Differences in Soil Fungal Communities between European Beech (*Fagus sylvatica* L.) Dominated Forests Are Related to Soil and Understory Vegetation

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**Abstract**

Fungi are important members of soil microbial communities with a crucial role in biogeochemical processes. Although soil fungi are known to be highly diverse, little is known about factors influencing variations in their diversity and community structure among forests dominated by the same tree species but spread over different regions and under different managements. We analyzed the soil fungal diversity and community composition of managed and unmanaged European beech dominated forests located in three German regions, the Schwäbische Alb in Southwestern, the Hainich-Dün in Central and the Schorfheide Chorin in the Northeastern Germany, using internal transcribed spacer (ITS) rDNA pyrotag sequencing. Multiple sequence quality filtering followed by sequence data normalization revealed 1655 fungal operational taxonomic units. Further analysis based on 722 abundant fungal OTUs revealed the phylum Basidiomycota to be dominant (54%) and its community to comprise 71.4% of ectomycorrhizal taxa. Fungal community structure differed significantly (p<0.001) among the three regions and was characterized by non-random fungal OTUs co-occurrence. Soil parameters, herbaceous understory vegetation, and litter cover affected fungal community structure. However, within each study region we found no difference in fungal community structure between management types. Our results also showed region specific significant correlation patterns between the dominant ectomycorrhizal fungal genera. This suggests that soil fungal communities are region-specific but nevertheless composed of functionally diverse and complementary taxa.


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**Introduction**

Fungi are an important and highly diverse component of soil microbial communities. In forest ecosystems, they perform essential ecological functions including decomposition, element cycling, and are involved in biotic interactions such as mycorrhizal symbioses [1,2]. Understanding factors shaping fungal diversity, community structure and spatial patterns is one of the central issues in soil microbial ecology [3]. The spatial distribution of soil fungal communities is thought to reflect their response to environmental factors such as soil nutrient availability [4], soil texture and water availability [5], and vegetation type [6,7]. These factors are further controlled by geographic differentiation, changes in plant community composition due to forest management, and the associated impact on soil conditions [5,8].

Studies on soil fungal diversity and community structure among geographic locations differing in soil, land-use or vegetation revealed contradictory results. For instance, Green et al [8] reported geographic differentiation in soil fungal community structure. In contrast, Kasel et al [5] only found weak regional differences, while land use within regions was important. Most studies in temperate forests focused on ectomycorrhizal fungi and root associated communities, where spatial variation in fungal communities was related to changes in soil environment, stand age, host tree species and herbaceous plant cover [7,9,10,11,12,13]. Recently spatial heterogeneity of soil fungal communities in temperate forests was also reported to be explained by host tree species and soil environment [10]. Massively parallel high throughput pyrotag sequencing has recently been employed to assess soil fungal diversity [10,14,15,16,17]. Use of the same technique for large-scale soil fungal community analysis of geographically separated forest sites dominated by the same tree species could help to elucidate the relative contribution of geographic location, soil environment, forest management, and understory vegetation cover to soil fungal community structure.

In this context, we used a massively parallel high throughput pyrotag sequencing approach to analyze the soil fungal diversity and community structure of 9 managed and 9 unmanaged European beech (*Fagus sylvatica* L.) dominated forests distributed in...
three German regions. Previous culture based study on the
distribution of yeasts [10] and 16S pyrotag based bacterial
diversity [19] studies reported that soil microbial community
diversity differs between these study sites. Accordingly, we
expected that the fungal community differs among the three study
sites and between the management types within the study sites.
Thus the main objectives of this study were to (i) assess the
influence of soil environment and understory vegetation related
parameters on the fungal community structure, (ii) evaluate the
impact of forest management on fungal community composition
within the study regions, and (iii) assess correlations and patterns of
coe-existence among the dominant ectomycorrhizal fungal taxa.

Materials and Methods

Study Site and Sample Collection

This study was conducted as part of the Biodiversity
Exploratories project ([20]; www.biodiversity-exploratories.de).
The three exploratories, hereafter referred as study regions, are
located in: (1) the Schwälbitsche Albs UNESCO Biosphere Area in
Southwestern Germany; (2) the Hainich National Park and its
surroundings (Hainich-Dun) in Central Germany; and (3) the
Schorfheide Chorin UNESCO Biosphere Reserve in North-
Eastern Germany. The study regions differ in climate, geography,
and topographical situations and are representative for large parts
of Central Europe (for details see Table 1 and [18]). We studied 18
20×20 m plots dominated by European beech (Fagus sylvatica L.).
Within regions, the six studied plots were typically separated by
several km separated from each other, and at least several hundred
meters. In each of the three regions there were three age-class
forests (characterized by homogeneous, even aged structure and
intensive management), and three unmanaged forests (characterized
by natural old-growth, uneven-aged stands with trees between 0
and 250 years old).

In April 2008 we took five soil samples per plot. First, the
organic layer was removed with a quadratic 400 cm² metal frame.
Then, the mineral soil was sampled with a motor-driven soil
cylinder (diameter 8.3 cm, length 1 m) to obtain undisturbed cores (Fischer et al. 2010). After removing roots and
stones, we pooled the A horizons of the five soil cores of each plot
to obtain a representative composite sample and stored the
samples at −20°C until molecular analysis. In addition, we
determined organic carbon content (Corg), total nitrogen content
(Nt), pH and soil texture as described in [21] (see also Table 1).

Furthermore, we recorded the vegetation of all plots in spring
and in late summer of the same year. We identified all vascular
plants and litter on each plot. The spring vegetation data was used
as the main objective of this study was to (1) assess the
influence of soil environment and understory vegetation related
parameters on the fungal community structure, (ii) evaluate the
impact of forest management on fungal community composition
within the study regions, and (iii) assess correlations and patterns of
coe-existence among the dominant ectomycorrhizal fungal taxa.

DNA Extraction, Amplicon Library Preparation and
Pyrosequencing

Soil microbial genomic DNA was extracted from 1 g of each
composite sample using a MoBio PowerSoil DNA Isolation Kit
(MoBio Laboratories Inc. Carlsbad, CA, USA), according to the
manufacturer’s instructions. Fungal ITS rDNA amplicon libraries
were produced using fusion primers designed with pyrosequencing
primer B, a barcode and the fungal specific primer ITS1F [22] as a
forward primer and pyrosequencing primer A and the universal
eukaryotic primer ITS4 [23] as a reverse primer. We used a set of
10 bp MID-barcode provided by Roche (Roche Applied Science).
Amplicon libraries were produced from a pool of two
dilution levels and three PCR replications. The PCR reactions
were performed in a total volume of 50 μl reaction mix containing
1 μl DNA template, 25 μl Go Taq Green Master mix (Promega)
and 1 μl 25 pmol of each of the two custom fusion primers. The
reactions were performed using touchdown PCR conditions with
an initial denaturation for 5 min at 95°C followed by: (1) 10 cycles
of 94°C for 30 sec, 60–50°C for 45 sec (−1°C per cycle) and 72°C
for 2 min; and (2) 30 cycles of 94°C for 30 sec, 50°C for 45 sec
and 72°C for 2 min with a final extension step of 10 min.

The PCR products were analyzed using a 1.5% agarose gel,
equimolar volumes of amplified products from three positive
amplicons of the six replicate PCRs per sample were pooled and
gel purified using a Qiagen Gel Extraction Kit (Qiagen, Hilden,
Germany). The amount of DNA in the purified amplicons was
measured using a fluorescence spectrophotometer (Cary Eclipse,
Agilent Technologies, Waldbronn, Germany). An equimolar mix
of the 18 amplicon libraries was subjected to unidirectional
pyrosequencing from the ITS1F end of the amplicons, using a 454
titanium amplicon sequencing kit and a Genome Sequencer FLX
454 System (454 Life Sciences/Roche Applied Biosystems,
Mannheim, Germany) at the Department of Soil Ecology,
Helmholtz Centre for Environmental Research (UFZ, Halle,
Germany).

Bioinformatic Analysis

Multiple levels of sequence processing and quality filtering were
performed. The 454 fungal ITS sequences were extracted based
on 100% barcode similarity. Simultaneously sequence reads with
an average quality score of <25, read length of <200 bp after
trimming of the last 30 bps, ambiguous bases and homo-polymers
of >8 bases were removed, barcodes and primers were trimmed
using the split libraries script available in the Quantitative Insights
In Microbial Ecology pipeline (QIIME) [24]. As our preliminary
analysis showed that the sequence quality score drops below 20
after the 500th bp of longer reads, sequences were trimmed to a
maximum read length of 450 bp using mothur [25]. Sequences
were then clustered and assigned to operational taxonomic units
(OTUs) using the QIME implementation of cdhit with a
threshold of 97% pairwise identity after pre-filtering of sequences
identical in the first 100 bases (n = 100). The representative
sequences, the most abundant sequence in the respective clusters,
were then clustered and classified taxonomically according to the NCBI
taxonomy based on a blast search against the NCBI nucleotide
database excluding uncultured sequences and environmental
samples followed by a 66% consensus level as implemented in
CANGS [26]. A total of 1744 reads, which were not assigned to
the fungal kingdom were cleared from the sequence dataset.

To facilitate screening of potentially chimeric sequences, we
established a reference fungal ITS rDNA sequence database,
containing of fungal ITS rDNA sequences downloaded from the
NCBI GenBank database, screened for sequences with a minimum
length of 400 bp, pre-filtered at 98% identity and clustered at a
97% similarity using cdhit as implemented in QIIME. A total of
6601 sequences representing individual clusters were aligned using
MAFFT [27] and used as core alignment sets. Representative
sequences of OTUs of the fungal ITS pyrotags assigned under the
fungal kingdom were aligned with the custom ITS reference
dataset and checked for chimeras using the chimera uchime
algorithm, as implemented in mothur. Subsequently a total of
6222 sequences including potentially chimeric reads and having less than 90% alignment length to the fungal reference database were removed from the sequence dataset.

Finally we found 29169 fungal sequences, which were grouped into 2271 OTUs. However, the number of reads per sample was variable ranging from 856 to 2505. Thus the number of sequences per sample was normalized to the smallest sample size by random removal of sequences using the normalized.shared command as implemented in mothur.

Statistical Analyses

Data were analyzed using R, version 2.13.2 [28]. All the statistical analyses were carried out using the sequence count within each OTU as abundance value [29] of the non-singleton fungal communities. The observed richness and the Chao1 and ACE estimates of the fungal communities were calculated using the estimateR function of the vegan package [30]. Diversity of the fungal community was assessed calculating Shannon-Wiener, invSimpson, and rarified diversity indices. Differences in the fungal diversity were compared using ANOVA followed by Tukey post hoc test. Similarity in the fungal community structure among the three regions and between the management types within each study region was analyzed using the functions ANOSIM and adonis of the vegan package respectively.

Relationships between fungal communities with environmental variables, which include study site, management type, and soil and vegetation parameters, were visualized using non-metric multidimensional scaling (NMDS) on the basis of Bray-Curtis distance matrix using the nmds function of the labdsv package [31]. The envfit function of vegan was used to fit a centroid to each level of the environmental variables. The function envfit calculates the goodness of fit statistics or squared correlation coefficient value as a measure of separation among the different levels of the variables. Significance or empirical p value of each variable was calculated using 999 random permutations. Model of multivariate analysis of variance was constructed using distance-based redundancy analysis (dbRDA) based on the Bray–Curtis distance using the function capscale of vegan to determine the most influential environmental variables on the fungal community composition. Marginal tests were performed to test the amount of variation explained by the selected variables. Significance tests were performed through non-parametric permutation, which do not rely on the assumption of multivariate normality [32].

In order to assess the influence of the low abundant fungal OTUs on the fungal community structure we performed a hierarchical cluster analysis. Before clustering, fungal OTUs were sorted by the sum of their abundance across all samples and less abundant OTUs were excluded from the analysis by maintaining
those OTUs occurring at least in four samples. Samples were then hierarchically clustered using the complete linkage clustering criteria of the hclust function of vegan using Spearman rank’s similarity metrics [33].

The fungal community assembly rule was tested using the C-score, the tendency for species to exclude one another from a given niche and checkerboard indices that corresponds to the number of species pairs that never co-occur [34] were determined using a null hypothesis of random community assembly. To assess the significance of the scores obtained from the datasets 5,000 matrices were randomly generated from the fungal and putative ectomycorrhizal fungal OTU datasets with EcoSim Version 7.0 [35]. C-score and checkerboard distributions and p values were determined from the simulations using EcoSim’s default settings. Furthermore, we used Spearman rank correlation tests to elucidate the relationship between the environmental parameters and the dominant ectomycorrhizal fungal communities at the Family and Genus level. The same analysis was also used to test the patterns of co-occurrence among the ECM fungal communities. Both spearman’s correlation coefficients and their significance values were calculated using the function corr.test of the psych package [36]. Based on preliminary normality tests, both species and environmental variables were log-transformed.

Results

Sequence Quality Control and Characterization

A total of 37135 reads were obtained after the first sequence processing and quality filtering steps. From this amount a total of 7966 reads were removed including 1744 non-fungal and 6222 potentially chimeric sequences. The remaining 29169 fungal sequences were distributed unevenly ranging from 856 to 2505 reads per sample. The number of sequences per sample was therefore normalized to 856 reads leading to 15408 fungal ITS sequences clustered into 1655 fungal OTUs. The 722 abundant
Figure 2. Observed and estimated (Chao1 and ACE) fungal richness across the three study regions, Schwäbische Alb (A), Hainich-Dün (H) and Schorfheide Chorin (S) presented using box plots for: (a) the fungal kingdom, (b) the phylum Basidiomycota, (c) the subphylum Agaricomycotina, (d) the phylum Ascomycota and (e) the subphylum Pezizomycotina. Different letters above bars indicate significant differences between the sites ($p \leq 0.05$) based on a Tukey post hoc pairwise comparison.

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OTUs excluding singletons were finally used for further analyses in order to address our questions.

Taxonomic assignment of the abundant fungal OTUs found in this study indicated members of the phylum Basidiomycota (390 OTUs/54%) as the most dominant, followed by Ascomycota (261 OTUs/36.1%), Mucoromycotina (24 OTUs/3.3%), Glomeromycota (7 OTUs/1%), Chytridiomycota (4 OTUs/0.6%) and Entomophthoromycotina (1 OTU/0.1%). The remaining 35 OTUs/36.1%) were assigned to the kingdom level according to the NCBI nucleotide taxonomy and represented unknown or unannotated environmental sequences (Figure 1). In general the vast majority of the fungal OTUs were assigned to the major taxonomic levels of subphylum (647 OTUs, 89.6%), class (622 OTUs, 86.2%), order (624 OTUs, 86.4%), Family (567 OTUs, 78.5%) and genus (583 OTUs, 80.6%).

### Fungal Diversity

Comparison of diversity showed that the relative soil fungal distribution at the phylum level differed between the management types within a study region particularly in Schorfheide-Chorin and Hainich-Dün and also among the three regions (Fig. 1). For example, the soils of the Schwäbische Alb region were characterized by a higher percentage (59.8%) of Basidiomycota compared to those of the Hainich-Dün (49.3%) and Schorfheide-Chorin (42.9%). On average, the soils in forests of Schorfheide-Chorin were characterized by a higher percentage of Ascomycota (43.6%) compared to those of the Hainich-Dün (39.1%).

ANOVA followed by a Tukey post hoc pair wise comparison showed no significant difference in the observed and estimated OTU richness among the three regions. In contrast, similar tests showed that the observed Basidiomycotan, Agaricomycotan, Ascomycotan and Pezizomycotan richnesses differed significantly ($p<0.05$) among the three regions. The Schwäbische Alb and Hainich-Dün regions exhibited significantly higher basidiomycotan and agaricomycotan OTU richnesses than Schorfheide-Chorin (Figure S2).

In all three taxonomic levels tested, extrapolative species richness estimates (chao1 and ACE estimators) were more than double compared to the observed richness, indicating the presence of highly diverse fungal communities in these forest ecosystems (Figure 2). The Shannon-Wiener diversity index ranged from 3.0 to 4.7, also indicating a diverse fungal community, especially in the Hainich-Dün forest soils. The invSimpson and rarified species diversity indices also followed a similar pattern (Figure S2).

### Fungal Communities and Factors Explaining the Community Structure

Analysis of the similarity of fungal communities using ANOSIM revealed a significant ($r=0.783$, $p<0.001$) variation among the three regions. Consistently, fitting of the study site to the NMDS ordination plot indicated significant differences in the fungal community structure among the study regions at the kingdom, phylum and subphylum levels ($r^2\geq 0.75$, $p<0.001$, Table 2). The soil physical and chemical parameters were also significantly related to differences in the fungal community composition. Among the vegetation parameters, the cover of the herbaceous layer influenced significantly the fungal community structure in all three taxonomic levels tested, where increased cover of the herbaceous layer was related to an increase in the fungal communities (Figure 3a, 4a and Figure S3).

The dbRDA model analysis indicated soil pH, sand content, and litter cover to be the most important factors shaping the fungal
community composition ($F = 3.925$, $p = 0.005$, Table 3). Marginal tests, however, showed that sand content and litter cover were significantly related to the fungal community composition ($pH - F = 1.381$, $p = 0.065$, Sand - $F = 1.975$, $p = 0.005$, litter cover - $F = 2.586$, $p = 0.005$). The litter cover was obviously a driver of the fungal community structure, which was mainly reflected by its positive correlations to the Ascomycotan ($p \leq 0.01$, Table 2, Figure S5) and ectomycorrhizal fungal communities ($p \leq 0.01$, Table 2, Figure 4a).

The observed change in fungal community composition among regions was also found when we compared datasets for the two management types separately (see Table 2). Overall, the number of shared fungal OTUs between age-class and unmanaged forests within the study regions ranged between

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**Figure 3.** Fungal community structure across the three study regions: (a) NMDs ordination plot of the study regions Schwäbische Alb (A), Hainich-Dün (H), and Schorfheide Chorin (S), based on the fungal community composition identified as members of the fungal kingdom (Stress = 8.17). In each diagram soil and vegetation parameters used as an explanatory variable and found to be significant ($p \leq 0.05$) are represented as vectors. Management types are abbreviated as AC for age-class and NF for unmanaged natural forests followed by the respective study site. (b) Hierarchical cluster based on the most abundant fungal OTUs identified at least in four of the study plots where the fungal OTUs clearly separated the three regions. Fungal community assembly is nonrandom: C-score distribution (c) and checkerboard indices (d) for observed and randomized fungal OTU occurrence.

doi:10.1371/journal.pone.0047500.g003
Table 3. Relationships between the predictor variables pH, sand content and litter cover to the fungal community composition.

<table>
<thead>
<tr>
<th></th>
<th>pH var</th>
<th>F</th>
<th>p</th>
<th>Sand var</th>
<th>F</th>
<th>p</th>
<th>Litter cover var</th>
<th>F</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fungi</td>
<td>0.342</td>
<td>1.634</td>
<td>0.005</td>
<td>0.495</td>
<td>2.362</td>
<td>0.005</td>
<td>0.576</td>
<td>2.752</td>
<td>0.005</td>
</tr>
<tr>
<td>Ascomycota</td>
<td>0.300</td>
<td>1.381</td>
<td>0.140</td>
<td>0.430</td>
<td>1.975</td>
<td>0.005</td>
<td>0.563</td>
<td>2.586</td>
<td>0.005</td>
</tr>
<tr>
<td>Pezizomyeota</td>
<td>0.338</td>
<td>1.564</td>
<td>0.026</td>
<td>0.473</td>
<td>2.189</td>
<td>0.010</td>
<td>0.613</td>
<td>2.837</td>
<td>0.005</td>
</tr>
<tr>
<td>Basidiomycota</td>
<td>0.300</td>
<td>1.381</td>
<td>0.065</td>
<td>0.430</td>
<td>1.975</td>
<td>0.005</td>
<td>0.563</td>
<td>2.586</td>
<td>0.005</td>
</tr>
<tr>
<td>Agaricomycotina</td>
<td>0.408</td>
<td>1.750</td>
<td>0.015</td>
<td>0.588</td>
<td>2.523</td>
<td>0.005</td>
<td>0.656</td>
<td>1.816</td>
<td>0.005</td>
</tr>
<tr>
<td>ECM fungi</td>
<td>0.407</td>
<td>1.566</td>
<td>0.026</td>
<td>0.586</td>
<td>2.253</td>
<td>0.005</td>
<td>0.661</td>
<td>2.543</td>
<td>0.005</td>
</tr>
</tbody>
</table>

Results show marginal tests using the dbRDA model, where var indicates the proportion of the fungal community variation explained by the predictor variable. Significant p values less than 0.05 are indicated in bold.

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37% and 50% (Figure S3). However, the contribution of management to variation in fungal community composition within the study regions was not significant (adonis, $R^2 = 0.049$, $p = 0.61$). Hierarchical cluster analysis based on the most abundant OTUs occurring at least in four of the study samples also separated the fungal communities into three major groups corresponding to the study regions (Figure 3b), which consistently demonstrated that the fungal community structure differs among the three regions but not between the management types within the study regions.

The fungal community co-occurrence test found that the C-score for the real fungal OTU dataset was 4.84, which is significantly greater than the simulated mean C-score of 4.75 obtained from the simulated dataset ($p < 0.0001$). The checkerboard measure for the fungal communities (162069.70) was also significantly greater than the simulated mean checkerboard measure (169235.00) was also obtained from the simulated dataset ($p = 0.61$). Hierarchical cluster analysis based on the most significant (R = 0.798, $p = 0.0001$) and was influenced by soil physico-chemical parameters (Figure 4a, Table 2). The dbRDA model analysis for the ECM fungal communities found that soil pH, sand content and litter cover to be the most important factors ($F = 3.598$, $p = 0.005$, Table 3), where all the three variables were significantly related to the community composition ($pH - F = 1.366$, $p = 0.026$, Sand - $F = 2.253$, $p = 0.005$, litter cover - $F = 2.543$, $p = 0.005$).

ANOVA followed by a Tukey HSD post hoc analysis indicated significant variation in ECM fungal family richness among the three regions. Similar analysis of individual families also revealed a significant variation in the richness of some families among the study regions and a significant correlation to soil parameters. For example richness of the Russulaceae was significantly lower in the Hainich-Dun site (p <= 0.05) compared to the highest richness in Schorfheide Chorin, where the observed richness was positively correlated with sand content and soil C:N ratio. The Sebacinaeae and Thelephoraceae showed relatively low richness in Schorfheide Chorin. Their richness was increasing with soil pH and decreasing with sand content and soil C:N ratio. However, richness of members of the Inocybaceae was increasing with soil pH. Their diversity was higher in the Schwabsiche Alb than in both other regions (Figure 5).

Consistent with the general fungal community structure, the observed change in ECM fungal community composition among regions was also found when we compared datasets for the two management types separately (see Table 2). But, we found no statistically significant effect of management within the respective study sites (adonis, $R^2 = 0.043$, $p = 0.779$). However, the relative distribution of the ECM fungal communities showed different patterns between the two management types particularly within the Schwabsiche Alb and Schorfheide Chorin regions (Figure S4).

The C-Score and checkerboard pairs analysis of ECM fungal co-occurrence also showed that both the observed C-Score of 4.22 and checkerboard measure of 36514.00 were significantly higher than the randomized datasets (C-Score = 4.11, $p < 0.0001$ and checkerboard = 34850.89, $p < 0.0001$) that the ectomycorrhizal fungal community is composed of non-random fungal communities. Spearman’s rank correlation analysis of the 10 most abundant ECM fungal genera among the study plots revealed some significant positive and negative correlations (Table 4). For example the genus Tomentella showed a strong positive correlation with Thelephora and Sebacinaceae. The genera Inocybe and Sebacinaceae on the other hand showed strong correlations with other ECM genera. Inocybe was significantly and positively correlated with Sebacinaceae and negatively with the genus Xerocomus, whereas Sebacinaceae was significantly and positively correlated with Cortinarius. Similar analysis within the individual study regions (Table 5) also showed region-specific correlation patterns consistent with the observed correlations of the fungal genera with the...
soil and vegetation parameters. Our results in general demonstrate that the observed differences in ECM fungal community structure among and within the three regions were rather characterized by the co-occurring and potential functional complementarity of ECM fungal taxa.

Discussion

Sequence Analysis

Pyrosequencing in microbial ecology has strongly improved resolution of community studies by increasing the numbers of sequences per sample compared to traditional cloning and sequencing approaches. A number of microbial diversity studies filtered out sequences by removing noisy and chimeric reads, thus reducing the bias and enabling documentation of large numbers of singletons as members of the “rare biosphere” [40,41,42,43,44]. However, most of the analyses in recent fungal diversity studies have focused on abundant sequence types (OTUs), while the ecological significance of singletons as rare biosphere is still being debated. Some authors recommend excluding all singletons from the analysis [16,17], while others consider them as an evidence for a large unexplored diversity [15,45].

In this study we were able to screen a total of 1655 fungal OTUs including 933 singletons. The vast majority of the singletons (62%) showed ≥97% identity at a minimum of 90% query coverage to sequences available in the NCBI GenBank database; the remaining 38% may correspond to the unexplored and rare fungal biosphere. We also observed that 287 (30.8%) of the singletons were non-singleton OTUs before the normalization step and 82% were taxonomically assigned to the Genus level. These observations provide evidence against the current practice to exclude singletons in general with the assumption that they are non-biological in nature [17]. However, we presented results based on the abundant fungal OTUs excluding singletons, although all the statistical analysis performed including the singletons showed similar results.

Fungal Diversity and Community Structure Among Study Regions

In this study we found a huge soil fungal diversity in the soils of the investigated European beech forests with clear differences in community composition among the three study regions located in North, Central and South Germany. The fungal community was dominantly composed of Basidiomycota followed by Ascomycota, which is in accordance with previous studies investigating temperate forest soils [10]. Noteworthy, significant differences in the observed fungal richness between the study regions were found at the phylum (Basidiomycota, Ascomycota) and subphyla (Agaricomycotina and Pezizomycotina) levels (Figure 2, Figure S2).

In general the fungal community structure was found to be significantly different among the three study regions. The NMDS ordination plot and ANOSIM using the abundant fungal OTUs and the hierarchical clustering using only the most abundant fungal OTUs occurring at least in four samples showed consistent clustering of the three study regions, indicating a consistent pattern of fungal community structure. Having in mind that the three study regions are distantly located in the North - South gradient across Germany, our finding is in line with the report of Green et al [8] who studied Ascomycotan fungal communities in four distinct land use systems in arid Australia that varied substantially in geology, topography and native vegetation. They analyzed a total of 1,536 soil samples with distances ranging from 1 m to 100 km using a pair wise sample comparison and found a strong differences in the structure of soil fungal communities among geographic distances, which contradicts the weak region effect on...
Figure 5. Relative distribution of the four dominant ectomycorrhizal fungal families *Russulaceae*, *Inocybaceae*, *Sebacinaceae* and *Thelophoraceae* among the three study regions and their relationships with soil pH, C:N ratio and Sand content determined using Box plots and linear regression analysis respectively. Different letters above bars in the box plots indicate significant differences between the sites ($p \leq 0.05$) based on a Tukey HSD post hoc pairwise comparison. Significant regression lines are presented with $p$-values.

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Table 4. Relationships among the ten dominant ectomycorrhizal (ECM) fungal genera determined using Spearman’s rank correlation *.

<table>
<thead>
<tr>
<th>Russula</th>
<th>Inocybe</th>
<th>Cortinarius</th>
<th>Phialophora</th>
<th>Sebacina</th>
<th>Lactarius</th>
<th>Elaphomyces</th>
<th>Xerocomus</th>
<th>Tomentella</th>
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*significant correlations with p<0.05 are in bold.

doi:10.1371/journal.pone.0047500.t004

fungal community structure found by Kasel et al [5] who studied soil fungal communities among four land uses located across three regions separated by distances of 50, 175 and 215 km in central Victoria, south-eastern Australia.

Relationships of Fungal Community Structure with Soil Physico-chemical Parameters

Differences in fungal community structure may result from different abiotic factors. A number of studies reported effects of soil physical and chemical parameters on fungal community structures [7,15,46]. We also found that the fungal communities were positively correlated to the first NMDS axis with the soil sand content and pH, C\text{org}, silt, and clay content (Figure 3a). The dbRDA based model explained the fungal community composition (Table 3). Compared to both other regions soil pH, C\text{org}, clay, and silt contents were significantly lower in Schorfheide-Chorin, while the C:N ratio and sand content were significantly higher at this site (Figure S1). The patterns of the NMDs ordination plot and the strong correlation with the soil parameters were consistent among tested taxa, whereby the Hainich-Dün and Schwäbische Alb regions were relatively close to each other indicating similar soil conditions.

Relationships of Fungal Community Structure with Vegetation and Litter Cover

We found evidence that vegetation characteristics, mainly the herbaceous plant and litter covers, affect the diversity and community composition of soil fungal communities in these European beech dominated forests. Our data indicates that the

Table 5. Relationships between the dominant ectomycorrhizal fungal genera and soil and vegetation parameters determined using Spearman’s rank correlation *.

<table>
<thead>
<tr>
<th>pH</th>
<th>Russian</th>
<th>Inocybe</th>
<th>Cortinarius</th>
<th>Phialophora</th>
<th>Sebacina</th>
<th>Lactarius</th>
<th>Elaphomyces</th>
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*significant correlations with p<0.05 are in bold.

Note: Hart cover: Cover of 5–10 m high trees; Tree cover 2: Cover of >10 m high trees; Tree cover 1 and 2: cumulative tree cover of all trees.

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herbaceous plant cover was significantly correlated with the soil fungal communities, which corroborates the report of Burke et al [7], who analyzed ECM roots from soil cores in a Mature Beech-Maple forest and found a strong correlation between root fungal communities and the herbaceous plant cover. They also found a strong correlation of the herbaceous layer with the genus Russula. Our data, however, showed that presence and relative abundance of the genera Cortinarius and, Phialophora correlated positively with the herbaceous plant cover. On the other hand the genera Phialophora and Inocybe showed a strong negative and positive correlation with the litter cover, respectively. This partially reflects the observed strong and negative correlation between herbaceous plant and litter cover in these beech forest systems (r = -0.642, p = 0.004) and their impact in the fungal community. However, the functional links underlying these correlations remain to be investigated.

**Management Effects on Fungal Community Structure**

It has been well documented that land use changes influence the composition of soil fungal communities indirectly by changing plant and soil properties, but such evidence presented previously has focused on comparisons between different dominant tree species [6], or near-natural vs. plantation forests [5]. In our study we found no influence of management on the fungal community structure within the study sites. Remarkably, we also found no effect of management on the soil parameters and vegetation cover within the study regions, which could partly explain the absence of management effect on the soil fungal community structure. However, although it is not statistically significant, the relative distribution of the fungal communities as exemplified by the ECM fungal families indicated differences between managed and unmanaged forest stands in the respective study regions (Figure S3). The high degree of specificity of fungal communities, especially ECM fungi to their host plants under similar edaphic conditions [11,47], could also lead to the observed weak impact of management on the fungal community structure.

**Correlation and Co-existence of Ectomycorrhizal Fungi**

Consistent with the total fungal community structure, the ectomycorrhizal fungal communities also differed significantly between the three regions, but no management effect was found within the study sites. The ECM fungal communities were dominated by the ECM genera Russula, Inocybe, Cortinarius, Lactarius, Thelephora, and Tomentella, which were also reported to be the most diverse and abundant groups of ECM fungi in a number of studies [13,39,48,49]. Besides the significant variation on the ECM fungal community structure among the study regions in response to the soil physico-chemical parameters (Figure 4a and Figure 5), we observed strong study region specific correlations between the ECM fungal genera, suggesting different patterns of co-existence. This is in line with previous studies that reported co-existence of ECM fungi in colonized roots [7,13]. The observed non-random patterns of co-occurrence, differences in the identity and number of correlated ECM fungal genera reflect the degree of variation in environmental preferences and niche partitioning [11,12].

**Conclusions**

The use of pyrosequencing in microbial ecology is a powerful tool and increasingly becomes a standard method, where strict quality filtering [44] and sequence normalization [3050] are crucial analysis steps. Although we presented our data based on abundant fungal OTUs, we found comparable results including singletons in the analysis. The observation that about 30% of the singletons were abundant OTUs before the sequence read normalization step suggests the need for methods to screen singletons in order to assess the contribution of the rare (or rarely detected) fungal biosphere in a given ecosystem, especially when considering temporal variations.

In general, in this study, based on ANOSIM of the abundant fungal OTUs and hierarchical cluster analysis of the most abundant fungal OTUs occurring at least in four samples, we found consistent results showing that the fungal community structure differs among the study regions. Our results also indicate that soil fungal community composition is mainly influenced by soil physico-chemical parameters and the herbaceous plant and litter cover, where soil pH, sand content and litter cover explained most of the variation in the fungal community composition. However, the forest management showed a very weak impact in the studied forests dominated by the same tree species. This suggests the need for large-scale biogeographic studies with ecologically broader sampling and analysis of soil fungal communities in order to find the functional relationship of biotic and abiotic parameters varying with forest management. Our study also demonstrated ECM fungal correlation patterns that differ between the three beech forest sites, supporting the functional diversity and complementarity of ECM fungi. Future research on comparative study of root and soil ECM fungal communities coupled with isolation and functional analysis of the dominant taxa is needed to explore functional links.

**Supporting Information**

**Figure S1** Soil and understory vegetation parameters among the three study regions depicted using box plots. Schwäbische Alb (A), Hainich-Dün (H) and Schorfheide Chorin (S) study sites. Different letters above bars indicate significant differences between the sites (p ≤ 0.05) based on a Tukey post hoc pairwise comparison. (TIF)

**Figure S2** Rarefied species richness, Shannon and inverse diversity indices across the three study regions, Schwäbische Alb (A), Hainich-Dün (H) and Schorfheide Chorin (S), for: (a) the fungal kingdom, (b) the phylum Basidiomycota, (c) the subphylum Agaricomycotina, (d) the phylum Ascomycota and (e) the subphylum Pezizomycotina. Based on a Tukey post hoc pairwise comparison at p ≤ 0.05 no significant differences were found. (TIF)

**Figure S3** Distribution of shared and unique fungal OTUs among the two management types of the three study regions (a) age class beech forests (b) among the unmanaged beech forests, and between the two management types of the study regions Schwäbische Alb (c), Hainich-Dün (d) and Schorfheide Corin (e). (TIF)

**Figure S4** Relative distribution of ectomycorrhizal fungal families between the two management types in the three study regions. (TIF)

**Figure S5** NMDs ordination of the study sites Schwäbische Alb (A), Hainich-Dün (H) and Schorfheide Chorin (S), based on the fungal community composition identified as members of the phylum Ascomycota (Ascomycotan communities, stress = 10.66), phylum Basidiomycota (Basidiomycotan communities, stress = 12.66), subphylum Pezizomycotina (Pezizomycotan communities, stress = 10.73) and subphylum Agaricomycotina (Agaricomycotan communities, stress = 12.80). Soil and plant parameters used as an explanatory variable and found to be significant (p ≤ 0.05) are represented as vectors. The two management types
are presented as AC = age class and NF = unmanaged beech forests followed by the respective study site abbreviations.

**Table S1** Ectomycorrhizal fungal community distribution.

Putative ECM fungal families and genera found in this study and the study sites and management types they are found. (Numbers refer to the number of fungal OTUs of the respective family found in the respective management type). Abbreviations: AC = age class and NF = unmanaged beech forest. Note: For Ascomycetes fungal taxa without a clearly defined family classification we used the genus names in the family column.

**DOCX**

**Acknowledgments**

We thank the managers of the three exploratories, Swen Renner, Sonja Gockel, Andreas Hemp, as well as Martin Gorte and Simone Pfeiffer for their work in maintaining the plot and project infrastructure, and Elisabeth Kalko, Eduard Linsermair, Dominik Hessenmoller, Jens Nieschulze, Daniel Prati, Ernst-Defel Schlulze and Wolfgang W. Weiser for their role in setting up the Biodiversity Exploratories project. Fieldwork permits were issued by the relevant state environmental offices of Baden-Württemberg, Thüringen, and Brandenburg (according to § 72 BbgNatSchG).

**Author Contributions**

Conceived and designed the experiments: FB, TW. Performed the experiments: SC MG BS. Analyzed the data: TW SC. Contributed reagents/materials/analysis tools: FB TW. Wrote the paper: TW SC FB. Contributed data on soil properties and analysis of the data: IS. Contributed vegetation data and analysis of the data: SB MF.

**References**


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