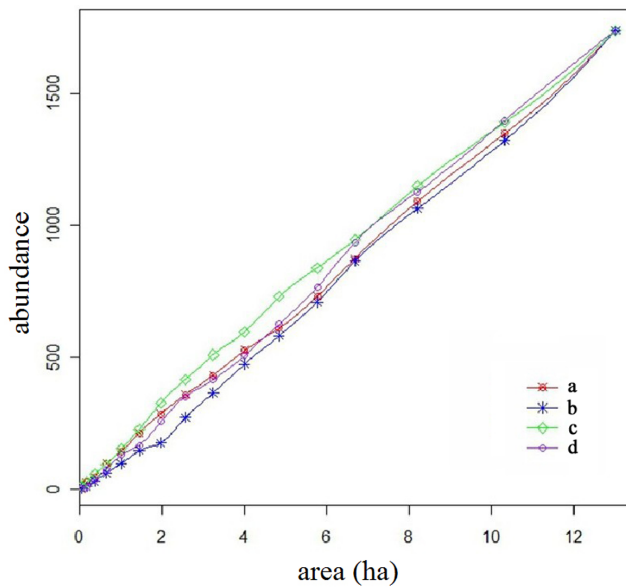


**Figure 3.** Logistic, Exponential and Power models compared to the observed species-area curve for sample starting point a.

**3.3 Abundance-area Relationship**

The relationships between the abundance and sampling area for each of the four starting points are approximately linear (Figure 4). Ordinary least square linear regression was used in the analysis, and the

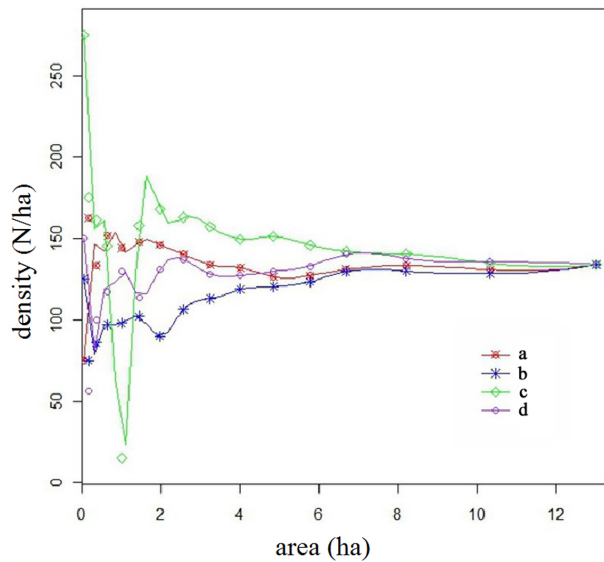
abundance of fungi was significantly correlated to the area, with the coefficients being above 0.99. The predicted values of abundance did not vary significantly for the different sample starting points.



**Figure 4.** Abundance-area relationships for the different sample starting points (a, b, c and d) shown in Figure 1 c.

The density (individuals/unit area)-area curves (Figure 5) indicate that the density varied greatly depending on where sampling started in the plot; this was particularly true for sampling areas less than 4 ha. This result indicated that the

variance of any estimates would be very large with smaller sample sizes and that the occurrence of the fungi is random. When the sampling area increased to areas greater than 8 ha, the density varied little.



**Figure 5.** Density-area relationships for the four different sample starting points (a, b, c and d) shown in Figure 1c.

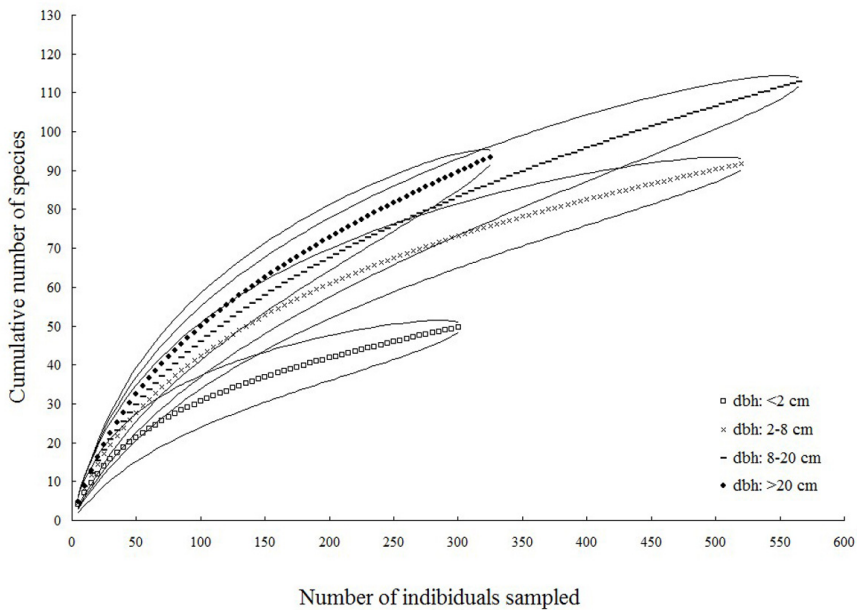
### 3.4 Distribution of Wood-decaying Fungi on Dead Wood Fragments of Different Sizes

Comparisons of cumulative species richness on fragments of dead wood of different sizes, based on rarefaction curves, showed that with relatively few individuals (less than 300), there was a positive relationship between dead wood fragment size and number of fungal species. Trunks with a diameter  $>20$ cm have the highest species richness and twigs with a diameter  $\leq 2$  cm have relatively lower species richness. When there were more than 300 individuals, the greatest number of species and individuals was on dead wood with a diameter between 8 and 20 cm. This may be because the sizes of dead wood fragments

were not evenly distributed. There were many fewer fragments with a diameter  $>20$ cm than with a diameter between 8 and 20 cm. The numbers of species and individuals on twigs (diameter  $\leq 2$  cm) were significantly lower (Figure 6). However, some species prefer twigs; for example, *Polyporus hemicapnodes* and *Irpex lacteus* were only found on twigs.

### 3.5 Distribution of Wood-decaying Fungi on Wood of Different Decay Stages

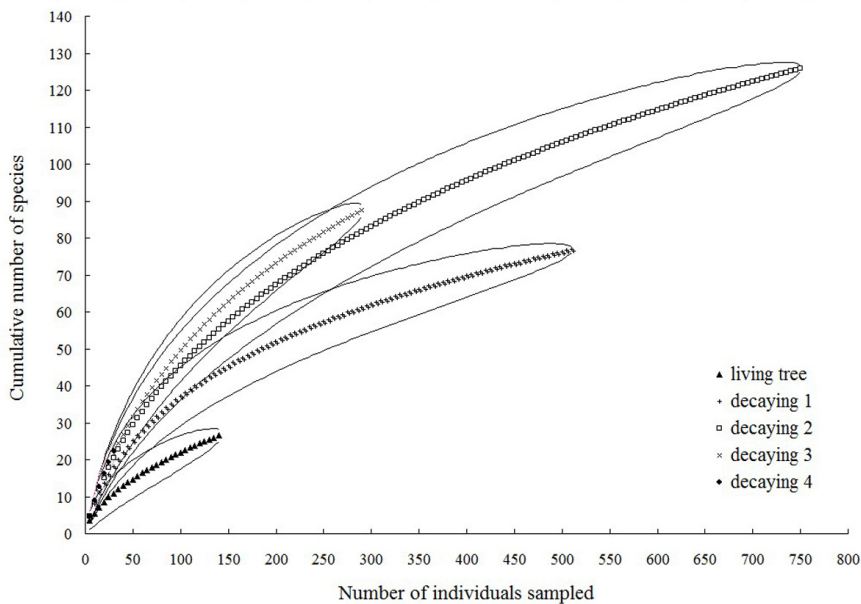
Besides the size of dead wood fragments, the decay stage is also an important factor in determining the distribution of wood-decaying fungi. By comparing cumulative species richness on dead wood in different stages of decay, we found that more species



**Figure 6.** Coleman rarefaction curves for wood-decaying fungi species richness in relation to dead wood fragment diameter size classes. The thin lines indicate 95% confidence intervals around the means for each substrate class.

and individuals were found on wood in decay stage 2 (Figure 7). Decay stage 4, i.e. soft wood with small to large pieces

missing and the trunk outline deformed, supported the lowest numbers of species and individuals.



**Figure 7.** Coleman rarefaction curves for wood-decaying fungi species richness in relation to decay stages. Thin lines indicate 95% confidence intervals around the means for each substrate class.

## 4. DISCUSSION

### 4.1. Species–area Relationship

Within certain limits, the numbers of species increased with increasing sampling size, but the relationship was not linear and the rate of increase gradually declined. Although an asymptote was not reached, if the sample size was increased further, then eventually, assuming a large enough forest, no more new species would be found. In contrast, the number of individual fungi increased linearly with area sampled up to our maximum plot size.

We found that species known to be generally common occurred more frequently than threatened species. Spatial heterogeneity in species distributions can be the result of dispersal, colonization and extinction and is considered a neutral process [35,36]. In theory, there is an equal chance that any species will be present. However, the spore production, dispersal and colonization ability of wood-decaying fungi control their spatial distribution [37,38]. Further research is required to elucidate the reasons for the distribution of our study species.

Our results indicate that the species–area relationship of wood-decaying fungi in the old-growth temperate forest studied are best described by a logistic model, although a power model provides nearly as good a fit. The latter indicates the presence of a dynamic equilibrium [39], so our results suggest that the wood-decaying fungi in this temperate forest are not currently in a state of equilibrium. If this is the case, species abundance could be estimated in an unbiased way by any sample size since fungi would be randomly distributed throughout the whole plot. In fact, the density in the different sample sets with different starting points varied greatly within small sampling areas, indicating that the fungi were not randomly distributed

at a small scale. In the 20 m × 20 m small plots, for example, the number, size and decay stage of dead wood fragments varied greatly. The spatial heterogeneity of the substrate means that wood-decaying fungi could be randomly distributed at small scale.

### 4.2 Factors Influencing Species Distribution

Dead wood size and decay stage are two important factors affecting fungal species composition and individual occurrence [24, 40-42]. Both characteristics and the spatiotemporal availability of dead wood are important in explaining the distribution patterns and population dynamics of wood-decaying fungal communities [43].

Our results showed that, in the old-growth temperate forest, the number of species was positively correlated with the diameter of the dead wood fragments (Figure 6). This sort of relationship has been reported previously [14,16].

The greatest numbers of wood-decaying fungi were found on moderately hard wood – substrate with hard wood and bark broken up into patches but covering > 50% – supported the most species and individuals. We recorded 126 species on substrate classified as decay stage 2, representing 72.4% of all the species in the plot. In contrast, only 25 species were recorded on wood in decay stage 4, and all these were present on wood in other decay stages, in fact, most of them were common in the forest. Once they colonize the fresh substrate successfully, such species are able to utilize the resource fully. Our results suggest that moderately hard wood is the most important substrate to enhance wood-decaying fungi diversity, as found by Yamashita et al. [44].

### 4.3 Conservation Relevance

Wood-decaying fungi have been extensively studied in China, but most studies focused on taxonomy and phylogeny [45-51], and only a few on the ecology and conservation [41-42, 52]. The present paper is to find the spatial distribution of wood-decaying fungi in the studied area, and the results will be important for conservation on wood-decaying fungi.

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