Title: The role of decaying logs in nursing soil fungal diversity varies with decay classes in the forest ecosystem

Running head: Soil fungi vary with log decay classes

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Abstract

Soil fungi are crucial drivers of log decomposition in forest ecosystems, but how soil fungal community composition varies during the process of log decomposition remains poorly understood. We conducted an experiment incubating decaying logs in a subalpine coniferous forest on the eastern Qinghai-Tibet Plateau, China. Five classes of decaying Minjiang fir (*Abies faxoniana*) logs were incubated on the forest floor, and the composition and diversity of fungal communities in soils underneath decaying logs were measured using high-throughput sequencing. A total of 4321 operational taxonomic units (OTUs) were detected by Illumina Novaseq sequencing analysis. Soil fungal diversity differed significantly during the process of log decomposition and was highest in decay classes III or IV. Basidiomycota and Ascomycota were dominant phyla regardless of log decay classes. Moreover, the proportion of arbuscular mycorrhiza, wood saprotroph and saprotroph increased during the process of log decomposition, but that of ectomycorrhiza decreased. The structure of soil fungal community underneath decaying logs varied greatly with decay classes. Different decay classes of logs favor special fungal groups, implying that the ecological effects of logs at differing decay classes on soil fungal communities were different.

Key words: *Abies faxoniana*, coarse woody debris, community composition, functional group, soil fungal, subalpine forest

1.Introduction

Decaying logs are an important habitat for many organisms and play crucial roles in

42 the global carbon cycle, soil formation, and water and soil conservation (Harmon et al.
43 1986; Lassauce et al. 2011; Forrester et al. 2012). During the process of log
44 decomposition, fungi exhibit strong priority effects (Fukami et al. 2010, Leopold et al.
45 2017). Fungal hyphae can penetrate into the woody debris and secrete extracellular
46 enzymes to decompose refractory organics such as lignocellulose (Baldrian and Banin
47 2017), finally releasing soluble substrates for microbial uptake (Moorhead et al. 2012).
48 The logs are in direct contact with soil surface and therefore might alter the fungal
49 community structure of underlying soil during the decomposition process. Zalamea et
50 al. (2016) and Semchenko et al. (2018) have reported that the decomposition of logs
51 directly affects the physical, chemical and biological properties of soils underneath the
52 logs. Minnich et al. (2021) have also found that deadwood can affect soil microbial
53 community structure. Previous studies have reported the role of deadwood in
54 conservation of macrofungi, plants and invertebrates (Bani et al. 2018), but the
55 responses of composition and functional groups of soil fungal community to log
56 decomposition have rarely been studied.

57 Soil fungi are key participants in the biogeochemical cycles of forest ecosystems,
58 playing essential roles in the formation and development of soil, storage of soil carbon
59 (C), nutrient cycling and energy flow (Tedersoo et al. 2014). The role of soil fungal
60 community is closely related to its structure and diversity, and the structure and
61 diversity of the soil fungal community are affected by biological and abiotic factors
62 such as soil moisture and temperature and substrate quality (Chen et al. 2017b;
63 Asemaninejad et al. 2018). Lindahl et al. (2007) have observed the presence of

saprotrophic, wood-decomposer fungi in soils. These fungi are main factors in decomposing organic matter and are critical in regulating nutrient cycling. Some fungal species are found solely in the soil underneath decaying wood (Mäkipää et al. 2017). Some mycorrhizal fungi have ability to colonize the wood substrate in contact with soil surface, break down organic matter, and even tend to produce fruiting bodies more often in wood than in soil (Lindahl and Tunlid 2015). In addition, previous studies have observed that the effect of deadwood on soil varies with the decay stage (Bł ońska et al. 2017; Zalamea et al. 2007), and that the stage of decomposition has an impact on the C:N:P stoichiometry of the soil (Wojciech et al. 2019). There is no obvious sign of decomposition in newly formed logs (Ganjegunte et al. 2004), while highly decayed logs have a larger contact area with the forest floor, thus favouring sediment adsorption (Barker, 2008), and releasing more ions into the surface layers of soil than less-decomposed wood, which may further cause differences in soil fungal community structure (Jarosł aw et al. 2017). Thereby, the composition and diversity of soil fungal community might be closely related with the log decay process.

Because it is affected by the limitation of low temperature and frequent geological disasters, such as earthquakes and mudslides, the soil in the subalpine forest on the eastern Qinghai-Tibet Plateau develops slowly (Yang and Wu 2021). Therefore, soil organic layer and the decaying logs on the ground play an important role for biodiversity conservation, nutrient cycling, and water and soil conservation (Yang and Wu 2021). The goal of this study was to analyze the effects of decaying logs on the composition of soil fungal communities and the response of the fungal community and

functional groups to the decay classes. We hypothesized that (1) decaying logs favoured different groups of soil fungi thus altering soil fungal communities; and (2) highly decayed logs would lead to stronger effects on soil fungal communities. We tested these hypotheses by incubating decaying logs in a subalpine coniferous forest on the eastern Qinghai-Tibet Plateau, China. Minjiang fir (*Abies faxoniana*) is the dominant tree species in this region. Minjiang fir logs at various stages of decay were incubated for six years on the forest floor, and the compositions of the soil fungal communities in the soil underneath the logs were determined using high-throughput sequencing. The objective of this study was thus to assess the ecological effects of logs at differing decay classes on soil fungal communities.

2. Materials and methods

2.1 Site description

The study was conducted at the Long-Term Research Station of Alpine Forest Ecosystems (31°14′-31°19′N, 102°53′-102°57′E; 2458-4619 m a.s.l.) in Li County, Sichuan Province, southwestern China. The region is a transitional area between the Tibetan Plateau and the Sichuan Basin. The annual mean temperature and precipitation are approximately 2-4 °C and 850 mm, respectively (Chang et al. 2019). The seasonal soil freeze-thaw period begins in early November and ends in April the following year. The soil is classified as Cambisols. The accumulation of large amounts of woody debris (53 $Mg \cdot ha^{-1}$) in this region (Xiao et al. 2016) plays crucial roles in maintaining soil fertility, controlling soil erosion and promoting biodiversity. The trees consist mainly of Minjiang fir (*Abies faxoniana*), cypress (*Sabina saltuaria*), larch (*Larix mastersiana*)

and red birch (*Betula albo-sinensis*), with Minjiang fir accounting for 80% of the total basal area at the site (Xiao et al. 2014). The main understory shrubs include willow (*Salix paraplesia*) and azalea (*Rhododendron lapponicum*).

2.2 Experimental design

We established a permanent 100 × 100 m plot of primary Minjiang fir forest in the nature reserve in August 2013 based on previous studies (Chang et al. 2019; Chang et al. 2020) and three 25 × 25 m subplots with similar slope aspects, slope degrees, canopy closures and tree heights. Logs of Minjiang fir with 35 ± 5 cm in diameter in five decay classes (I-V, at increasing levels of decay) described in detail by Chang et al. (2019) and Wang et al. (2021) were collected. The logs of decay class I were from newly felled trees, representing the start of decomposition, and the logs of classes II-V were collected from the primary Minjiang fir forest neighbored the permanent plot. All logs were sawed on-site into lengths of 120 cm and carefully placed on the forest floor under the closed canopy in each subplot. See Chang et al. (2020) and Wang et al. (2021) for more details about the placement and arrangement of decaying logs.

2.3 Sampling

In August 2019, after decaying logs were carefully removed, soil samples were collected in each subplot using an auger (10 cm long, 5 cm diameter) from the organic layer of the forest floor. Control samples (CK) were also collected 3 m away from the decaying logs. The samples were transported to the laboratory on ice packs in a cooler. A total of 54 soil samples were collected, i.e., (1 CK + 5 decay classes) × 3 replicates

× 3 subplots. Visible living plant material was removed from the samples, and about 20g of soil was used to determine the water content (WC). The samples were passed through a 2-mm sieve, about 10g of air-dried soil samples were used for pH determination, and subsamples were stored at -70 and 4 °C for molecular and biochemical analysis, respectively. Five of the nine replicate samples were randomly selected for molecular biochemical analysis, thus making a total of 30 samples.

2.4 Soil physiochemical and biological analyses

Water content was determined by weighing the samples before and after drying. Soil pH was measured using a pH meter at a soil: water ratio of 1:2.5 (m/v). The concentrations of organic C (OC), total nitrogen (TN) and total phosphorus (TP) in soil were measured using potassium dichromate oxidation-ferrous sulfate titrimetry, Kjeldahl determination and molybdenum‐antimony colorimetry, respectively (Lu 1999). Soil microbial biomass C (MBC) and nitrogen (MBN) were measured using chloroform fumigation and K_2SO_4 extraction (Brookes et al. 1985; Vance et al. 1987). Soil microbial biomass phosphorus (MBP) was measured using chloroform fumigation and $NaHCO_3$ extraction (Brookes et al. 1982).

2.5 DNA extraction, PCR amplification and high-throughput sequencing

Microbial DNA was extracted from the samples using the FastDNA Spin Kit for Soil (MP Biomedicals, Solon, USA) following the manufacturer's instructions. DNA was checked for quality using agarose gel electrophoresis and ultraviolet absorbance (ND1000, Nanodrop, Thermo Fisher Scientific, Waltham Mass, USA). The DNA was diluted to 1 ng/μl using sterile water and stored at -20 °C until analysis.

A region of the fungal ITS2 gene was amplified, purified, quantified, pooled and sequenced on an Illumina NovaSeq platform at Novogene Genomics Institute (Beijing, China). The fungal ITS2 gene was amplified using the primer pair ITS3-2024F (GCATCGATGAAGAACGCAGC)/ITS4-2409R (TCCTCCGCTTATTGATATGC). All the samples were amplified in 3 replicates, and no-template controls were included in all steps of the process. Triplicate PCR amplicons were pooled together, after which they were detected by electrophoresis in a 2% (w/v) agarose gel, and bands were excised, mixed in equal density ratios and purified using a GeneJET Gel Extraction Kit (Thermo Fisher Scientific, Waltham Mass, USA). The purified PCR products were sequenced on the Illumina NovaSeq platform by Pair-End 250 The barcode sequences were spliced with FLASH (v 1.2.7) software to obtain the raw tags (Zhang et al. 2014). The clean tags were obtained by quality filtering the raw tags using Quantitative Insights Into Microbial Ecology (QIIME) (v1.9.0) software (Caporaso et al. 2010; Bokulich et al. 2013). Chimeric sequences were removed using the UCHIME algorithm (Edgar et al. 2011). USEARCH was used to identify and remove chimeras, and the remaining sequences were clustered to generate operational taxonomic units (OTUs) at the 97% similarity level (Edgar 2010; Magoč and Salzberg 2011). The UNIT (v 7.2) database (Kõljalg et al., 2013) and QIIME (v 1.9.0) (Altschul, 1990) software were selected as species annotation analysis for ITS. A rapid multiple sequence alignment was performed using MUSCLE (Edgar, 2004) software to obtain the phylogenetic relationship of all OTUs representing sequences. Normalization was performed based on the least amount of data in each sample, and subsequent analyses were based on the

normalized data.

In addition to fungal community composition, functional groups were assigned based on FUNGuild (Nguyen et al. 2016). For analysis, we classified the fungal taxa into six functional groups (i.e., animal pathogen, arbuscular mycorrhiza, ectomycorrhiza, plant pathogen, wood saprotroph and saprotroph) with some overlaps. 'other' (including ericoid mycorrhizal fungi, foliar endophytes, lichenized fungi, mycoparasites, etc.), and undetermined (OTUs that were not identified to genus or whose genus was not represented in the FUNGuild database) were included in analysis but the results on guild level were not shown. We considered only FUNGuild assignments with a confidence score of 'probable' or 'highly probable' and classified taxa with assignment scores below these as undetermined (Lankau and Keymer. 2016).

2.6 Statistical analyses

The Shannon and Simpson diversity indices, metrics of alpha diversity of the soil fungal communities, were calculated. The significance of the differences in alpha diversity of soil fungi among log decay classes was tested by Tukey's honestly significant difference (HSD) test when the results of variance analysis conducted with general linear models were significant at P =0.05. One-way ANOVA and HSD test were also performed to test the effects of decay class on the abundance of the fungal community. The effects of log decay classes on soil fungal communities were tested using permutational multivariate analysis of variance (PERMANOVA) based on Bray-Curtis distance and the analysis of similarity (ANOSIM), and visualised using two-dimensional Non-metric multidimensional scaling (NMDS) analysis based on Bray-

195 Curtis distance. Heatmap was used to show the relative abundance of dominant genera
196 and the proportion of functional groups of soil fungi from different decay classes of
197 logs. Spearman correlation analysis was used to identify relationships between soil
198 physicochemical properties and the relative abundances of fungal taxa. One-way
199 ANOVA was performed using SPSS 20.0 (IBM Corporation, Armonk, USA). Other
200 statistical analyses were performed using the VEGAN package in R (Oksanen et al.
201 2013; R Development Core Team 2015). The statistical tests were considered
202 significant at $P < 0.05$.

203 # 3. Results

204 ## 3.1 Characteristics of the sequence data and species alpha diversity

205 Across 30 soil samples underneath decaying logs, a total of 3 344 637 raw fungal
206 sequences, and 1 926 264 high-quality fungal sequences were retained after the raw
207 sequences were controlled for quality. The sequence data were classified into 4321
208 fungal OTUs at a cutoff in sequence similarity of 97%. The Shannon and Simpson
209 diversity indices for the fungal communities differed significantly among the decay
210 classes ($P < 0.05$) and were the highest for decay classes III and IV (Table 1).
211 However,the number of OTUs of soil fungal community was not significantly different
212 among log decay classes and neither between CK and presence of logs ($P > 0.05$) (Table
213 1). Compared with CK, soil fungi communities under decaying logs had more
214 independent OTUs (Fig. S1a), which was most for decay classes II and V (Fig. S1b).

3.2 Composition of fungi

Basidiomycota (22.0-49.3%), Ascomycota (15.7-41.5%) and Mortierellomycota (2.4-11.9%) were the most dominant fungal phyla, representing >65% of the total reads (Fig. 1a). The relative abundance of Mortierellomycota was significantly higher in the soil underneath decaying logs than in CK and was the lowest in decay class II and the highest in decay class IV ($P < 0.05$), while the relative abundances of Basidiomycota and Ascomycota did not differ significantly among the classes ($P > 0.05$) (Figs. 1a and S2a). The relative abundances of other phyla, including Rozellomycota, Glomeromycota, Chytridiomycota and Mucoromycota, were less than 2%. The relative abundances of these phyla were significantly affected by the decaying logs except Mucoromycota.

A total of 24 fungal genera (with relative abundance >1%) were identified across all samples (Fig. 1b). *Piloderma*, *Inocybe* and *Mortierella* were the three most abundant genera. The relative abundance of *Piloderma* in soils under decaying logs for decay classes I, II and IV was significantly higher than in CK, and significantly lower for decay classes III-V than I-II. The relative abundance of *Inocybe* in soils under decaying logs for decay classes I, II, IV and V was lower than in CK, and were lowest for decay class V. The relative abundance of *Mortierella* in soils under decaying logs for all decay classes was significantly higher than in CK (Figs. 1b and S2b). The relative abundances of most of the other genera, such as *Ilyonectria*, *Fusarium*, *Phlebia*, *Humicola* and *Pleotrichocladium*, were significantly higher in general under the logs than in CK (Fig. S2b).

Based on Bray-Curtis, PERMANOVA, ANOSIM and NMDS were used to compare the difference in composition of soil fungi between decay classes (Fig. 2). The composition of the soil fungal communities differed significantly among the classes (stress <0.2, ANOSIM, R = 0.628, P = 0.001). Additionally, PERMANOVA test verified that soil fungal communities significantly differed among log decay classes and were also affected by presence of logs (Table S1).

3.3 Compositions of fungal functional group inferred by FUNGuild

The relative abundance of most putative fungal functional groups was significantly affected across the treatments (Fig. 3). The proportion of arbuscular mycorrhiza, wood saprotrophs and saprotroph increased with the increase of decay classes of logs, while the proportion of ectomycorrhiza decreased, while the relative abundance of wood saprotrophs did not differ between CK and decay class I - III. The relative abundance of animal pathogen was highest for decay class IV, while the relative abundance of plant pathogen was highest for decay class III. Additionally, heatmap made based on fungal community composition and functional guilds showed that the community composition of soil fungi was similar under decay classes IV and V of logs, but different from that of CK, while those of soil fungi communities under early decomposition stage were more similar to that of CK (Fig. 4a and Fig. 4b).

3.4 Correlations between fungal composition and soil physicochemical properties

Spearman correlation heatmaps were analyzed to identify the relationships of the fungal communities with biochemical properties and environmental factors (Fig. 5).

Soil pH, microbial biomass carbon, microbial biomass nitrogen and total phosphorus were important factors correlated to soil fungal community composition. The relative abundance of Basidiomycota was correlated positively with microbial biomass carbon, microbial biomass nitrogen and total phosphorus, while the opposite trend was found for Ascomycota, Glomeromycota and Chytridiomycota (Fig. 5a). Microbial biomass carbon, microbial biomass nitrogen, total phosphorus and water content were negatively correlated with the relative abundances of the genera *Ilyonectria*, *Fusarium*, *Humicola*, *Pleotrichocladium*, *Chaetomium*, *Tetracladium*, *Dactylonectria*, and *Didymosphaeria*, but microbial biomass carbon, microbial biomass nitrogen, microbial biomass phosphorus and organic carbon were positively correlated with the relative abundances of *Cortinarius* and *Meliniomyces*. Soil pH was positively correlated with the relative abundances of *Ilyonectria*, *Fusarium*, *Humicola*, *Pleotrichocladium*, *Chaetomium*, *Tetracladium* and *Dactylonectria* (Fig. 5b).

4. Discussion

Level of decay in logs affects soil fungal community, consistent with our hypotheses. The diversity of soil fungal community was highest in decay classes III or IV (Table 1), and it tended to stabilize after that. Changes in fungal community were mostly explained by changes in genera that were not detected on phylum level. Additionally, the proportion of functional groups varied with decay classes of logs (Fig. 4), indicating that decaying logs favor different groups of soil fungi thus altering the composition of soil fungal communities. The composition of soil fungal communities underneath

decaying logs was closely related to physicochemical properties (e.g., microbial biomass nitrogen, total phosphorus concentrations and water content. Our results indicated the ecological effects of logs at differing decay classes on soil fungal community were different.

4.1 The diversity of soil fungal communities differed significantly among log decay classes

The Shannon and Simpson diversity of fungal communities in soils underneath decayinglogs increased during the decaying process, while it tended to stabilize after that. This is likely that decaying logs provide an additional source of nutrients, and some microbial species, such as fungi utilizing wood, occur in soil only under decaying logs (Mäkipää et al. 2017). Additionally, highly decayed logs provide a more stable moisture content of the soil surface (Zalamea et al. 2016), offering beneficial habitat conditions for some fungal species. However, logs in decay class V were basically fragmented material, with more refractory substances, leading to the replacement of some fungi, so the fungal diversity of soils underneath decay class V was lower than underneath decay class IV and then tended to be stable.

4.2 Effect of decaying logs on composition of soil fungi

Basidiomycota and Ascomycota were the two dominant phyla across CK and all decay classes, consistent with previous studies (Chen et al. 2017a; Zhang et al.2021). Some species of Basidiomycota and Ascomycota have the ability to decompose refractory substances such as lignin and cellulose, but the existence of so many species

300 in these two phyla, lead to the absence of any significant difference in the relative
301 abundance of these phyla between decay classes. Mortierellomycota, a typical phylum,
302 is mostly saprophytic in soil (Lindahl et al. 2007), and its relative abundance was
303 significantly different in soil among decay classes, which is consistent with a previous
304 study (Mäkipää et al. 2017). The significant differences in microbial biomass nitrogen
305 and total phosphorus concentrations among decay classes may to some extent account
306 for the separation of Mortierellomycota.

307 *Piloderma* and *Cortinarius* declined in abundance during the process of log
308 decomposition, while *Inocybe, Russula* and *Lactarius* had highest abundance in decay
309 class III. All these genera have species known to form ectomycorrhizal symbiosis with
310 plant roots. Lindahl and Tunlid (2015) have demonstrated that some ectomycorrhizal
311 fungi have retained mechanisms of decomposition similar to those of brown- and white-
312 rot fungi and actively participate in the decomposition of organic matter. Nitrogen
313 availability is a major factor structuring ectomycorrhizal fungal communities. As
314 nitrogen increases, ectomycorrhizal fungal communities shift from taxa specialized in
315 N uptake under low-N conditions (e.g., *Cortinarius*, *Piloderma*) toward taxa
316 specialized in P uptake under high-N, low-P, acidified conditions (e.g., *Lactarius*)
317 (Lilleskov et al. 2002). The nutrient conditions of decaying logs and pH value of soil
318 under middle decomposition stage may be more suitable for the propagation of *Inocybe*,
319 *Russula* and *Lactarius*. Additionally, the abundance of *Fusarium* and *Humicola*
320 significantly increased during the decomposition process due to the strong positive
321 correlation between the organic matter decomposition and these two genera (Banerjee

et al. 2016), which can produce ligninase and cellulase to decompose refractory substances.

4.3 Response of soil fungal functional group to log decomposition

According to the classification results of FUNGuild, the relative abundance of fungal functional groups varied greatly with the trophic mode in the decomposing process of logs. The soil underneath decaying Minjiang fir logs was dominated by saprotrophic fungi. Wood saprotrophs and saprotroph were heterotrophic organisms that obtain a major fraction of their metabolic carbon from dead organic matter (Lindahl and Tundia 2015). In this study, the relative abundance of wood saprotrophs and saprotroph increased drastically at decay classes IV and V (Fig. 4), indicating that saprotrophic fungi is favoured underneath the highly decayed logs. The relative abundance of arbuscular mycorrhizal fungi increased during the decomposing process of logs. Although the reason for the increase remains to be further studied, these arbuscular mycorrhizal fungi likely play a role in early stages of decomposition. Besides, ectomycorrhizal fungi in our study decreased during the decomposition process, which might be related to the changes in soil nutrients and environmental conditions.Additonally, the interaction between fungi with different trophic modes also affected the proportion of fungal functional groups on guilds (Lindahl et al. 1999). The results indicated that logs with different decay classes favoured different functional groups on guilds of soil fungi.

4.4 Influencing factors of soil fungal community composition

Correlation between soil fungal community and physicochemical properties could be

attributed to the following reasons. Organic matter strongly affects the structure and function of soil microbial communities (Grayston et al. 2004). Both carbon composition and nitrogen addition can affect soil microbial community structure and function, such as symbiotic mycorrhizal fungi (Morrison et al. 2016; Corrales et al. 2017; Zhang et al. 2020). Cao et al. (2016) have demonstrated that the concentration of phosphorus is among the main factors influencing microbial activity at regional spatial scales. Besides, water content was strongly correlated with the characteristics of the microbial communities (Brockett et al. 2012). The relative abundance of some genera in our study did not differ significantly among decay classes, suggesting that fungal genera in the soil underneath decaying logs might respond to the changes in water content by the allocation of limited resources. Soil pH is also a critical factor for the diversification of fungi (Geisseler and Scow 2014). This is probably because pH indirectly affects the structure of some microbial communities through interactions among soil elements (e.g. precipitation of ions) (Lammel et al. 2018). The results showed that logs with different decay classes provided various carbon and nutrient sources for soil fungal communities, and highly decayed logs provided favorable water and pH conditions for functional groups such as saprophytes.

Conclusion

This study examined the effects of decay classes of logs on the composition of soil fungal communities in a subalpine forest. Our results showed that decaying logs altered the compositions of soil fungal communities. The diversity of soil fungal community

and the relative abundance of dominant genera of soil differed significantly by the decomposition of logs. Additionally, groups of fungi on guilds varied with decay classes of logs, indicating that decaying logs favoured different functional groups of soil fungi thus altering soil fungal community structures. Physicochemical properties (e.g., microbial biomass nitrogen, total phosphorus concentrations and water content) in our study accounted to some extent for the difference of the fungal community structures among decay classes. Therefore, the ecological effects of logs at differing decay classes on soil fungal community were different. Log decomposition is a long-term and complex biological process, so the response of soil microorganisms to the decomposition of logs needs long-term experimental research.

Author contributions

W.Q.Y. and B.T. conceived and designed the experiment and contributed resources. Q.W. completed laboratory analysis and led the writing of the manuscript. Q.W., B.T., Z.W., H.L., R.C., C.H.C., and Y.R.J. contributed to field work. W.Q.Y., and J.P. provided writing assistance. All authors have read and agreed to the published version of the manuscript.

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Declaration of competing interest

All authors certify that they have no affiliations with or involvement in any organization or entity with any financial interest or non-financial interest in the subject matter or materials discussed in this manuscript.

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Figure captions

Fig. 1 Relative abundances (>1%) of soil fungi at the phylum (a) and genus (b) levels in the control (CK) and the decay classes (ranked by the sum of means). Groups accounting for <1% of the relative abundance are integrated into 'others'. CK, control; I - V, decay classes I -V. Data are the means of five samples for each group.

Fig. 2 Nonmetric multidimensional scaling (NMDS) analysis of the composition of soil fungal communities based on Bray-Curtis distances. CK, control; I - V, decay classes I -V.

Fig. 3 Fungal functional groups (guild) under different treatments (mean ± *SD*, $n = 5$). CK, control; I - V, decay classes I -V. Different letters indicate significant differences ($P < 0.05$) among the decay classes.

Fig. 4 Heatmap of the relative abundance of dominant genera (a) and the proportion of functional groups (b) from soil fungi. Blue denotes a low relative value across a taxon (row); red denotes a high relative value. The color key for the Z score indicates correspondence between the blue-red coloring and standard deviations from the mean value of each taxon. CK, control; I-V, decay classes I-V.

Fig. 5 Correlation heatmap of soil physicochemical properties and the relative abundances of soil fungi at phylum (a) and genus (b) level. MBC: microbial biomass carbon, MBN: microbial biomass nitrogen, MBP: microbial biomass phosphorus, OC: organic carbon, TN: total nitrogen, TP: total phosphorus, WC: water content. * $P < 0.05$, ** $P < 0.01$.

621 **Table 1** Number of operational taxonomic units (OTUs) and indices of Shannon and Simpson
622 diversity for the fungal communities in the soil underneath decaying logs for the decay classes (mean
623 ± *SD*, n = 5). CK, control; I - V, decay classes I -V. Different letters within a column indicate
624 significant differences ($P < 0.05$) among the classes.
625

Class	No. OTUs	Shannon	Simpson
CK	607±199a	3.84±0.72b	0.734±0.055c
I	684±48a	4.63±0.40b	0.832±0.050b
II	663±166a	3.76±0.48b	0.722±0.053c
III	845±160a	6.14±0.45a	0.951±0.016a
IV	790±178a	6.07±0.92a	0.954±0.029a
V	890±115a	5.94±1.09a	0.929±0.059a

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