

Supporting Information

Life in leaf litter: novel insights into community dynamics of bacteria and fungi during litter decomposition

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Appendix S1. PCR conditions

Samples were amplified for pyrosequencing using a forward and reverse fusion primer. For bacteria, the forward primer was constructed with (5'-3') the Roche A linker (CCATCTCATCCCTGCGTGTCTCCGACTCAG), an 8-10bp barcode, and the BAC 341F primer ([CCTACG GGAGGCAGCAG, Muyzer & Smalla, 1998; Muyzer et al, 1995]). The reverse fusion primer was constructed with (5'-3') a biotin molecule, the Roche B linker (CCTATCCCCTG TGTGCCTTGGCAGTCTCAG), and the BAC 907R primer ([CCGTCAATTCMTTGTGAGTTT, Muyzer & Smalla, 1998; Muyzer et al, 1995]). We sequenced the samples from the forward primer. For fungi, the forward primer was constructed with (5'-3') the Roche A linker, an 8-10bp barcode, and the ITS1F primer ([CTTGGTCATTTAGAGGAAGTAA, Gardes & Bruns, 1993]). The reverse fusion primer was constructed with (5'-3') the Roche B linker, and the ITS4 primer ([TCCTCCGCTTATTGATATGC, White et al, 1990]). We sequenced the samples from the ITS4 (reverse primer). Amplifications were performed in 25 µl reactions with Qiagen HotStar Taq master mix (Qiagen Inc, Valencia, California), 1 µl of each 5 µM primer, and 1 µl of template. Reactions were performed on ABI Veriti thermocyclers (Applied Biosystems, Carlsbad, California) under the following thermal profile: 95 °C for 5 min, then 35 cycles of 94 °C for 30 sec, 54 °C for 40 sec, 72 °C for 1 min, followed by one cycle of 72 °C for 10 min and 4 °C hold.

Appendix S2. Decomposition of European beech leaf litter

Information related to the decomposition of beech leaf litter used in this study, i.e. variations in microbial biomass, enzyme activity patterns (five hydrolytic and three oxidative enzymes) and nutrient dynamics, has been published elsewhere (Purahong et al, 2014a, b). Briefly, after 473 days, almost 40 % of the total leaf litter mass was lost (Purahong et al, 2014a), and the decomposition rate was consistent with other litterbag studies carried out at the same location and using the similar leaf litter (Jacob et al, 2009, 2010). Substantial amounts of lignin were decomposed between days 284 to 473 (~20 % – 40 %), demonstrating that leaf litter in our litterbag experiment had reached the later (second phase) decomposition stage mentioned in Berg (2000). C:N and Lignin:N ratios also leveled out at 284 days. The microbial biomass measured with phospholipid fatty acid (PLFA) clearly showed that fungi dominated during the entire decomposition processes (fungal:bacterial ratios ranged from 5.74 at 89 days to 1.36 at 473 days) (Purahong et al, 2014b). Enzyme activities in leaf litter sampled at different times were observed to fluctuate. Interestingly, the two lignin-degrading enzymes (laccase and manganese peroxidase activity (MnP)) that were measured, exhibited patterns linked to lignin decomposition rate in the unmanaged beech forests under investigation (Purahong et al, 2014a). While oxidative activities in the leaf litter were dominated by laccase over the whole sampling time, from 284 days on there was a strong increase of MnP that has a higher redox potential than laccase, (Lundell et al, 2010) coupled with a significantly decreased lignin content (Purahong et al, 2014a). We hypothesized that there should be a community shift perhaps involving newly arriving microbes by 284 – 473 days (Purahong et al, 2014a). The dynamics of most macronutrients (C, N, P, K, Ca, Mg) were studied. Nitrogen immobilization was clearly observed from the first sampling date (89 days) to 362 days (Purahong et al, 2014a).

Appendix S3. Bacterial community dynamics

The initial leaf litter (day 0) was highly dominated by two common bacterial OTUs: OTU 2 (closest hit: Actinobacteria, *Frigoribacterium* sp., 8.9 %) and OTU 4 (closest hit: Proteobacteria, *Sphingomonas* sp., 8.4 %) (Figure 1 a, Figure 2). These two were also the most dominant OTUs in the leaf litter at 89 and 180 days with relative abundances ranging from 5.2 % – 12.8 %, but their respective abundances gradually decreased to between 1.4 % and 3.5 % at 473 days. Six bacterial OTUs (closest hit: *Pseudomonas* sp.1, *Rhizobiales* OTU 27, *Massilia* sp.2, *Novosphingobium* sp., *Janthinobacterium* sp., *Massilia* sp.1; relative abundances 3 % - 4 %) co-dominated freshly fallen leaf litter. The abundance of the majority of dominant bacterial OTUs in freshly fallen leaf litter decreased or became absent by the next sampling dates (Figure 1 a, Figure 2). At 89 and 180 days, the

bacterial communities were also co-dominated by ten further OTUs (closest hit: *Pedobacter* sp., *Novosphingobium* sp., *Massilia* sp.1, *Rhizobium* sp.1, *Kineosporia* sp., *Nitrobacter* sp., *Flavobacterium johnsoniae*, *Flavobacterium* sp., *Caulobacter* sp. and *Chitinophaga* sp. (Figure 1 a, Figure 2). The two bacterial OTUs from the early stages of decomposition (*Nitrobacter* sp. and *Kineosporia* sp.) maintained their high levels of abundance at all sampling dates until the later stages of decomposition at the end of the experiment (180 – 473 days). The abundance of *Flavobacterium johnsoniae* and *Flavobacterium* in leaf litter had declined markedly by 284 and 362 days and became co-dominant at 473 days. *Streptomyces* and *Bradyrhizobium* appeared and co-dominated the later decompositional stage of leaf litter (284 – 473 days) (Figure 1 a, Figure 2). Interestingly, almost all of them were already present in 0 day leaf litter, mostly at low levels of abundance, except for *Pseudomonas* and *Rhizobium*, which were already very abundant at this early stage. This result can be partly explained by some studies which have shown that *Rhizobium* and *Pseudomonas* could be transported from root to leaf or to the top of the plant and live there as bacterial endophytes (Bodenhausen et al., 2013). Such endophytic *Rhizobium* and *Pseudomonas* may serve as inoculum and start to fix nitrogen shortly after leaf fall. One might argue that some of these genera (*Frankia*, *Rhizobium* and *Bradyrhizobium*) commonly found as symbionts in roots of trees and shrubs (e.g. *Alnus*, *Robinia*, *Genista*) or herbaceous legumes (e.g. *Lupinus*, *Vicia*, *Lathyrus*) were detected in leaf litter because the roots of their host plant might have entered the litterbags during the experiment. However, we can rule out this hypothesis in our experiment as we did not find any roots in the litterbags and all small plants that grew near by the litterbags were removed.

Appendix S4. Fungal community dynamics

The initial leaf litter (day 0) was highly dominated by an aquatic hyphomycetes (Ingoldian fungi; closest hit: *Gyoerffyyella* sp.1) that alone contributed 71.9 % of the total sequences at this stage (Figures 1 b, Figure 3). *Mycosphaerella* sp. was also frequently detected in freshly fallen leaf litter where it accounted for 10.7 %. Its abundance had dropped sharply by the next sampling time (89 days) and almost disappeared after 180 days (Figure 1 b, Figure 3). *Ceratobasidium* sp. was the most frequently detected basidiomycete fungus in freshly fallen leaf litter, but it only contributed to 1.6 % of total sequences (Figure 1 b). *Gyoerffyyella* sp.1 was still dominant or frequently detected but its abundance declined markedly to 31.7 % and 7.4 % at 89 and 180 days, respectively, and had almost disappeared from the leaf litter at 284 – 473 days (Figure 1 b, Figure 3). The abundance of six fungal OTUs increased greatly from the freshly fallen leaf stage to co-dominate the leaf litter at 89 – 180 days (closest hit: *Ceratobasidium* sp., 10.9 % – 20.6 %; Xylariales OTU 3, 9.4 % – 19.9 %; *Cylindrosyndonium* sp.1, 6.5 %; Leotiomycetes OTU 12, 5.7 %; Ceratobasidiaceae OTU 79, 3.9 % – 5.0 %;

Apodus sp., 6.4 %). These six OTUs also co-dominated until 362 or 473 days (Figure 1 b, Figure 3). Some Basidiomycota significantly increased in their abundance (*Mycena* spp., cumulative relative abundance = 4.3 % – 15.6 %) or were newly detected (*Clitocybe phaeophthalma* 11.4 % – 15.5 %; Agaricomycetes OTU 7, 6.8 %; *Lepiota clypeolaria* 5.6 %) and co-dominated leaf litter at 284 – 473 days (Figure 1 b, Figure 3).).

Appendix S5. Factors significantly corresponding with microbial community successions

Our work has identified factors that correspond with successions within the microbial community (see below). It is worth noting that, in the investigated litter, the abiotic factors correlating with both bacterial and fungal community successions were identical, and that the directions of the correlations were also similar. In particular, leaf litter quality parameters, microbial macronutrients, micronutrients and pH were significant factors. Leaf litter quality e.g. C:N ratio is an important factor influencing microbial communities as it relates both to the nutrient status of the leaf litter and to its stage of decomposition (Purahong et al, 2014a, 2015). Macronutrients such as C, N, K, Mg and Ca are required in large amounts for microbial growth and reproduction (Prescott et al, 1999). Specifically, C and N are important elements in all macromolecules including carbohydrates, proteins, lipids, and nucleic acids (Aggarwal, 2007). K and Mg are needed for the activity of enzymes as cofactors (Aggarwal, 2007). Ca is cofactor for certain enzymes and is also a constituent of bacterial endospores. Micronutrients such as Co, Cu and Mn have important roles as structural components of enzymes involved in catalysis of reactions (Aggarwal, 2007). Co is biologically important for microorganisms as it is involved in diverse enzymatic reactions (Antony et al, 2010): it forms an essential component of non corrin-cobalt-containing enzymes (methionine aminopeptidase, prolidase, nitrile hydratase, glucose isomerase, methylmalonyl-CoA carboxytransferase, aldehyde decarboxylase, lysine-2,3-aminomutase, and bromoperoxidase) (Kobayashi and Shimizu, 1999). In this ecosystem, decomposing leaf litter is dominated by laccase - the so-called ‘blue copper proteins’ or ‘blue copper oxidases’, which are proteins containing four catalytic copper atoms (Kunamneni et al, 2007). Thus, we can deduce that Cu must be important for all microbes that produce laccase. In fact, Cu is required by most living organisms as it is the component of many metalloenzymes and proteins involved in electron transport, redox, and other important reactions, and as a cofactor in many proteins (Mendez de Souza et al, 2005). Mn is an essential micronutrient required for the growth, metabolism, reproduction and survival of microorganisms (Sujith & Bharathi, 2011). It is important for scavenging trace metals and breaking down complex organic matter such as lignin as it has roles in general as well as carbohydrate metabolic pathways (Crowley et al, 2000). Four metalloenzymes including manganese superoxide dismutase, mangani-catalase, arginase, and O-phosphatases are containing Mn

(Christianson, 1997; Shi, 2004). The Mn^{2+} containing O-phosphatases are known to regulate many important processes for microbial growth and reproduction such as spore formation, the assimilation of carbon and nitrogen, vegetative growth, the development of fruiting bodies, and cell segregation (Shi, 2004; Sujith & Bharathi, 2011). Mn is also required for microbial protection against toxic metals, UV light, viruses and oxidative stress (Christianson, 1997; Spiro et al, 2010; Sujith & Bharathi, 2011).

Goodness-of-fit statistics (R^2) of environmental variables fitted to the nonmetric multidimensional scaling (NMDS) ordination of bacterial and fungal communities

| Variables | Bacterial community | | Fungal community | |
|---------------|---------------------|--------------|------------------|--------------|
| | R^2 | P value | R^2 | P value |
| Total C | 0.6363 | 0.001 | 0.627 | 0.002 |
| Total N | 0.9088 | 0.001 | 0.8374 | 0.001 |
| C: N | 0.8849 | 0.001 | 0.8716 | 0.001 |
| pH | 0.4898 | 0.008 | 0.3425 | 0.045 |
| Mg | 0.6197 | 0.002 | 0.4171 | 0.021 |
| K | 0.742 | 0.001 | 0.7953 | 0.001 |
| Ca | 0.7983 | 0.001 | 0.7107 | 0.002 |
| P | 0.1218 | 0.377 | 0.1387 | 0.300 |
| Mn | 0.4271 | 0.013 | 0.3684 | 0.036 |
| Fe | 0.1275 | 0.375 | 0.0458 | 0.744 |
| Cu | 0.4599 | 0.017 | 0.4478 | 0.012 |
| Co | 0.5371 | 0.003 | 0.3042 | 0.05 |
| V | 0.207 | 0.175 | 0.1168 | 0.417 |
| Water content | 0.3094 | 0.048 | 0.3201 | 0.05 |
| Lignin | 0.3236 | 0.049 | 0.2064 | 0.176 |
| L: N | 0.8569 | 0.001 | 0.8297 | 0.001 |

Fig. S1 Individual rarefaction analysis for each sample. TP = time point: TP0 = 0 day, TP1 = 89 days, TP2 = 180 days, TP3 = 284 days, TP4 = 362 days, TP5 = 473 days.

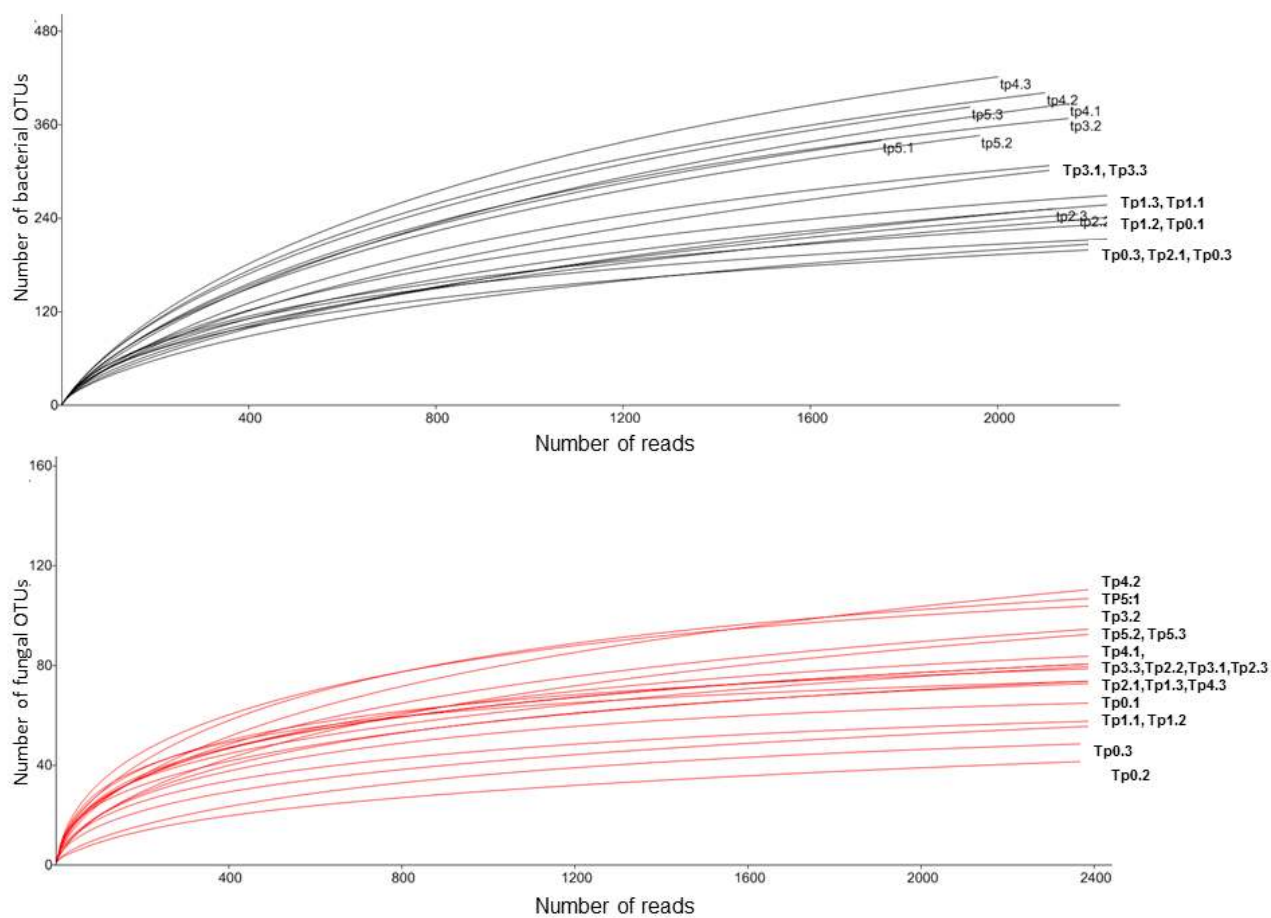


Fig. S2 Heat-map of relative abundances of dominant bacterial (a) and fungal (b) OTUs which account for at least 1 % of the relative abundance at one or more sampling times (mean and standard error (SE), n = 3). The heatmap was overlaid with overall values. TP = time point: TP0 = 0 day, TP1 = 89 days, TP2 = 180 days, TP3 = 284 days, TP4 = 362 days, TP5 = 473 days.

| Bacterial OTU | Mean TP0 | SE TP0 | Mean TP1 | SE TP1 | Mean TP2 | SE TP2 | Mean TP3 | SE TP3 | Mean TP4 | SE TP4 | Mean TP5 | SE TP5 |
|------------------------------------|----------|--------|----------|--------|----------|--------|----------|--------|----------|--------|----------|--------|
| <i>Nitrobacter</i> sp. | 0.76 | 0.22 | 3.80 | 0.62 | 9.70 | 1.33 | 12.25 | 0.88 | 13.32 | 2.45 | 9.22 | 0.50 |
| <i>Frigonibacterium</i> sp. | 8.88 | 0.39 | 8.25 | 1.14 | 12.83 | 2.30 | 4.97 | 1.08 | 3.69 | 0.72 | 3.45 | 0.57 |
| <i>Kineosporia</i> sp. | 1.70 | 0.50 | 3.01 | 0.29 | 10.05 | 2.07 | 17.37 | 1.36 | 5.55 | 0.98 | 4.53 | 0.23 |
| <i>Sphingomonas</i> sp. | 8.38 | 1.39 | 5.22 | 0.76 | 8.65 | 1.26 | 4.02 | 0.83 | 2.49 | 0.49 | 1.39 | 0.24 |
| <i>Rhizobium</i> sp.1 | 2.26 | 0.23 | 3.92 | 0.69 | 3.88 | 1.27 | 2.19 | 0.44 | 1.84 | 0.14 | 1.80 | 0.10 |
| <i>Flavobacterium</i> sp.1 | 0.52 | 0.09 | 4.77 | 0.95 | 3.94 | 0.79 | 0.67 | 0.04 | 1.04 | 0.38 | 3.37 | 1.32 |
| <i>Flavobacterium johnsoniae</i> | 0.55 | 0.16 | 4.05 | 1.24 | 3.19 | 1.24 | 0.42 | 0.18 | 0.39 | 0.11 | 4.41 | 1.52 |
| <i>Pedobacter</i> sp. | 2.18 | 0.41 | 5.41 | 1.68 | 3.42 | 1.18 | 0.23 | 0.07 | 0.20 | 0.10 | 0.38 | 0.19 |
| <i>Novosphingobium</i> sp. | 2.95 | 0.08 | 3.63 | 0.51 | 2.36 | 0.41 | 0.79 | 0.28 | 0.44 | 0.18 | 0.37 | 0.08 |
| <i>Caulobacter</i> sp. | 0.42 | 0.03 | 2.39 | 0.53 | 2.80 | 0.28 | 1.88 | 0.36 | 1.16 | 0.13 | 1.92 | 0.22 |
| <i>Bradyrhizobium</i> sp. | 0.07 | 0.05 | 0.16 | 0.10 | 0.12 | 0.04 | 2.20 | 0.33 | 3.50 | 0.91 | 4.61 | 0.27 |
| <i>Massilia</i> sp.1 | 2.60 | 0.13 | 3.80 | 0.81 | 2.20 | 0.37 | 0.36 | 0.14 | 0.34 | 0.17 | 0.16 | 0.09 |
| <i>Actinoplanes</i> sp. | 0.25 | 0.14 | 1.33 | 0.71 | 0.92 | 0.29 | 2.11 | 0.43 | 2.17 | 0.36 | 1.88 | 0.23 |
| <i>Massilia</i> sp.2 | 3.58 | 0.77 | 2.27 | 0.64 | 0.81 | 0.06 | 0.51 | 0.12 | 0.44 | 0.15 | 0.17 | 0.09 |
| <i>Pseudomonas</i> sp.1 | 4.26 | 0.69 | 1.16 | 0.51 | 1.31 | 0.93 | 0.12 | 0.07 | 0.34 | 0.11 | 0.14 | 0.08 |
| <i>Chitinophaga</i> sp. | 0.21 | 0.09 | 1.31 | 0.21 | 2.87 | 1.42 | 1.47 | 0.30 | 0.96 | 0.48 | 0.66 | 0.15 |
| <i>Variovorax paradoxus</i> | 1.59 | 0.21 | 0.97 | 0.20 | 0.90 | 0.11 | 0.73 | 0.14 | 0.92 | 0.01 | 0.67 | 0.16 |
| <i>Flavobacterium</i> sp.2 | 0.33 | 0.11 | 2.33 | 0.70 | 0.85 | 0.05 | 0.56 | 0.16 | 0.36 | 0.13 | 1.38 | 0.64 |
| <i>Streptomyces</i> sp.1 | 0.00 | 0.00 | 0.00 | 0.00 | 0.05 | 0.03 | 2.51 | 1.21 | 1.09 | 0.10 | 1.79 | 0.32 |
| <i>Devosia</i> sp.1 | 0.64 | 0.18 | 1.40 | 0.13 | 0.73 | 0.16 | 0.59 | 0.13 | 0.56 | 0.11 | 0.87 | 0.19 |
| <i>Umezawaea tangerina</i> | 0.02 | 0.02 | 0.13 | 0.09 | 0.29 | 0.06 | 1.07 | 0.33 | 1.86 | 0.45 | 1.56 | 0.21 |
| <i>Janthinobacterium</i> sp. | 2.64 | 0.42 | 1.10 | 0.47 | 0.40 | 0.04 | 0.12 | 0.06 | 0.17 | 0.01 | 0.03 | 0.03 |
| <i>Polaromonas</i> sp. | 0.89 | 0.29 | 1.28 | 0.33 | 0.83 | 0.22 | 0.34 | 0.20 | 0.67 | 0.13 | 0.35 | 0.05 |
| <i>Devosia</i> sp.2 | 0.40 | 0.21 | 1.33 | 0.44 | 1.05 | 0.13 | 0.50 | 0.10 | 0.68 | 0.12 | 0.40 | 0.03 |
| <i>Rhizobium</i> sp.2 | 0.45 | 0.05 | 0.72 | 0.14 | 0.55 | 0.05 | 0.62 | 0.08 | 1.00 | 0.19 | 0.89 | 0.09 |
| <i>Rhizobiales</i> OTU27 | 3.77 | 0.16 | 0.01 | 0.01 | 0.00 | 0.00 | 0.08 | 0.08 | 0.00 | 0.00 | 0.00 | 0.00 |
| <i>Luteibacter rhizovicius</i> | 0.01 | 0.01 | 0.01 | 0.01 | 0.03 | 0.02 | 0.98 | 0.24 | 1.00 | 0.49 | 1.90 | 0.47 |
| <i>Rhizobacter</i> sp. | 1.64 | 0.47 | 0.32 | 0.05 | 0.67 | 0.31 | 0.15 | 0.09 | 0.21 | 0.09 | 0.46 | 0.03 |
| <i>Micromonospora</i> sp. | 0.04 | 0.04 | 0.04 | 0.03 | 0.15 | 0.02 | 0.82 | 0.27 | 1.28 | 0.68 | 1.25 | 0.35 |
| <i>Dyadobacter</i> sp. | 1.25 | 0.26 | 1.00 | 0.14 | 0.68 | 0.13 | 0.09 | 0.05 | 0.11 | 0.03 | 0.03 | 0.02 |
| <i>Xylophilus</i> sp. | 2.10 | 0.43 | 0.40 | 0.09 | 0.11 | 0.08 | 0.05 | 0.03 | 0.22 | 0.06 | 0.19 | 0.06 |
| <i>Rhizomicrobium</i> sp. | 0.01 | 0.01 | 0.00 | 0.00 | 0.08 | 0.03 | 0.96 | 0.25 | 1.02 | 0.10 | 1.18 | 0.03 |
| <i>Methylobacterium adhaesivum</i> | 2.19 | 0.19 | 0.27 | 0.07 | 0.11 | 0.02 | 0.12 | 0.08 | 0.03 | 0.02 | 0.02 | 0.02 |
| <i>Hymenobacter</i> sp. | 2.47 | 0.20 | 0.03 | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| <i>Streptomyces</i> sp.2 | 0.00 | 0.00 | 0.01 | 0.01 | 0.00 | 0.00 | 0.76 | 0.22 | 0.85 | 0.29 | 1.06 | 0.16 |
| <i>Duganella</i> sp. | 1.05 | 0.50 | 0.44 | 0.13 | 0.35 | 0.07 | 0.05 | 0.03 | 0.05 | 0.05 | 0.04 | 0.04 |
| <i>Flavobacterium</i> sp.3 | 1.81 | 0.86 | 0.12 | 0.05 | 0.03 | 0.03 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| <i>Pedobacter roseus</i> | 1.44 | 0.17 | 0.32 | 0.04 | 0.11 | 0.05 | 0.00 | 0.00 | 0.02 | 0.02 | 0.02 | 0.02 |
| <i>Kineococcus</i> sp. | 1.07 | 0.23 | 0.18 | 0.09 | 0.17 | 0.10 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| <i>Friedmanniella</i> sp. | 1.07 | 0.12 | 0.12 | 0.05 | 0.01 | 0.01 | 0.05 | 0.03 | 0.02 | 0.02 | 0.06 | 0.06 |
| <i>Pseudomonas</i> sp.2 | 0.00 | 0.00 | 1.12 | 1.12 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| <i>Acidiphilium</i> sp. | 1.07 | 0.32 | 0.04 | 0.03 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |

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Fig. S2 (continue)

| Fungal OTU | Mean TP0 | SE TP0 | Mean TP1 | SE TP1 | Mean TP2 | SE TP2 | Mean TP3 | SE TP3 | Mean TP4 | SE TP4 | Mean TP5 | SE TP5 |
|----------------------------------|----------|--------|----------|--------|----------|--------|----------|--------|----------|--------|----------|--------|
| <i>Apodus</i> sp. | 0.00 | 0.00 | 0.23 | 0.16 | 6.40 | 3.61 | 13.90 | 5.72 | 16.98 | 2.12 | 38.09 | 13.47 |
| <i>Gyoeffiyella</i> sp.1 | 71.91 | 5.42 | 31.72 | 6.47 | 7.40 | 2.04 | 0.00 | 0.00 | 0.06 | 0.04 | 0.03 | 0.01 |
| <i>Xylariales</i> otu3 | 0.36 | 0.28 | 9.35 | 1.66 | 19.87 | 0.57 | 9.00 | 1.25 | 1.64 | 0.52 | 2.23 | 0.39 |
| <i>Ceratobasidium</i> sp. | 1.61 | 0.55 | 20.60 | 3.93 | 10.87 | 4.74 | 4.21 | 1.30 | 15.51 | 7.72 | 8.15 | 3.78 |
| <i>Cylindrosympodium</i> sp.1 | 0.10 | 0.05 | 1.12 | 0.41 | 6.49 | 1.19 | 10.00 | 1.24 | 1.31 | 0.48 | 0.85 | 0.08 |
| <i>Cercophora</i> sp. | 0.00 | 0.00 | 0.00 | 0.00 | 1.27 | 1.09 | 0.95 | 0.78 | 4.85 | 3.79 | 1.47 | 1.37 |
| <i>Agaricomycetes</i> otu7 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.56 | 0.54 | 6.85 | 6.85 | 0.00 | 0.00 |
| <i>Cylindrosympodium</i> sp.2 | 0.11 | 0.09 | 0.52 | 0.32 | 3.61 | 0.34 | 9.23 | 1.24 | 2.42 | 0.65 | 1.72 | 0.18 |
| <i>Etibulobasidium albescent</i> | 0.08 | 0.04 | 4.13 | 2.79 | 1.94 | 1.07 | 0.00 | 0.00 | 0.38 | 0.38 | 0.00 | 0.00 |
| <i>Clitocybe phaeophthalma</i> | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 11.38 | 10.52 | 15.53 | 7.98 | 0.07 | 0.04 |
| <i>Mycosphaerella</i> sp. | 10.72 | 1.69 | 1.81 | 0.63 | 0.62 | 0.04 | 0.00 | 0.00 | 0.08 | 0.05 | 0.00 | 0.00 |
| <i>Leotiomycetes</i> otu12 | 0.04 | 0.02 | 1.59 | 1.08 | 5.73 | 1.17 | 4.98 | 0.97 | 1.72 | 0.20 | 2.50 | 0.45 |
| <i>Flagellospora</i> sp. | 2.10 | 0.62 | 3.24 | 0.68 | 1.27 | 0.49 | 0.67 | 0.10 | 0.26 | 0.07 | 0.22 | 0.04 |
| <i>Mycena terena</i> | 0.00 | 0.00 | 0.32 | 0.32 | 0.68 | 0.35 | 1.05 | 0.54 | 3.42 | 2.02 | 6.35 | 5.16 |
| <i>Podospora</i> sp. | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.54 | 0.54 | 4.46 | 2.82 |
| <i>Hydnodontaceae</i> otu16 | 0.00 | 0.00 | 0.19 | 0.19 | 1.57 | 1.57 | 0.00 | 0.00 | 0.03 | 0.03 | 0.00 | 0.00 |
| <i>Tricholomataceae</i> otu17 | 0.00 | 0.00 | 3.63 | 3.30 | 0.97 | 0.77 | 0.04 | 0.04 | 0.01 | 0.01 | 0.00 | 0.00 |
| <i>Leptodiscella</i> sp. | 0.00 | 0.00 | 0.10 | 0.08 | 1.70 | 0.52 | 2.48 | 0.39 | 0.26 | 0.12 | 0.32 | 0.18 |
| <i>Lepiota clypeolaria</i> | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.01 | 0.01 | 0.01 | 5.60 | 4.12 |
| <i>Cylindrotrichum gorii</i> | 0.00 | 0.00 | 0.11 | 0.09 | 1.01 | 0.56 | 1.51 | 0.30 | 0.07 | 0.05 | 0.07 | 0.01 |
| <i>Apiognomonia</i> sp. | 1.53 | 0.94 | 0.03 | 0.03 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| <i>Aureobasidium</i> sp. | 0.03 | 0.01 | 1.23 | 0.23 | 1.90 | 0.38 | 2.62 | 1.12 | 0.47 | 0.22 | 0.65 | 0.13 |
| <i>Hydropisphaera</i> sp. | 0.00 | 0.00 | 0.19 | 0.17 | 2.54 | 1.34 | 0.92 | 0.54 | 0.07 | 0.03 | 0.03 | 0.03 |
| <i>Cryptosporiopsis</i> sp. | 1.25 | 0.28 | 1.08 | 0.71 | 0.22 | 0.03 | 0.15 | 0.05 | 0.22 | 0.01 | 0.17 | 0.08 |
| <i>Mycena</i> sp.1 | 0.00 | 0.00 | 0.00 | 0.00 | 0.05 | 0.04 | 1.08 | 0.53 | 0.40 | 0.03 | 2.94 | 0.41 |
| <i>Phialea strobilina</i> | 0.38 | 0.06 | 1.98 | 0.32 | 0.96 | 0.36 | 0.14 | 0.08 | 0.23 | 0.11 | 0.26 | 0.10 |
| <i>Xylariales</i> otu30 | 0.00 | 0.00 | 0.00 | 0.00 | 0.70 | 0.29 | 1.09 | 0.28 | 0.72 | 0.55 | 0.04 | 0.00 |
| <i>Helotiales</i> otu31 | 0.67 | 0.18 | 2.67 | 0.40 | 2.26 | 0.55 | 1.20 | 0.28 | 0.34 | 0.12 | 0.25 | 0.02 |
| <i>Chalara holubovae</i> | 0.00 | 0.00 | 0.03 | 0.03 | 0.52 | 0.14 | 1.23 | 0.93 | 0.22 | 0.10 | 0.77 | 0.60 |
| <i>Phaeohelotium monticola</i> | 0.00 | 0.00 | 0.03 | 0.03 | 0.26 | 0.24 | 0.25 | 0.25 | 2.57 | 1.77 | 0.08 | 0.08 |
| <i>Podospora glutinans</i> | 0.00 | 0.00 | 0.00 | 0.00 | 1.30 | 0.46 | 0.52 | 0.20 | 0.95 | 0.48 | 0.15 | 0.09 |
| <i>Venturiaceae</i> otu35 | 0.00 | 0.00 | 0.08 | 0.06 | 0.53 | 0.11 | 1.72 | 0.66 | 0.14 | 0.08 | 0.14 | 0.01 |
| <i>Helotiales</i> otu40 | 0.19 | 0.07 | 1.27 | 0.42 | 0.66 | 0.39 | 0.00 | 0.00 | 0.01 | 0.01 | 0.00 | 0.00 |
| <i>Clitocybe metachroa</i> | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 1.46 | 0.77 |
| <i>Herpotrichia</i> sp. | 0.00 | 0.00 | 0.11 | 0.06 | 0.37 | 0.18 | 0.40 | 0.33 | 1.07 | 0.46 | 0.19 | 0.11 |
| <i>Mycena</i> sp.3 | 0.00 | 0.00 | 0.00 | 0.00 | 0.89 | 0.81 | 2.18 | 0.53 | 2.59 | 1.24 | 3.23 | 1.44 |
| <i>Ceratobasidiaceae</i> otu79 | 0.01 | 0.01 | 5.00 | 1.78 | 3.91 | 2.85 | 1.70 | 0.99 | 3.39 | 3.03 | 1.09 | 0.50 |
| <i>Ascomycota</i> otu144 | 0.00 | 0.00 | 0.14 | 0.04 | 1.11 | 0.46 | 0.86 | 0.28 | 0.39 | 0.10 | 0.44 | 0.10 |

b

Fig. S3 Observed bacterial and fungal OTU richness (a and c) and Shannon diversity (b and d) (mean \pm SE, n = 3) in leaf litter across different sampling dates.

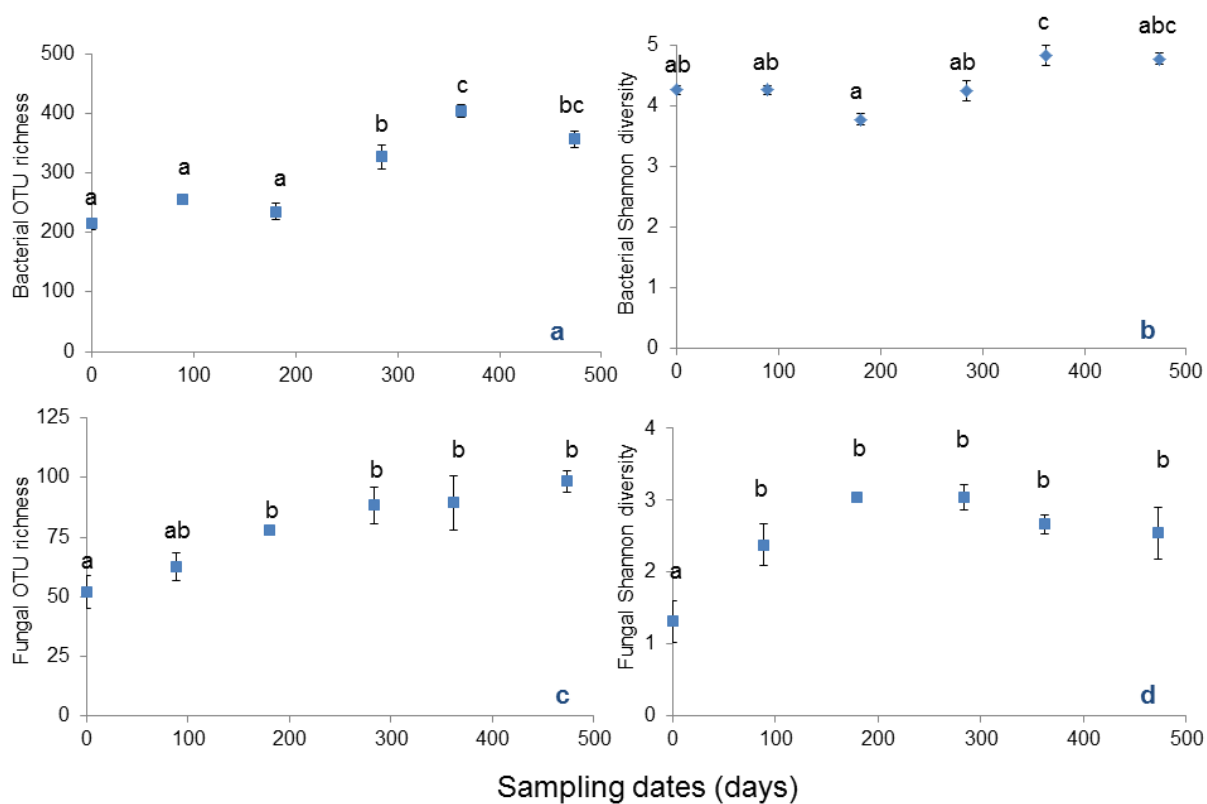


Fig. S4 Spearman's rank correlations between specific bacterial (a) and fungal (b) OTUs (account for at least 1 % of the relative abundance at one or more sampling times) and leaf litter quality parameters and physicochemical properties. The heatmap was overlaid with overall values.

| Bacterial OTU | C | N | C/N | Mg | K | Ca | Mn | Cu | Co | pH | Water | Lignin |
|----------------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|
| <i>Nitrobacter</i> sp. | -0.64 | 0.84 | -0.73 | 0.54 | -0.57 | 0.83 | 0.30 | 0.53 | 0.76 | 0.10 | 0.03 | 0.11 |
| <i>Frigoribacterium</i> sp. | 0.78 | -0.74 | 0.78 | -0.17 | 0.69 | -0.64 | -0.11 | -0.50 | -0.68 | -0.19 | -0.37 | 0.49 |
| <i>Kineosporia</i> sp. | -0.53 | 0.68 | -0.56 | 0.53 | -0.49 | 0.68 | 0.23 | 0.39 | 0.45 | 0.02 | -0.36 | 0.46 |
| <i>Sphingomonas</i> sp. | 0.79 | -0.64 | 0.77 | 0.06 | 0.74 | -0.48 | 0.15 | -0.45 | -0.52 | -0.40 | -0.43 | 0.61 |
| <i>Rhizobium</i> sp.1 | 0.54 | -0.48 | 0.55 | -0.17 | 0.53 | -0.47 | -0.17 | -0.19 | -0.59 | 0.20 | -0.22 | 0.27 |
| <i>Flavobacterium</i> sp.1 | -0.14 | -0.06 | -0.04 | -0.55 | -0.25 | -0.15 | -0.75 | 0.29 | -0.25 | 0.67 | 0.26 | -0.20 |
| <i>Flavobacterium johnsoniae</i> | -0.04 | -0.33 | 0.15 | -0.57 | -0.18 | -0.26 | -0.82 | 0.10 | -0.42 | 0.72 | 0.48 | -0.12 |
| <i>Pedobacter</i> sp. | 0.68 | -0.72 | 0.66 | -0.44 | 0.60 | -0.75 | -0.33 | -0.32 | -0.78 | 0.01 | -0.20 | 0.17 |
| <i>Novosphingobium</i> sp. | 0.83 | -0.71 | 0.75 | -0.39 | 0.81 | -0.76 | -0.14 | -0.38 | -0.70 | -0.09 | -0.30 | 0.20 |
| <i>Caulobacter</i> sp. | -0.11 | 0.09 | -0.04 | -0.20 | -0.21 | -0.01 | -0.51 | 0.21 | -0.33 | 0.60 | 0.05 | 0.26 |
| <i>Bradyrhizobium</i> sp. | -0.84 | 0.71 | -0.79 | 0.10 | -0.81 | 0.64 | -0.04 | 0.34 | 0.62 | 0.34 | 0.40 | -0.36 |
| <i>Massilia</i> sp.1 | 0.82 | -0.70 | 0.74 | -0.35 | 0.80 | -0.73 | -0.08 | -0.30 | -0.78 | -0.15 | -0.25 | 0.23 |
| <i>Actinoplanes</i> sp. | -0.65 | 0.64 | -0.65 | -0.01 | -0.50 | 0.48 | 0.02 | 0.24 | 0.54 | 0.34 | 0.09 | -0.24 |
| <i>Massilia</i> sp.2 | 0.87 | -0.72 | 0.77 | -0.27 | 0.88 | -0.72 | 0.01 | -0.46 | -0.66 | -0.25 | -0.25 | 0.24 |
| <i>Pseudomonas</i> sp.1 | 0.73 | -0.74 | 0.67 | -0.23 | 0.63 | -0.60 | 0.01 | -0.37 | -0.51 | -0.27 | -0.18 | 0.04 |
| <i>Chitinophaga</i> sp. | -0.24 | 0.35 | -0.35 | 0.17 | -0.16 | 0.37 | -0.01 | 0.47 | 0.11 | 0.20 | 0.09 | 0.30 |
| <i>Variovorax paradoxus</i> | 0.63 | -0.48 | 0.61 | -0.09 | 0.51 | -0.40 | 0.21 | -0.09 | -0.48 | -0.27 | -0.16 | -0.04 |
| <i>Flavobacterium</i> sp.2 | -0.07 | -0.15 | -0.01 | -0.58 | -0.04 | -0.33 | -0.64 | 0.11 | -0.40 | 0.57 | -0.01 | -0.12 |
| <i>Streptomyces</i> sp.1 | -0.84 | 0.77 | -0.82 | 0.28 | -0.74 | 0.63 | 0.06 | 0.23 | 0.63 | 0.15 | -0.21 | -0.05 |
| <i>Devosia</i> sp.1 | 0.24 | -0.26 | 0.28 | -0.63 | 0.11 | -0.49 | -0.52 | -0.14 | -0.53 | 0.58 | 0.13 | -0.17 |
| <i>Umezawaea tangerina</i> | -0.80 | 0.78 | -0.82 | 0.22 | -0.74 | 0.64 | 0.03 | 0.25 | 0.75 | 0.22 | 0.09 | -0.26 |
| <i>Janthinobacterium</i> sp. | 0.91 | -0.72 | 0.83 | -0.15 | 0.84 | -0.63 | 0.05 | -0.32 | -0.59 | -0.29 | -0.22 | 0.18 |
| <i>Polaromonas</i> sp. | 0.50 | -0.41 | 0.47 | -0.28 | 0.52 | -0.42 | -0.06 | -0.27 | -0.47 | 0.09 | -0.18 | -0.02 |
| <i>Devosia</i> sp.2 | 0.28 | -0.10 | 0.22 | -0.14 | 0.08 | -0.07 | -0.21 | 0.37 | -0.34 | 0.41 | -0.06 | 0.13 |
| <i>Rhizobium</i> sp.2 | -0.60 | 0.42 | -0.53 | -0.21 | -0.56 | 0.38 | -0.17 | 0.32 | 0.50 | 0.48 | 0.45 | -0.60 |
| Rhizobiales OTU27 | 0.61 | -0.61 | 0.61 | -0.08 | 0.73 | -0.60 | 0.29 | -0.66 | -0.33 | -0.56 | -0.18 | 0.11 |
| <i>Luteibacter rhizovicinus</i> | -0.84 | 0.80 | -0.84 | 0.29 | -0.85 | 0.65 | 0.05 | 0.43 | 0.58 | 0.07 | 0.56 | -0.22 |
| <i>Rhizobacter</i> sp. | 0.26 | -0.70 | 0.44 | -0.16 | 0.17 | -0.41 | -0.24 | -0.54 | -0.41 | -0.17 | -0.04 | 0.09 |
| <i>Micromonospora</i> sp. | -0.79 | 0.79 | -0.77 | 0.20 | -0.79 | 0.62 | -0.05 | 0.27 | 0.68 | 0.18 | 0.13 | -0.18 |
| <i>Dyadobacter</i> sp. | 0.88 | -0.75 | 0.86 | -0.38 | 0.77 | -0.69 | -0.16 | -0.41 | -0.64 | -0.13 | -0.16 | 0.20 |
| <i>Xylophilus</i> sp. | 0.57 | -0.59 | 0.54 | -0.42 | 0.45 | -0.62 | -0.09 | -0.46 | -0.36 | -0.11 | -0.10 | -0.34 |
| <i>Rhizomicrobium</i> sp. | -0.92 | 0.77 | -0.85 | 0.43 | -0.90 | 0.81 | 0.12 | 0.47 | 0.70 | 0.11 | 0.39 | -0.15 |
| <i>Methylobacterium adhaesiv</i> | 0.85 | -0.75 | 0.82 | -0.17 | 0.82 | -0.71 | 0.08 | -0.49 | -0.50 | -0.36 | -0.19 | 0.18 |
| <i>Hymenobacter</i> sp. | 0.77 | -0.72 | 0.73 | -0.24 | 0.75 | -0.72 | 0.07 | -0.42 | -0.47 | -0.37 | -0.15 | -0.08 |
| <i>Streptomyces</i> sp.2 | -0.83 | 0.72 | -0.79 | 0.20 | -0.75 | 0.62 | 0.15 | 0.39 | 0.65 | 0.17 | 0.25 | -0.42 |
| <i>Duganella</i> sp. | 0.82 | -0.79 | 0.84 | -0.23 | 0.79 | -0.72 | -0.11 | -0.46 | -0.72 | -0.24 | -0.21 | 0.27 |
| <i>Flavobacterium</i> sp.3 | 0.85 | -0.81 | 0.84 | -0.37 | 0.75 | -0.81 | -0.03 | -0.54 | -0.63 | -0.29 | -0.13 | 0.03 |
| <i>Pedobacter roseus</i> | 0.73 | -0.84 | 0.77 | -0.35 | 0.79 | -0.70 | -0.11 | -0.40 | -0.57 | -0.24 | -0.16 | -0.05 |
| <i>Kineococcus</i> sp. | 0.81 | -0.82 | 0.83 | -0.12 | 0.69 | -0.66 | 0.01 | -0.47 | -0.66 | -0.38 | -0.19 | 0.29 |
| <i>Friedmanniella</i> sp. | 0.51 | -0.51 | 0.51 | -0.29 | 0.66 | -0.64 | 0.10 | -0.51 | -0.48 | -0.43 | -0.19 | 0.00 |
| <i>Pseudomonas</i> sp.2 | 0.16 | -0.21 | 0.21 | -0.40 | 0.26 | -0.21 | -0.26 | -0.16 | -0.21 | 0.35 | 0.17 | -0.07 |
| <i>Acidiphilium</i> sp. | 0.77 | -0.70 | 0.72 | -0.25 | 0.74 | -0.72 | 0.07 | -0.40 | -0.50 | -0.38 | -0.14 | -0.08 |

a

Fig. S4 (continue)

| Fungal OTU | C | N | C/N | Mg | K | Ca | Mn | Cu | Co | pH | Water |
|------------------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| <i>Apodus</i> sp. | -0.88 | 0.75 | -0.83 | 0.28 | -0.85 | 0.77 | -0.12 | 0.44 | 0.71 | 0.33 | 0.47 |
| <i>Gyoeffya</i> sp.1 | 0.82 | -0.86 | 0.83 | -0.42 | 0.78 | -0.79 | -0.20 | -0.52 | -0.65 | -0.20 | -0.26 |
| <i>Xylariales</i> otu3 | -0.03 | 0.13 | -0.07 | 0.08 | -0.11 | 0.15 | -0.18 | 0.42 | -0.21 | 0.35 | -0.11 |
| <i>Ceratobasidium</i> sp. | 0.10 | 0.14 | -0.10 | -0.48 | 0.02 | -0.27 | -0.25 | 0.27 | -0.20 | 0.18 | -0.01 |
| <i>Cylindrosyndrium</i> sp.1 | -0.38 | 0.55 | -0.46 | 0.42 | -0.32 | 0.53 | 0.14 | 0.33 | 0.35 | 0.08 | 0.01 |
| <i>Cercophora</i> sp. | -0.50 | 0.57 | -0.40 | 0.43 | -0.57 | 0.75 | 0.14 | 0.57 | 0.55 | 0.18 | 0.27 |
| <i>Agaricomycetes</i> otu7 | -0.18 | 0.42 | -0.29 | 0.47 | -0.14 | 0.34 | 0.51 | 0.13 | 0.38 | -0.11 | -0.42 |
| <i>Cylindrosyndrium</i> sp.2 | -0.52 | 0.68 | -0.57 | 0.51 | -0.50 | 0.66 | 0.25 | 0.34 | 0.48 | -0.05 | 0.00 |
| <i>Efibulobasidium albescentis</i> | 0.39 | -0.45 | 0.44 | -0.12 | 0.34 | -0.18 | -0.17 | -0.08 | -0.50 | 0.23 | -0.14 |
| <i>Clitocybe phaeophthalma</i> | -0.66 | 0.58 | -0.76 | 0.30 | -0.47 | 0.49 | 0.43 | 0.24 | 0.47 | -0.17 | 0.17 |
| <i>Mycosphaerella</i> sp. | 0.87 | -0.84 | 0.87 | -0.33 | 0.86 | -0.70 | -0.06 | -0.47 | -0.60 | -0.24 | -0.27 |
| <i>Leotiomyces</i> otu12 | -0.48 | 0.40 | -0.41 | 0.37 | -0.37 | 0.56 | 0.03 | 0.30 | 0.22 | 0.19 | 0.17 |
| <i>Flagellospora</i> sp. | 0.80 | -0.67 | 0.70 | -0.20 | 0.72 | -0.65 | 0.07 | -0.21 | -0.69 | -0.17 | -0.39 |
| <i>Mycena terena</i> | -0.78 | 0.69 | -0.75 | 0.20 | -0.78 | 0.66 | -0.01 | 0.39 | 0.55 | 0.23 | 0.54 |
| <i>Podospora</i> sp. | -0.70 | 0.28 | -0.51 | -0.27 | -0.65 | 0.23 | -0.45 | 0.15 | 0.29 | 0.25 | 0.62 |
| <i>Hydnodontaceae</i> otu16 | -0.02 | -0.14 | 0.04 | 0.10 | 0.07 | 0.24 | -0.05 | 0.02 | 0.12 | 0.39 | 0.28 |
| <i>Tricholomataceae</i> otu17 | 0.30 | -0.23 | 0.26 | -0.33 | 0.29 | -0.30 | -0.19 | 0.05 | -0.52 | 0.27 | -0.20 |
| <i>Leptodiscella</i> sp. | -0.48 | 0.55 | -0.43 | 0.50 | -0.44 | 0.62 | 0.13 | 0.29 | 0.33 | 0.10 | -0.06 |
| <i>Lepiota clypeolaria</i> | -0.61 | 0.31 | -0.42 | -0.16 | -0.46 | 0.21 | -0.13 | 0.13 | 0.25 | 0.04 | 0.28 |
| <i>Cylindrotrichum gorii</i> | -0.40 | 0.45 | -0.41 | 0.40 | -0.30 | 0.49 | 0.04 | 0.20 | 0.27 | 0.07 | 0.02 |
| <i>Apiognomonina</i> sp. | 0.64 | -0.71 | 0.71 | -0.20 | 0.73 | -0.55 | 0.10 | -0.68 | -0.38 | -0.44 | -0.14 |
| <i>Aureobasidium</i> sp. | -0.18 | 0.28 | -0.25 | 0.23 | -0.17 | 0.30 | 0.00 | 0.43 | -0.03 | 0.25 | -0.01 |
| <i>Hydropisphaera</i> sp. | -0.14 | 0.40 | -0.24 | 0.42 | -0.20 | 0.33 | 0.23 | 0.38 | 0.04 | -0.09 | -0.46 |
| <i>Cryptosporiopsis</i> sp. | 0.52 | -0.47 | 0.44 | -0.23 | 0.56 | -0.43 | 0.03 | -0.41 | -0.49 | -0.23 | 0.01 |
| <i>Mycena</i> sp.1 | -0.89 | 0.72 | -0.82 | 0.21 | -0.77 | 0.60 | -0.11 | 0.24 | 0.68 | 0.19 | 0.35 |
| <i>Phialea strobilina</i> | 0.49 | -0.59 | 0.49 | -0.41 | 0.35 | -0.51 | -0.31 | -0.08 | -0.52 | 0.32 | 0.05 |
| <i>Xylariales</i> otu30 | -0.49 | 0.74 | -0.56 | 0.63 | -0.47 | 0.77 | 0.37 | 0.43 | 0.59 | -0.10 | -0.04 |
| <i>Helotiales</i> otu31 | 0.51 | -0.31 | 0.41 | -0.16 | 0.41 | -0.35 | -0.05 | 0.08 | -0.50 | 0.05 | -0.26 |
| <i>Chalara holubovae</i> | -0.63 | 0.49 | -0.49 | 0.40 | -0.54 | 0.65 | 0.03 | 0.23 | 0.37 | 0.18 | 0.08 |
| <i>Phaeohelotium monticola</i> | -0.16 | 0.36 | -0.21 | 0.28 | -0.25 | 0.36 | 0.06 | 0.38 | 0.32 | 0.17 | -0.23 |
| <i>Podospora glutinans</i> | -0.57 | 0.57 | -0.58 | 0.54 | -0.49 | 0.75 | 0.27 | 0.39 | 0.47 | -0.10 | 0.14 |
| <i>Venturiaceae</i> otu35 | -0.33 | 0.46 | -0.34 | 0.46 | -0.36 | 0.45 | 0.14 | 0.24 | 0.31 | 0.13 | -0.10 |
| <i>Helotiales</i> otu40 | 0.71 | -0.69 | 0.70 | -0.40 | 0.61 | -0.61 | -0.25 | -0.20 | -0.73 | 0.09 | -0.20 |
| <i>Clitocybe metachroa</i> | -0.64 | 0.13 | -0.39 | -0.30 | -0.65 | 0.08 | -0.64 | -0.05 | 0.13 | 0.42 | 0.59 |
| <i>Herpotrichia</i> sp. | -0.54 | 0.56 | -0.59 | 0.15 | -0.34 | 0.51 | 0.08 | 0.28 | 0.36 | 0.19 | 0.11 |
| <i>Mycena</i> sp.3 | -0.79 | 0.76 | -0.73 | 0.29 | -0.74 | 0.68 | 0.06 | 0.43 | 0.65 | 0.01 | 0.22 |
| <i>Ceratobasidiaceae</i> otu79 | -0.14 | 0.33 | -0.27 | -0.28 | -0.26 | -0.02 | -0.36 | 0.27 | -0.05 | 0.38 | 0.21 |
| <i>Ascomycota</i> otu144 | -0.59 | 0.54 | -0.49 | 0.43 | -0.51 | 0.64 | 0.00 | 0.29 | 0.39 | 0.25 | 0.03 |

b

Fig. S5 Mean manganese peroxidase activities (mU/g litter dry mass) in beech leaf litter at different sampling times (n = 3): Tp1 = 89, Tp2= 180, Tp3= 284, Tp4 = 362, Tp5 = 473 days (**reproduced** from Purahong et al., 2014).

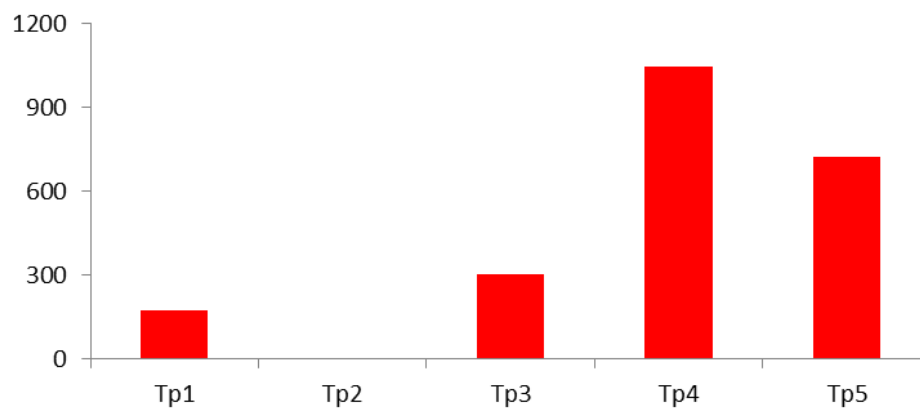
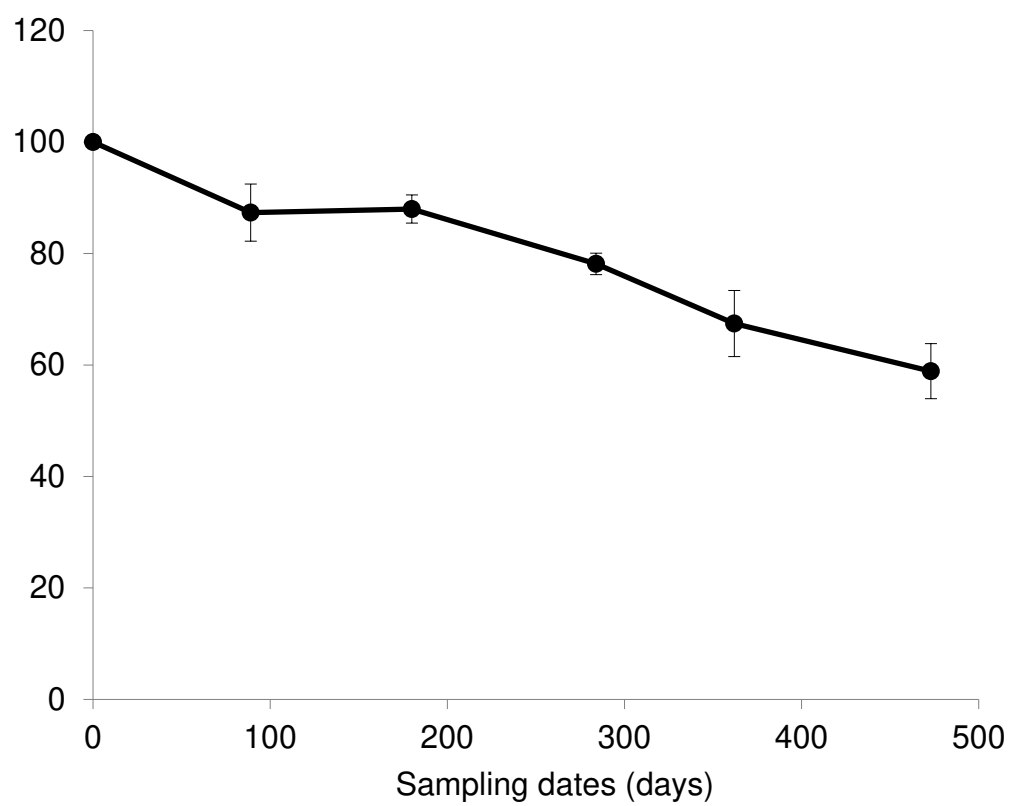


Fig. S6 Mean amount of total lignin remaining during decomposition (mean \pm SE, n = 3) (reproduced from Purahong et al., 2014).



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