Title: Soil fungal communities and succession following wildfire in Ethiopian dry Afromontane forests, a highly diverse underexplored ecosystem

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Abstract

Ethiopian dry Afromontane forests are complex ecosystems that have important economic and ecological roles. However, recurrent fire has been a source of disturbance for these forests. We assessed the effect of fire on soil fungal communities in a remnant dry Afromontane forest in Wondo Genet, southern Ethiopia, by analysing soil samples collected from unburned stands and from stands one and ten years after fire using DNA metabarcoding of the ITS2 rDNA. The analysis indicated that the soil fungal community was most diverse soon after a fire disturbance and declined over time. Fungal community composition also differed among stands. Our results also indicated that differences in fungal diversity were stand dependent rather than due to the chronology of the fire history in this forest system. We found higher numbers of mycorrhizal species in burned stands, suggesting that these fungal symbionts could compensate for the effects of nutrient stress caused by fire in these areas. Fungal community composition was also significantly correlated with organic matter content, potassium and magnesium in soil. This work could be considered as a case study since the plots were established in a single stand for each treatment in the dry Afromontane forests of Ethiopia. Thus, we recommend further studies and conclusions regarding other stands need to be taken with caution.

Keywords: *Edaphic variable, Ethiopia, Forest fire, fungal functional groups, ion torrent sequencing, tropics*

1. Introduction

Ethiopia is an ecologically diverse country owing to the varied topographic features and altitudinal variations (Bongers and Tenngkeit, 2010). The country also experiences a high variation in macro- and mesoclimatic conditions that have contributed to the formation of biologically diverse ecosystems. According to Friis et al. (2010), the vegetation of Ethiopia is classified into 12 types based on the elevation zones in which they occurred. Out of which, the natural high-elevation forests , that include the Afromontane vegetation, are exclusively found in the highland regions of Ethiopia between 1500 to 3400 m above sea level (Lemenih and Bekele, 2008).

The highlands of Ethiopia occupy more than 44% of the country's land area (Kidanu, 2004; McCann, 1995). Dry Afromontane forests dominate these highlands and are found mainly in the central, northern and western parts of the country (Friis et al., 2010). This forest is a complex ecosystem and is characterized by high humidity, a variable rainfall pattern, and a prolonged dry season (Friis et al., 2010). The dry Afromontane forest provides important ecosystem services such as watershed protection and carbon sequestration (Wassie et al., 2005). The dominant tree species in this forest are *Juniperus procera*, *Podocarpus falcatus*, *Hagenia abyssinica* and *Olea africana*, which are the main source of timber in Ethiopia. In addition, the dry Afromontane forest harbours various types of non-timber forest products, including wild edible mushrooms (Dejene et al., 2017b).

Anthropogenic factors are negatively affecting the forest resources in Ethiopia (Lemenih and Bekele, 2008). Fire is a potentially destructive disturbance, affecting the distribution, diversity and composition of the forest resources (Lemenih and Bekele, 2008; Wassie et al., 2005). Human-induced fire, mainly for subsistence and economic reasons, is the most important reason for the depletion and degradation of natural resources in Ethiopia. For instance, the most destructive forest fires, which occurred in 2000, destroyed over 150,000 ha of forest (Senbeta and Teketay, 2001). More recently, in 2019, a fire in the northern part of Ethiopia affected 340 ha of forest (New Business Ethiopia, 2019). This trend is more common in the highland areas, where the dry Afromontane forest is found, and has a direct impact on the biodiversity in the forest ecosystem (Lemenih and Bekele, 2008). This loss of biodiversity could also occur in the

forest soil, which harbours a great diversity of microbial organisms (Fierer and Jackson, 2006), including fungi. Depending on the severity and frequency, fire could directly or indirectly affect edaphic variables in the forest ecosystem (Reazin et al., 2016), which in turn could have an impact on fungal communities dwelling in the soil (Cairney and Bastias, 2007; Dahlberg et al., 2001; Rincón and Pueyo, 2010).

Forest fungi comprise a crucial functional component and contribute to the high ecological significance of forest ecosystems (Crabtree et al., 2010). Their roles can be described in terms of nutrient addition and cycling, the carbon pool, soil formation, and the formation of symbiotic links with plants (Claridge et al., 2009; Fontaine et al., 2007; Van Der Heijden et al., 2008). Saprotrophic fungi play a key role in the decay of organic matter (Hobbie et al., 1999), whereas mycorrhizal fungi form symbiotic associations with plants, and can form up to 80% of the fungal biomass in forest soils in northern temperate regions (Nehls, 2008). The fungal mycelium also plays an essential role in soil stabilization and helps to increase the water-holding capacity of the soil (Kennedy and Gewin, 1997). Furthermore, some species of fungi are pathogenic, causing disease in both above- and belowground components of the forest system (Narayanasamy, 2011).

Despite recent advances in determining the diversity and composition of forest fungi in various biomes, fundamental questions regarding their distribution and function, and the factors that influence them remain unanswered, particularly in under-sampled biomes (Guo et al., 2013; Krashevska et al., 2015). The majority of soil fungi are unexplored and, the functional relationship between fungi, soil, and plants remains understudied (Bridge and Spooner, 2011; Van Der Heijden et al., 2008). Previous investigations have estimated that there are about 5.1 million fungal species worldwide (Taylor et al., 2014). Of these, 2–6% have been described (O'Brien et al., 2005) and ~1200 new species are described each year (Hibbett and Thorn, 2001), indicating that there are many more fungal species to be explored, named, and identified. In addition, further studies are required to increase our understanding of the dynamics of soil fungi and their community structure (Dhruba et al., 2015) and the impact of various environmental and anthropogenic factors. Furthermore, to date, most studies of soil fungal communities have focussed on temperate and Mediterranean forest ecosystems; less consideration has been given to soil fungal communities in tropical forest ecosystems (Taudière et al., 2017).

The effects of fire on soil fungi are determined by the fire severity, changes in soil properties and post-fire environmental conditions (Bastias et al., 2006; Buscardo et al., 2012, 2010; Neary et al., 1999; Reazin et al., 2016). A change in vegetation following a fire may also impact on fungi living in a symbiotic or saprophytic relationship with trees. Thus, the subsequent structure of fungal communities might be influenced by the dynamics of post-fire plant communities (Cairney and Bastias, 2007). In addition, factors such as the fuel load (Dahlberg et al., 2001), soil moisture and temperature (Bonet et al., 2010) and other environmental and weather conditions during the fire event can also influence the effects on soil biota. Furthermore, differences in the sensitivity of fungal propagules to fire determine the degree to which the composition of fungal communities changes after the fire (Hernández-Rodríguez et al., 2013). However, the inconsistency of results from individual studies makes it difficult to provide a general conclusion regarding the possible dynamics of fire, fungi and ecosystem function. Consequently, location-based studies are necessary to obtain a better understanding of the effect of fire on the soil fungal community at a specific location (Taudière et al., 2017).

A limited number of studies have investigated fungal communities in the forest systems of Ethiopia; however, these were mainly focused on above-ground fungal communities (Dejene et al., 2017b, 2017a). Recently, Castaño et al. (2019) also investigated the soil fungal community and ecological guilds associated with *Eucalyptus grandis* plantations in Ethiopia. However, the soil fungal communities associated with the dry Afromontane forests in Ethiopia are undescribed and the potential effect of fire on soil fungal communities in these ecosystems where forest fire is a recurrent phenomenon has not yet been analysed. Forest fires are expected to change the edaphic variables on which the fungi depend for their trophic as well as their community composition. In addition, it is important to understand how fungal communities respond to the post-fire environment and to identify which are the most important environmental factors driving fungal community structure and function to supplement our knowledge of Ethiopian fungal resources as well as to promote their conservation and development. Thus, the aim of this study was to provide baseline information on soil fungal communities in the dry Afromontane forests along a post-fire, secondary succession gradient in Ethiopia.

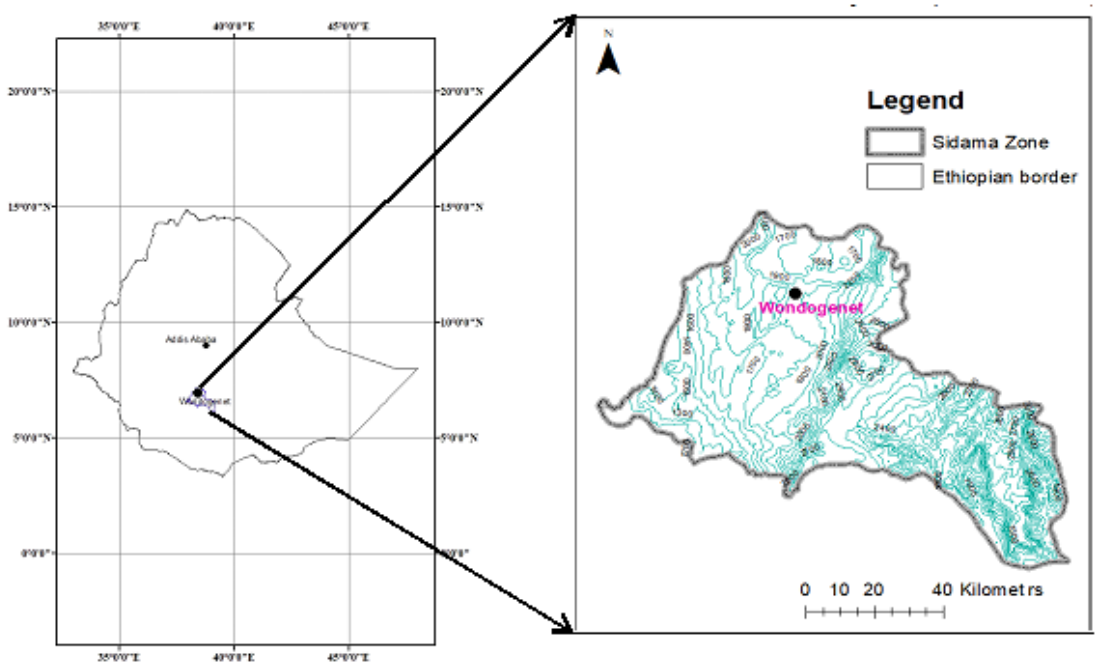
We hypothesized that the richness and composition of the entire soil fungal communities would change substantially during a post-fire forest succession and would differ from those in

unburned forest (Hypothesis 1). Specifically, we expected that soils would be more fertile immediately after fire with a gradual decrease in soil fertility over time and that the community turnover would partially be explained by these changes in edaphic conditions (Hypothesis 2). As a consequence, we expected ruderal, generalist saprotrophic fungi, mainly utilizing simple and easily absorbable forms of nutrients, to be more abundant and species-rich shortly after fire than in unburned forests (Hypothesis 3). By contrast, root-associated symbiotic fungi were expected to be more diverse in older burned forests and unburned forests (Hypothesis 4).

2. Materials and Methods

2.1. The study area description

The study was conducted in Wondo Genet natural forest area, which is located in southern Ethiopia, approximately 265 km from Addis Ababa (Figure 1) (between 7°06' N–7°07' N and 38°37' E–38°42' E) at 1,600 to 2,580 m above sea level (Belaynesh, 2002; Fenta, 2014). Wondo Genet is characterized by remnant dry Afromontane forest patches (Ango and Bewket, 2007; Belaynesh, 2002; Fenta, 2014). The climate is characterized by the Weyna-Dega agro-climatic zone, with a bimodal rainfall pattern: the main rainy season is in the summer and a lesser rainy season is in spring. The mean annual rainfall and mean annual temperature of the study area are 1210 mm and 20°C, respectively (Belay, 2016; Fenta, 2014). The soil is an Andisol with a sandy loam texture (Eriksson and Stern, 1987) and an average pH value of 5.7 (Eshetu and Högberg, 2000). The study area covers about 797 ha of natural forests lands (Ango and Bewket, 2007; Belaynesh, 2002; Fenta, 2014) that are characterized by remnant Dry Afromontane forest patches, home to important fauna and flora. The dominant tree species in the study forest are *Juniperus procera*, *Albizia gummifera*, *Afrocarpus falcatus*, *Bersama abyssinica*, *Prunus africana*, *Podocarpus falcatus*, *Cordia africana*, *Croton macrostachys* and *Olea africana* (Ango and Bewket, 2007; Zerga and Berta, 2016). These trees are reported to be associated with arbuscular mycorrhizal fungi (Wubet et al., 2003). Human-induced fire is a recurrent phenomenon, occurring yearly in small patches of this natural forest (Bekele et al., 2013; Dejene et al., 2017b).



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190 **Figure 1:** Location of the study area, Wondo Genet, Ethiopia.

191 Sample plots were established in the forest in 2015 in stands with similar environmental
192 conditions such as climate, altitude and soil. Information about the forest fire history of these
193 stands was obtained from the Department of Forest Management at the Wondo Genet College of
194 Forestry. The control stand of unburned natural forest (UB) was representative of the original
195 natural forest and had not been affected by fire for at least 40 years. Burned stands selected for
196 the study were similar in terms of fire severity, i.e., the canopy and understory had burned and
197 the soil organic layer had been consumed (Rincón and Pueyo, 2010). In these burned areas, two
198 forest stands were selected based on their fire history: (1) one-year-old burned forest (B1); and
199 (2) ten-year-old burned forest (B10). Within each of these forest stands, three transects were
200 established about 250 m apart from each other. Each transect covered an area of 100 m^2, with a
201 rectangular shape (2 m x 50 m). Because the plots were established in a single stand for each
202 treatment, this work could be considered as a case study and conclusions regarding other stands
203 need to be taken with caution.

204 **2.2. Soil sampling for molecular work**

A total of nine (2 m × 50 m) transects, three per each studied stands (UB, B1 and B10), were established perpendicular to the slope following Luoma et al. (1991) and Smith et al. (2002). Five soil cores were extracted 5 m apart along the centreline of each transect using a cylindrical (2 cm radius, 20 cm long, 250 cm^3) soil borer (De la Varga et al., 2012; Taylor, 2002) to sample spatial variability and to minimize the probability of sampling the same genet repeatedly. From these cores, well-decomposed organic layers and mineral soils were sampled. The litter layer (intact and partially decomposed leaves) was discarded because the fungal community composition in litter tends to diverge from that in soil (Voříšková et al., 2014). The five cores from each transect were pooled to obtain a composite soil sample for each transect for the final DNA extraction. Soil cores were dried, sieved through a 1 mm^2 mesh and ground to a fine powder using a mortar and pestle. A subsample of each pooled sample was stored at –20°C for molecular analysis and the rest of the sample was used for determining selected physical and chemical properties of the soil (Table 1).

2.3. Molecular analysis

DNA was extracted from 0.25 g of soil per sample using a PowerSoil™ DNA Isolation Kit (MoBio Laboratories Inc., Carlsbad, CA, USA). PCR reactions were performed in triplicate for each sample to minimize PCR biases. PCR reactions were performed in 20 µl reaction volumes containing 11.22 µl of MQ water, 1.60 µl of DNA template, 2.00 µl of 10× buffer, 1.40 µl of $MgCl_2$ (50 mM), 1.60 µl of dNTPs (10 mM), 0.50 µl of BSA (2%), 0.80 µl of reverse and forward primers (10 µM) and 0.08 µl of Platinum Taq DNA polymerase (Invitrogen, Carlsbad, CA, USA). We used the following PCR conditions: an initial denaturation step at 94°C for 3 min; then 35 cycles of 94°C for 45 s, 50°C for 1 min and 72°C for 1.5 min; and a final cycle of 72°C for 10 min. The ITS2 rDNA region was amplified using the forward primer fITS7 (Ihrmark et al., 2012) and the barcoded reverse primer ITS4 (White et al., 1990). The ITS4 primer was labelled with sample-specific Multiplex Identification DNA-tags. A negative control consisting of MQ water instead of DNA was included in each PCR run. The absence of bands on gels indicated that negative controls were amplicon free. Ion Torrent sequencing was carried out at the Naturalis Biodiversity Center. We used the Ion 318^{TM}Chip to allow for the highest possible sequencing coverage.

2.4. Soil sampling and edaphic variables analysis

To relate soil fungal composition to explanatory edaphic variables, additional soil samples were collected from each transects. Composite soil samples, from the centre and from the four corners of each plot, were extracted after clearing plant matter and debris from the soil surface. Soil was extracted to a depth of 20 cm with the aid of an auger and spade. After mixing the samples thoroughly, approximately 500 g of soil was placed in a plastic bag for transport back to the laboratory for analysis. After air drying the soil in shade, the chemical and physical properties of the soil were determined using DTPA extraction, KH_2PO_4 extraction, Olsen, Kjeldahl digestion, Walkley–Black, ammonium acetate and instrumental methods. The analysis was conducted by Water Works Design and Supervision Enterprise, a laboratory test service for soil fertility at Addis Ababa, Ethiopia. A soil: water (1:2.5) suspension and the supernatant of the same suspension were measured using a pH meter and an electrical conductivity meter, respectively, to determine the soil pH (Reeuwijk, 2002). Organic carbon (C) content was determined using wet digestion (Walkley and Black, 1934). Total nitrogen (N) content was determined using the Kjeldahl digestion procedure (Kim, 1996). Available phosphorus (P) was determined using sodium bicarbonate (0.5M $NaHCO_3$) as an extraction solution (Olsen and Sommer, 1982). Available sodium (Na), potassium (K), calcium (Ca) and magnesium (Mg) were extracted using ammonium acetate. Soil particle size was analysed with a hydrometer (Bouyoucos, 1951), using sodium hexametaphosphate (Calgon solution) as the dispersing agent. Once the proportion of sand, silt and clay separates were calculated, the soil was assigned textural class name using ASTM software. We also used the following formula to convert organic carbon to organic matter. Organic matter (%) = Total organic carbon (%) x 1.72. The selected soil properties of the studied plots are provided in Table 1.

2.5. Bioinformatic analysis

Raw sequence reads were obtained from the Ion Torrent output that comprised demultiplexed sample reads. Primers and poor-quality ends were trimmed off based on a 0.02 error probability limit in Geneious Pro 8.1.8 (BioMatters, Auckland, New Zealand). Subsequently, sequences were filtered using USEARCH based on the following settings: all sequences were truncated to 200 bp and sequences with an expected error of >1 were discarded.

The remaining sequences were collapsed with USEARCH v.8.0 (Edgar, 2010) into unique sequence types on a per-sample basis while preserving read counts. Singleton sequence types were discarded; the resulting 305,520 high-quality sequences were grouped into 3,286 operational taxonomic units (OTUs) with USEARCH at 97% sequence similarity while simultaneously excluding 181 chimeric sequences. We assigned sequences to taxonomic groups based on pairwise similarity searches against the curated UNITE+INSD fungal ITS sequence database containing identified fungal sequences with assignments to species hypothesis groups (Kõljalg et al., 2013). After excluding OTUs with <70% similarity or with <150 bp pairwise alignment length to a fungal sequence, the dataset contained 2,898 fungal OTUs, representing a total of 296,384 high-quality sequences. Functional classification of OTUs at the genus level was performed using the FUNGuild database.

Table 1: Selected soil physic chemical properties of study plots in the dry Afromontane forest of the Wondo Genet area (Ethiopia).

	Stand age after burn[a]		
Soil properties	**Unburned**	**One year**	**Ten years**
Clay	1.60 (0.01)	1.72 (0.02)	1.27 (0.03)
Silt	1.30 (0.1)	1.40 (0.10)	1.38 (0.12)
Sand	1.76 (0.08)	1.38 (0.12)	1.79 (0.04)
pH-H_2O (1:2.5)	6.51 (0.30)	6.46 (0.1)	6.81(0.30)
Na (meq 100 g^{-1} of soil)	0.83 (0.07)	1.00 (0.4)	0.99 (0.10)
K (meq 100 g^{-1} of soil)	0.55 (0.12)	0.62 (0.35)	0.80 (0.08)
Ca (meq 100 g^{-1} of soil)	28.43 (13.67)	20.85 (5.18)	24.15 (4.98)
Mg (meq 100 g^{-1} of soil)	9.77 (5.18)	7.42 (1.42)	8.05 (1.50)
CEC (meq 100 $g^{-1}$of soil)	52.44 (14.91)	43.97(10.9)	42.66 (5.10)
OM	6.05 (1.77)	2.93 (0.36)	5.08 (1.88)
Nitrogen (%)	0.67 (0.17)	0.40 (0.06)	0.54 (0.11)
C/N	5.25 (0.20)	4.25(0.03)	5.46 (3.89)
P (mg P_2O_5/kg soil)	43.33 (12.72)	28.89 (4.36)	32.59 (5.18)

[a] Numbers in parentheses are the standard deviation of the mean.

Abbreviations: CEC, cation exchange capacity; OM, organic matter.

2.6. Statistical analysis

We normalized the OTU table for subsequent statistical analyses by rarefying the number of high-quality fungal sequences to the smallest library size (8,361 reads). Shannon's H' diversity index, $H = -\Sigma pi\ (\ln pi)$ (Shannon and Weaver, 1949), was estimated for each stand, where p_i indicates the relative abundance of fungal OTUs (Kent and Coker, 1993). The Simpson's diversity, $D = 1 - \Sigma\ (p_i^2)$, where p_i is the importance probability in element i; and the Evenness, $J = H'/H'\max$, where H' is the number derived from the Shannon diversity index and the H' max is the maximum possible value of H' were also calculated (Magurran, 1988). In addition, the richness values of all fungal OTUs (S) based on stand type were estimated. All diversity measures were calculated using the BiodiversityR GUI package in R version 3.5.3 (R Core Team, 2019). Diversity indices and richness were compared across stands using one-way ANOVA using R (R Core Team, 2019). Data were scaled using R when needed to normalize for ANOVA. Tukey HSD was used to determine significant differences between means ($P \leq 0.05$) among stands.

To compare the entire fungal OTU community composition across the studied stands, we used PC-ORD v. 6.0 (McCune and Grace, 2002) to run detrended correspondence analyses (DCAs) on the presence-absence data matrix. Data were also analysed using PERMANOVA (Adonis) in R to determine the effect of forest types and edaphic variables on the fungal community (Anderson, 2001). We performed an analysis of Similarity Percentages (SIMPER) to identify fungal species that are most responsible for the observed patterns (Clarke, 1993) and to determine the percentage contribution of fungal taxa to significant dissimilarities among the three stands (Parravicini et al., 2010). Canonical correspondence analysis (CCA) was also used to relate the selected edaphic variables (Table 1) with the mycorrhizal fungal community composition using CANOCO version 5.0 (Smilauer and Lepš, 2014). The statistical significance of the environmental variables was tested using a Monte Carlo permutation test (999 permutations).

3. Results

3.1. Sequencing outputs and fungal diversity

A total of 2,898 fungal OTUs of a total of 296,384 sequences were found across all samples before rarefaction. The taxonomic classification revealed that Ascomycota was the most diverse fungal phylum, with 1708 OTUs; 52% of the total (Figure 2A). The ranking of taxonomic orders in Ascomycota, based on the number of representative OTUs, was as follows Chaetothyriales (128), Pleosporales (106) and Hypocreales (77), followed by many other orders with less than 50 fungal OTUs (Figure 3A). In Basidiomycota, Agaricales was the most species-rich order followed by other orders with less than 50 OTUs each. Unidentified fungi were classified down to kingdom level and represented about 645 OTUs; 20% of the total (Figure 2A). The number and proportional distribution of fungal OTUs describing all known taxonomic phyla and orders are shown in Figure 3.

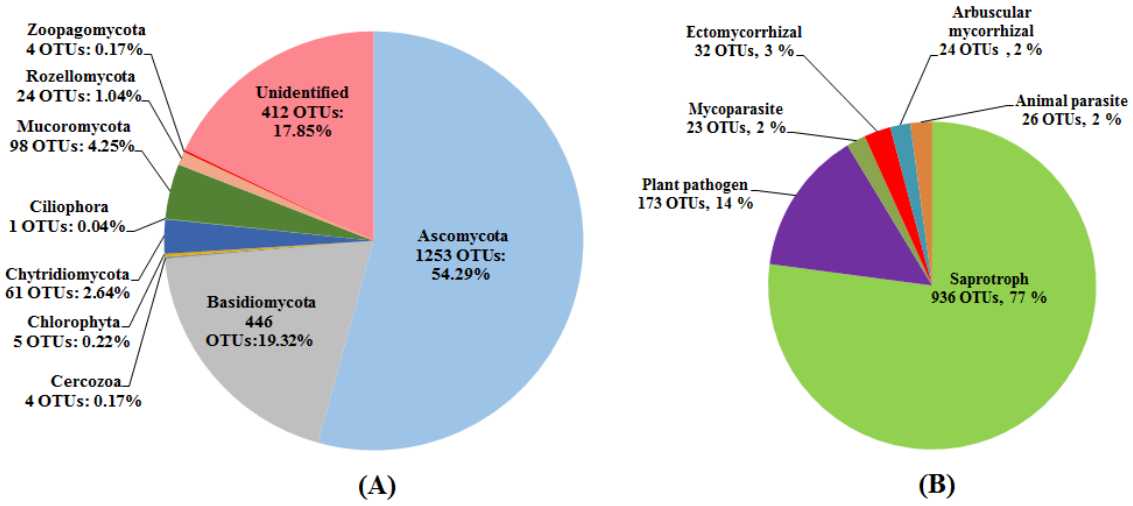


Figure 2: Relative proportions of fungal operational taxonomic units (OTUs): (A) taxonomical classification at the phylum level (name of phylum; the number of OTUs; percentage); (B) classification of fungal ecological function at the genus level (ecological function; the number of OTU; percentage) based on a FUNGuild (www.funguild.org) search.

About 42% (1217 OTUs) of the fungal OTUs were classified to the genus level. These genera were assigned to ecological functional groups, i.e. symbionts (ectomycorrhizal and arbuscular mycorrhizal fungi) and non-mutualistic fungi, including saprotrophs, parasites and pathogens. The proportion of fungal OTUs at the genus level sharing the same ecological function is presented in Figure 2B.

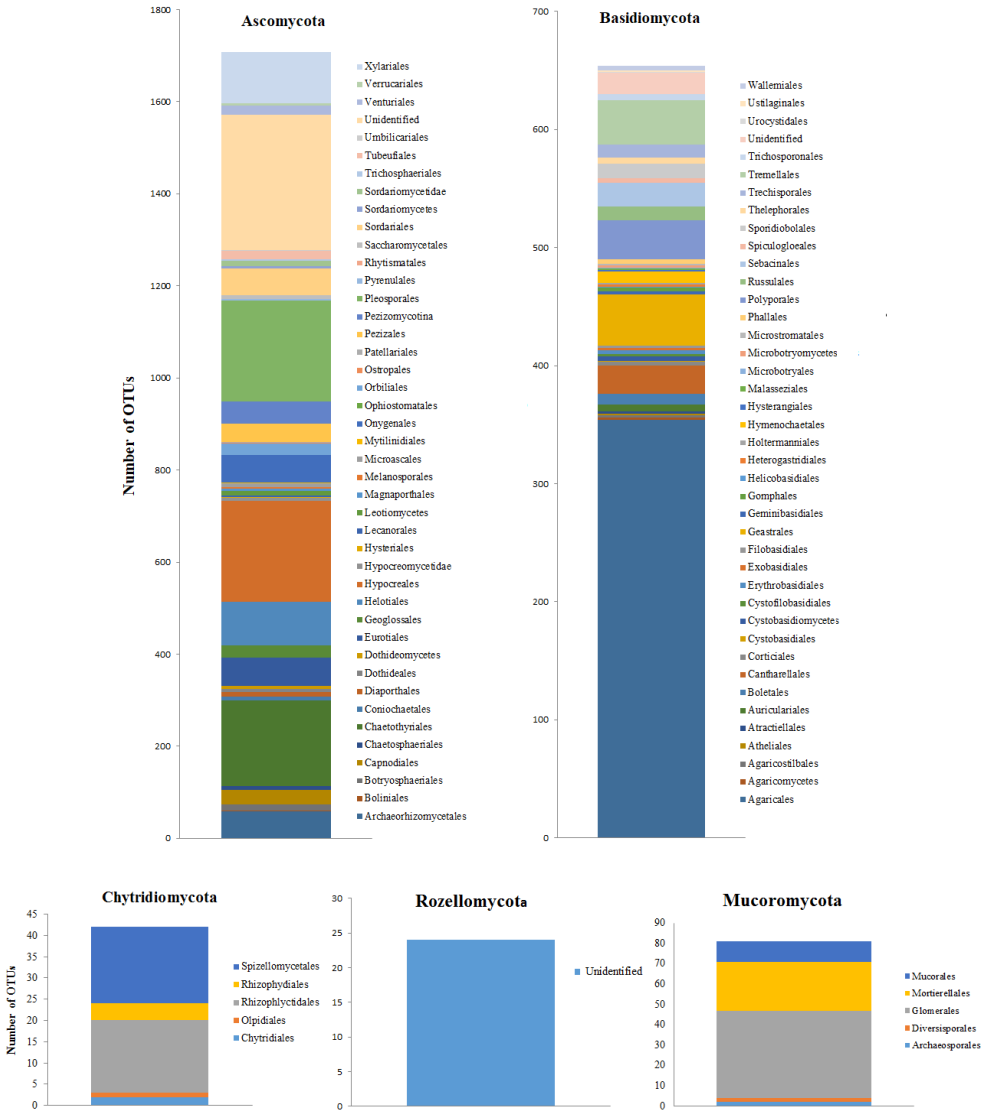


Figure 3: Numbers and proportional distribution of fungal operational taxonomic units (OTUs) representing all taxonomic phyla and orders found in soil samples collected from the dry Afromontane forest of Wondo Genet, Ethiopia.

3.2. Fungal richness and diversity changes after fire

The observed total fungal OTU richness was significantly affected by fire (P = 0.002; F = 12.48; Figure 4) and was higher in one and ten years after fire, compared with the unburned site. The highest richness value was observed in one-year-old burned stands, whereas the lowest was observed in unburned stands, which had an average richness value that was 50% and 18% lower than that of one- and ten-year old burned stands, respectively.

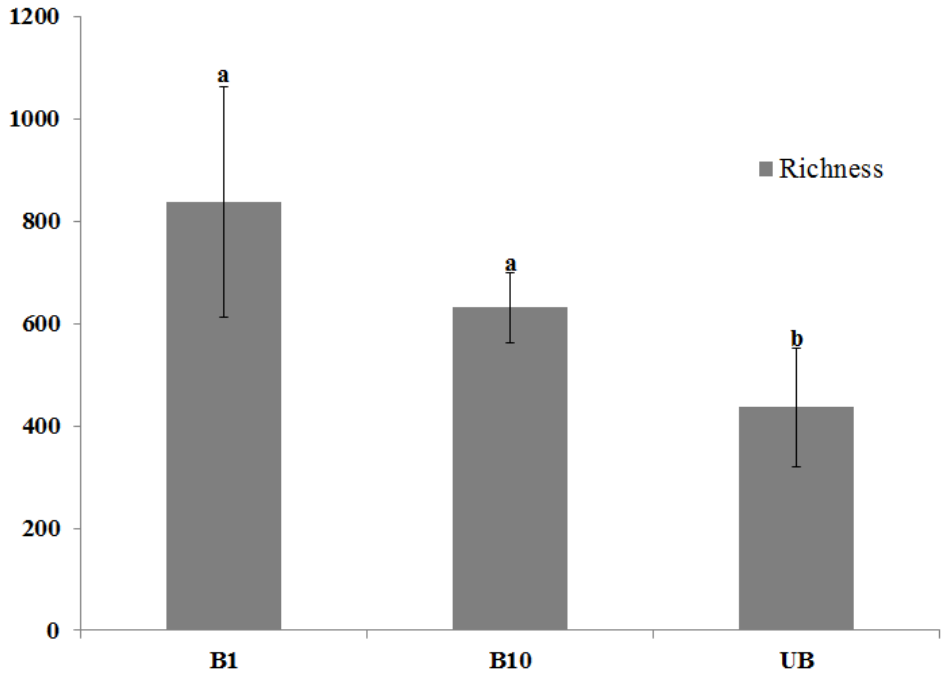


Figure 4: Mean total fungal community richness values in a dry Afromontane forest of Wondo Genet, Ethiopia, following fire. Abbreviations: UB, unburned stand; B1, one-year-old burned stand; B10, ten-year-old burned stand. Bars denote standard deviation. Different letters above the bars indicate a significant difference in richness between stand types (P< 0.01, n = 3 transects per stand).

Diversity indices for each ecological guild did not differ significantly among treatments (P> 0.05; Figure 5). The observed evenness values also did not differ significantly among treatments (F = 0.18, P = 0.72; Figure 5). However, the trend observed for evenness values

indicated that ecological guilds are distributed more uniformly in B10 and UB stands than in B1 stands (Figure 5).

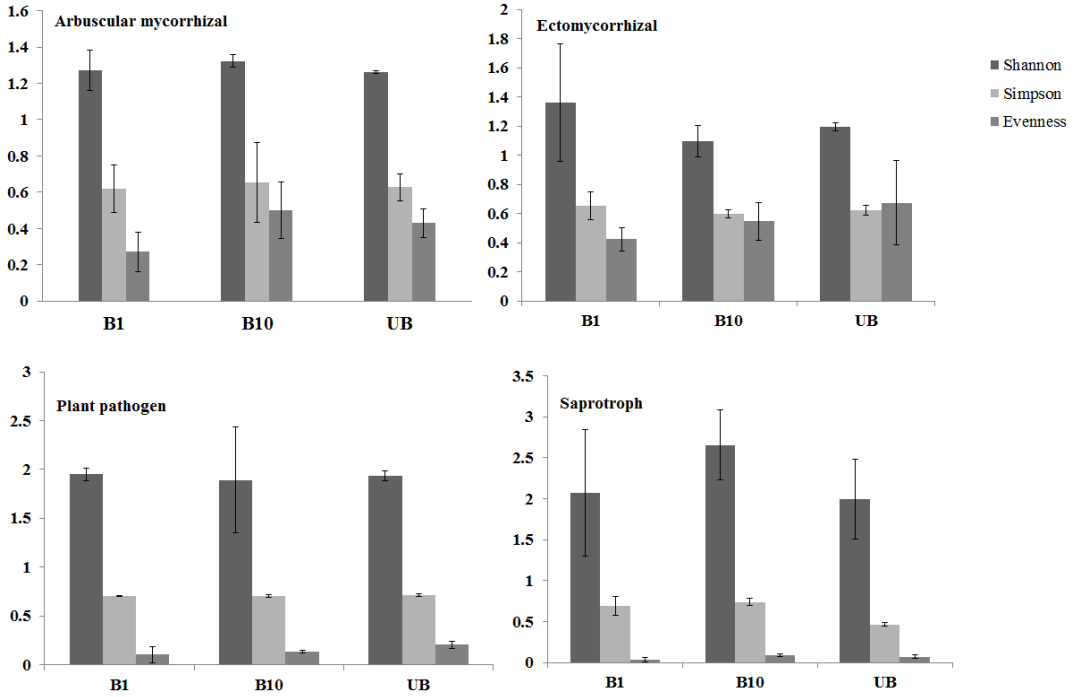
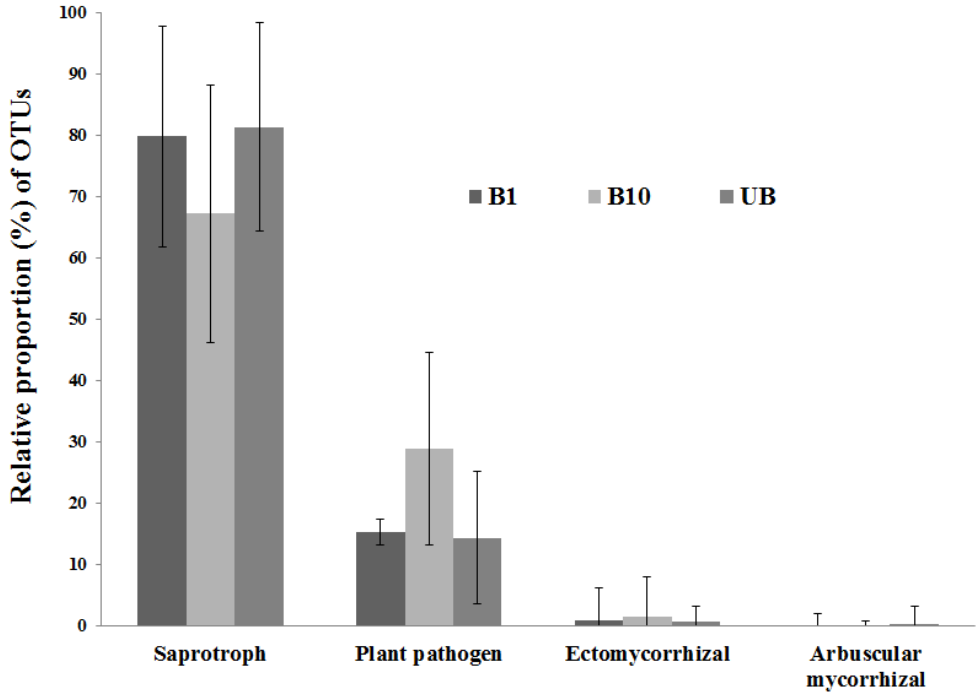


Figure 5: Mean soil fungal community diversity and evenness estimated for functional guilds detected in three types of forest stand with different fire histories. Abbreviations: UB, unburned stand; B1, one-year-old burned stand; B10, ten-year-old burned stand; Key: Shannon = Shannon diversity values; Simpson = Simpson diversity values; Evenness = evenness values. Bars denote standard deviation, n = 3 transects per stand.

When the relative proportions of each of the ecological guilds in each of the different types of forest stand were considered separately, only the proportions of plant pathogens differed significantly in the different types of forest stand. The relative proportion of plant pathogens in B10 soils was significantly greater than in UB or B1 soils ($P = 0.001$; $F = 5.04$; $n = 3$ transects). The relative proportions of the other ecological guilds were not significantly different ($P > 0.05$) in burned and unburned forest stands (Figure 6).



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367 **Figure 6:** Relative proportions of fungal operational taxonomic units (OTUs) in different
368 ecological guilds in unburned stands (UB), one-year-old burned stands (B1) and ten-year-old
369 burned stands (B10). Bars denote standard deviation.

370 **3.3. Soil fungal communities and environmental variables**

371 The DCA showed that the variation in fungal community composition can be partially
372 explained by the successional stage following fire (Figure 7), indicating distinct fungal
373 compositions in each treatment. The PERMANOVA analyses confirmed that the composition of
374 the fungal OTUs in the three stand types were significantly different ($F = 1.54$, $P = 0.02$),
375 indicating that the fungal communities are differently associated with the three forest stands due
376 primarily to soil fertility. With respect to the edaphic variables, Nitrogen (N) ($R^2= 0.5685$), C/N
377 ration ($R^2= 0.6355$), and Phosphorus (P) ($R^2= 0.6387$) correlated most strongly with fungal
378 community composition ($P<0.05$). The SIMPER analysis identified fungal species that typified
379 and distinguished between the three treatments (Table S1). The overall between-group
380 dissimilarity was 79.59% for UB and B1 treatments, 74.47% for UB and B10 treatments and

72.91% for B1 and B10 treatments. *Agaricus campestroides* and *Gymnopilus ochraceus* were the most influential species and, along with other species such as *Hypocreales* sp. and *Onygenales* sp., made the greatest cumulative contribution towards differences between the three stands, often accounting for more than 25% of the observed value of dissimilarity (Table S1). Furthermore, the one-year-old burned treatment (B1) dataset contained a relatively higher number of OTUs as compared to the ten-year old burned (B10) and unburned (UB) treatments.

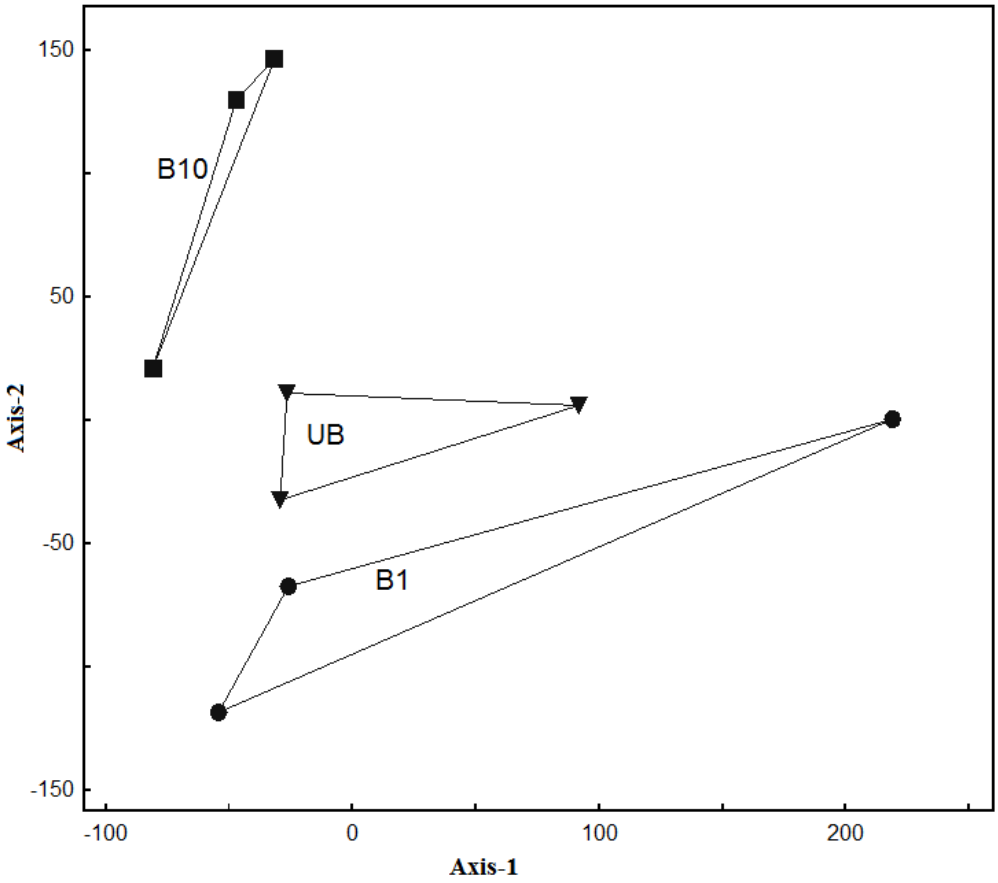


Figure 7: Detrended Correspondence Analysis ordination plot for soil fungal communities detected in the three treatment groups: B1, plots in one-year-old burned stands; B10, ten-year-old burned stands; UB, unburned stands. Plots with the same symbol are in the same treatment group.

CCA of ectomycorrhizal fungal OTUs based on simple term effects revealed that edaphic variables such as the Mg, K and OM were significantly correlated with ectomycorrhizal fungal

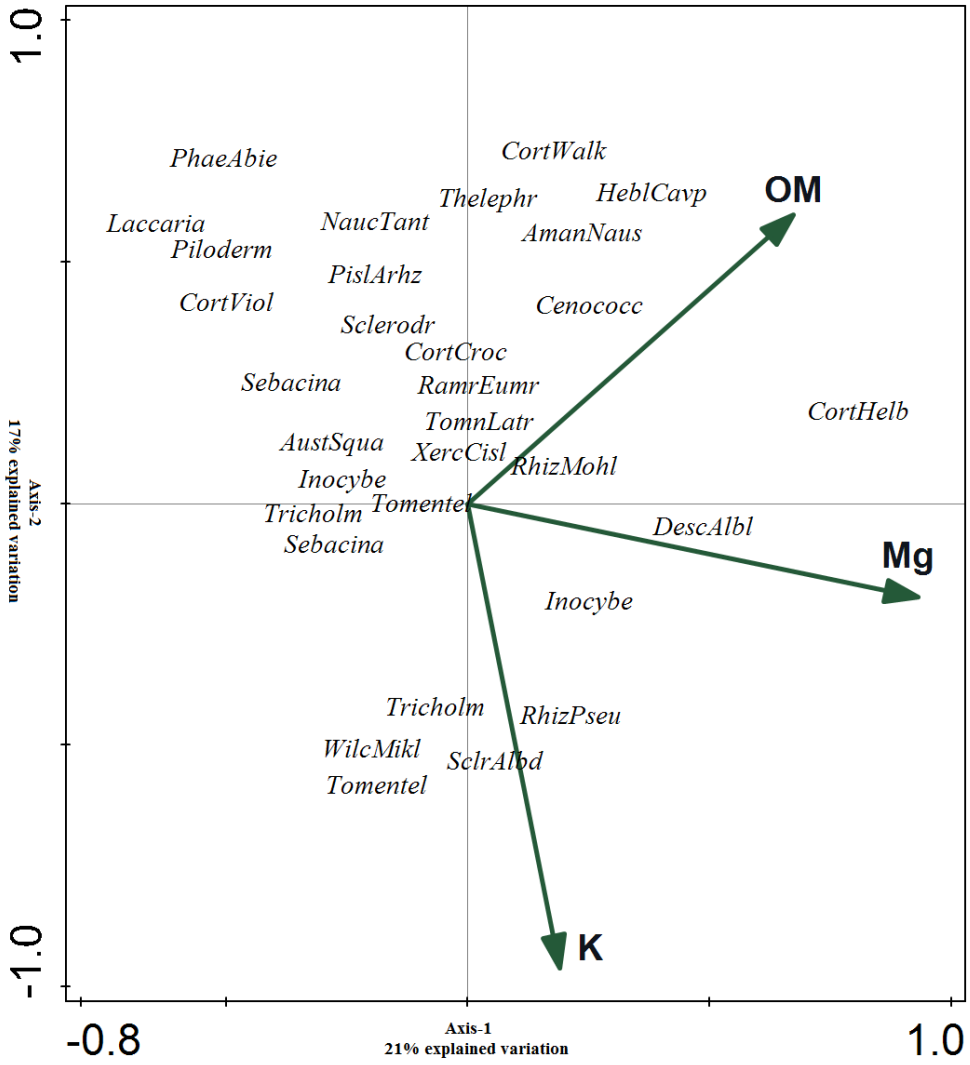
394 community composition in our forest study area (Table 2; Figure 8). The cumulative contribution
395 of the explained variation data for the interaction between ectomycorrhizal soil fungal
396 composition and soil variables are shown in Figure 8.

397 The response of the ectomycorrhizal species was unique to the different types of stands. In
398 contrast to our expectation, number ectomycorrhizal taxa were associated with recently burned
399 stands, which had lower soil fertility levels compared with unburned and 10-year-old burned
400 stands (Table 1). Species such as *Tricholoma* sp. and *Inocybe* sp. were among the observed taxa
401 associated to these 1-year-old burned stands. In older stands i.e. the 10-year-old burned and
402 unburned stands, where the soil fertility was high, species such as *Amanita* sp. and *Laccaria* sp.
403 were found together with other species. Other species such as *Entoloma* sp. and *Cortinarius* sp.
404 were associated with all stand age groups in the forest study area.

405 **Table 2:** Canonical correspondence analysis showing the significance ($P < 0.05$) of edaphic
406 variables based on simple term effects on the mycorrhizal fungal species.

Variable	Simple term effects		
	Explains %	pseudo-F	P
Mg	22.6	1.71	0.032
K	19.7	1.63	0.036
OM	17.0	1.40	0.047

407



408

409 **Figure 8:** Canonical Correspondence Analysis (CCA) of the species level community
410 composition of ectomycorrhizal fungi in a dry Afromontane forest in Ethiopia. Abbreviations:
411 OM, organic matter; Mg, magnesium; K, potassium. Species names are abbreviated (the full
412 names of the ectomycorrhizal species used in the ordination are provided in supplementary Table
413 S2).

414

415

4. Discussion

4.1. Fungal OTU diversity

Afromontane forests in Ethiopia are considered to be a major reservoir of biodiversity (Lemenih and Bekele, 2008), and may support a high level of microorganism diversity, including fungi. Our study revealed that the dry Afromontane forest in our study area harbours many more fungal species than previously reported in studies based on sporocarps sampling at a given period of time (Dejene et al., 2017b). However, the taxonomic classification was challenging owing to the lack of matches in the database. Thus, only about 48% and 24.13% of the OTUs detected could be identified to the genus and species level, respectively, indicating that the majority of fungal in this region had not been sequenced before this study and that many possibly are undescribed species. This may also be due to the uniqueness of the dry Afromontane forests in terms of the diversity of soil fungi as well as the lack of scientific studies that have investigated the local mycota (Dejene et al., 2017a). Furthermore, about 20% of sequences were not identified even at the phylum level, highlighting the current lack of data from understudied tropical and subtropical forest ecosystems (Tedersoo et al., 2014), such as the forest systems in Ethiopia. In light of this, the present study provides important information that contributes to the Ethiopian fungal biodiversity knowledge base.

The largest group of fungi found in this study belonged to the Ascomycota; previous studies of different forest ecosystems have also reported a dominance of Ascomycota taxa in the soil (Dhruba et al., 2015; Geml et al., 2014; Reazin et al., 2016; Smith et al., 2017). The Ascomycota is the most species-rich phylum of fungi (Araujo and Hughes, 2016), which may explain its dominance. The Hypocreales, Pleosporales, and Chaetothyriales were the three largest orders of Ascomycota found in this study. The order Hypocreales is a group whose taxonomy has been relatively well studied and identification aids are widely available (Chaverri and Samuels, 2003; Schroers, 2001). The fungi in this order can also be saprotrophic, entomopathogenic, and mycoparasitic (Rossman et al., 1999). In addition to their ecological and economic importance, the Hypocreales are also considered to be the most important regulators of insect and fungal populations and, therefore, are used in agriculture as biocontrol agents (Carruthers and Hural, 1990; Esser and El-Gholl, 1993; Rossman et al., 1999; Samuels, 1996). The second largest order of Ascomycota detected in this study was the Pleosporales. This order

446 comprises saprotrophs or fungi that are parasites of vascular plants (Kruys et al., 2006). Some
447 species from this order are also found on animal dung (Kruys et al., 2006), a small number occur
448 as lichens (Semenova-Nelsen et al., 2019) and as rock-inhabiting fungi (Ruibal et al., 2009). The
449 epiphytic or endophytic fungi of the Pleosporales are mainly saprotrophic but also play a key
450 role in causing plant diseases such as stem canker (Zhang et al., 2009). A considerable number of
451 fungi belonging to the order Chaetothyriales were also detected in this study. This order includes
452 fungi that are known to be epiphytes, colonizing the leaves and the bark of trees in tropical forest
453 ecosystems (Arnold et al., 2000; Batista and Ciferri, 1962).

454 The order Agaricales was the largest order of Basidiomycota detected in this study:
455 members of this order produce the familiar gilled mushroom (Binder et al., 2005; Hibbett and
456 Thorn, 2001; Stajich, 2015). Agaricales are widespread in diverse ecosystems (Kirk et al., 2008)
457 and many form ectomycorrhizae by engaging in mutualistic symbioses with vascular plants
458 (Alexopoulos et al., 1996). Some Agaricales are known to be termite symbionts, some are
459 valuable as a source of food for animals, including humans (Kirk et al., 2008), whereas others
460 have hallucinogenic properties or produce toxins lethal to humans (Nichols, 2003). Most of the
461 species of Agaricales detected in this study are well known soil saprotrophs, such as those
462 belonging to the genera *Agaricus*, *Calvatia*, *Coprinellus*, *Gymnopilus*, *Leucoagaricus*,
463 *Lycoperdon*, *Marasmius*, *Psathyrella* and *Psilocybe*, have been reported previously as fruit
464 bodies from our study area (Dejene et al., 2017b) providing validation of our molecular
465 techniques.

466 **4.2. Fungal richness and diversity changes after fire**

467 Our results from the post-fire successional chronosequence showed that soil fungal richness
468 was related to fire. In this study, we found higher total richness and diversity values in the forest
469 stands recently affected by fire than unburned stands. This may be attributed to the new
470 ecological conditions created owing to differences in fire severity, which may incite or support
471 spore germination of several fungal species in the soil (Heino, 2012) following the fire in the
472 investigated forests. In addition, the mycelium of fungal species in the rhizosphere may persist
473 (Cowan et al., 2016; Shen et al., 2016) or the fungal community may be resilient to the effects of
474 fire to some extent (Cowan et al., 2016; Jennings et al., 2012). Furthermore, the intensity of the

fire might not have been high enough to affect the below-ground fungal communities given that low-intensity fires may have little effect on below-ground fungal communities (Bárcenas-Moreno et al., 2009; Egidi et al., 2016). Thus, the responses of soil fungi to reoccurring low-intensity fire also appear to be minimal (Johnson et al., 2013; Oliver et al., 2015) and ephemeral (Hart et al., 2005). Contrary to our expectations, we found that the amount of time since the fire did not seem to affect fungal guild diversity. These results agree with the findings of a meta-analysis of fire effects on soil fungi (Egidi et al., 2016), which highlighted the absence of a significant change in fungal diversity following fire. This might be because little heat is transferred to the soil because fuel loads are low (Lunt and Morgan, 2002) or might indicate that the fungal guild communities in burned and unburned forest stands shared similar gene profiles, which may promote functional similarities among fungal communities with differing compositions (Mundra, 2015). On the other hand, the absence of significant difference in fungal richness and diversity in fire affected areas might be due to the fact that recurrent fires consume less fuel and produce less heat, which does not penetrate into soil as deeply as during high-intensity fires (Reazin et al., 2016; Semenova-Nelsen et al., 2019). Accordingly, fungal community shifts in such recurrent fire ecosystems, like that of the dry Afromontane forest, may be relatively modest (Choromanska and DeLuca, 2001; Korb et al., 2004) and the change may be driven by indirect fire-induced changes in soil properties or by the change in the plant communities (Hart et al., 2005; Oliver et al., 2015; Ponder et al., 2009; Trappe et al., 2009). Also, fungi in a recurrent forest ecosystem may be adapted to frequent fires. Some fungi produce heat- and smoke-activated spores (Semenova-Nelsen et al., 2019) and some may benefit from post fire ash deposits (Dean et al., 2015; Hart et al., 2005) or reduced competition from other species (Semenova-Nelsen et al., 2019). However, factors other than fire might have a greater effect on the richness and diversity of soil fungal communities. Therefore, further research is needed to better understand the dynamics and characteristics of soil fungal communities.

A previous study reported the absence of ectomycorrhizal fungi in the dry Afromontane forests of Ethiopia (Dejene et al., 2017a). This finding was not exceptional as the majority of tropical woody tree species are unable to form associations with ectomycorrhizal fungi (Brundrett, 2009). However, in this study, we observed different groups of mycorrhizal fungi and

505 they were identified and classified as ectomycorrhizal and arbuscular mycorrhizal (Figure 2).
506 This association may be due to the diverse vegetation (Friis et al., 2010) and, hence, there may
507 be more trees present that can act as hosts for mycorrhizal fungi, or may be due to the dispersion
508 of mycorrhizal inocula from nearby plantation forests, which are dominated by *Eucalyptus* and
509 *Pinus* species (Castaño et al., 2019; Dejene et al., 2017a; Urcelay et al., 2017). Thus, the findings
510 presented here may have important implifications for the indigenous forest system for the
511 maintenance of functional guild diversity in Ethiopia given that mycorrhizal fungi have
512 previously only been reported from exotic tree plantations (Dejene et al., 2017a). However, the
513 importance of ectomycorrhizae and arbuscular mycorrhizae in indigenous forest systems in
514 Ethiopia needs empirical data to confirm. In addition, the coexistence of these fungi has many
515 practical advantages, such as the exchange of water and nutrients through mycorrhizal hyphal
516 networks (Brundrett, 2002, 2004). Thus, our analysis of the fungal communities in these forest
517 soils presents an insight into the conservation of functional guilds in the forest system in the
518 study area.

519 The vegetation changes after a fire may affect the soil microbial community (Hart et al.,
520 2005). Previous studies have reported that the loss of host plants after fire decreases mycorrhizal
521 fungal diversity (Pattinson et al., 2006; Smith et al., 2005). In our study, both the richness and
522 diversity of ectomycorrhizal fungi increased in the recently burned stands, which could indicated
523 an immediate post-fire mycorrhizal colonization in fire-affected forest stands (Dahlberg, 2002;
524 Rincón et al., 2015), while the saprotrophic fungi mineralize nutrients and stabilize the soil
525 moisture after the fire (Dighton et al., 1986). The ectomycorrhizal taxa may also have established
526 dominance immediately after burning owing to their tolerance of fire effects (Dahlberg, 2002;
527 Kipfer et al., 2010) or they may have survived in a mycelial state during the fire event (Hewitt et
528 al., 2013). However, the colonization of mycorrhizal fungi could also be governed by burn
529 severity and by the depth of burning in the soil profile (Hewitt et al., 2013). Thus, the effect of
530 fire on mycorrhizae could be reduced when the fire only occurs at the soil surface, and the effect
531 of the fire reduces with soil depth (Danielson, 1984; Pattinson et al., 2006; Visser, 1995). Thus,
532 the fire that occurred in our forest study area might not have been strong enough to affect the
533 mycorrhizal fungi or may have only affected fungi on the soil surface. It may also be influenced
534 by the host plant's response to fire. However, in Ethiopia the mycorrhizal-associations for most

plants are not yet well known. Thus, this should be investigated in future studies, including ectomycorrhizal root-tip samples, to learn more about the diversity of ectomycorrhizal host tree species and their associated fungi in dry Afromontane forests.

4.3. Soil fungal communities and environmental variables

The DCA indicated that the fungal communities detected in the three stand types were different. The SIMPER analysis also distinguished the total dissimilarity between stands and the relative contribution of each fungal species to the observed dissimilarity. The species making the highest contributions to the dissimilarity between the one- and ten-year-old burned stands (10.95%) and the one-year-old burned stands and the unburned stands (10.92%) was *Agaricus campestroides*. This species was highly abundant (N ~14916) in one-year-old burned stands but much less abundant in ten-year-old burned and unburned stands (N= 2 and N= 386, respectively). The contribution of the species might be partially responsible for the differences between stands, suggesting that time after fire is also probably responsible for the variation in the dominance of some species and their exclusive occurrence in certain stands. This is supported by previous findings that, for a given stand, certain fungal species tend to be abundant and characterize its composition (Zhu et al., 2010). Thus, a species with a consistently high contribution to the dissimilarity is a good discriminating species (Clarke, 1993).

Soil microorganisms, including fungi, are influenced by edaphic parameters (Drenovsky et al., 2004; Lauber et al., 2009, 2008). Our edaphic data from the dry Afromontane forest showed that more fungal species were detected in the burned forest areas (B1 and B10) where the soil fertility was relatively low than in unburned areas, which could be related to depositions of ash after the fire (Hul et al., 2015). Ash depositions could create empty niches that provide opportunities for the area to be rapidly colonized by fungal species at the early stages of succession (Fritze et al., 1993). However, the dry Afromontane forest area has suffered erosion caused by heavy rainfall soon after the fire events. As a result, there is a potential for sediment transportation from fire-affected areas and, thus, changes in soil fertility levels among stands. For instance, pH was assumed to be increased in newly burned areas, owing to the production of oxides and hydroxides (Hul et al., 2015). However, in our study forests, we recorded slightly high soil pH values in unburned forest stands. We found also a significant influence of the N,

C/N ration and P on the entire fungal community in this study. For example, N and P reported could affect the structure of fungi in the soil, particularly of the mycorrhizal fungi (Zhao et al., 2018). The higher availability of these elements could decrease plant dependency on mycorrhizal fungi. This condition could also reduce the carbon allocation to fungi (Liu et al., 2019), which could increase competition and affect community composition (Wang and Wang, 2008; Zhao et al., 2018). Our result also confirmed that the fungal richness is low in stands where the soil C/N ratio is higher.

Previous studies have reported that after fire, the abundance of ectomycorrhizal fungi is reduced owing to the loss of host plants (Hart et al., 2005). However, in our study, the total fungal OTU richness in fire-affected stands, which had poor soil fertility, was high compared with that of unburned stands (Fig. 4), although such conditions remain to be interpreted. However, Castaño et al. (2019), reported high levels of ectomycorrhizal fungi in stands with poor soil quality. The occurrence of mycorrhizal species in poor quality soils suggests that the nutrient stress created in the fire-affected area could be compensated for by the increased dependency of trees on fungal symbionts (Read and Perez-Moreno, 2003). In this regard, the mycorrhizal ruderal guild in the spore bank would play an important role by quickly colonizing roots of plants, and will likely aid the survival of trees after the fire (Glassman et al., 2016). Species of *Wilcoxina*, *Tomentella*, *Tricholoma* and *Laccaria* were among the ectomycorrhizal species represented in the fire-affected stands, where soil fertility was low. Some of these genera such as *Laccaria* are considered ruderal species (Ishida et al., 2007) and are known to form an ectomycorrhizal association with several host tree species (Glassman et al., 2016; Hul et al., 2015).

4.4. Conclusions

This pioneer study is the first attempt to describe the soil fungal community in a dry Afromontane forest system of Ethiopia using next-generation sequencing and to investigate the effect of fire disturbance on these fungal communities. Data obtained in this study will significantly contribute to the body of knowledge regarding soil fungal communities in Ethiopia; however, the taxonomy of these fungi remains challenging and about 20% of the fungal species detected have not been described even at the phylum level. We conclude that, in general, the

fungal diversity in Ethiopian forest systems is as yet largely undescribed and likely includes many taxa unknown to science. Thus, we advise that additional scientific investigations of this highly diverse but unexplored forest ecosystem are needed to consolidate the Ethiopian fungal biodiversity database. Also in this study, the soil fungal communities expected to be changed substantially along a post-fire forest succession and in comparison to those in unburned forest. However, we found that fire did not have a significant negative effect on fungal richness and diversity in the burned stands. Our study also highlighted that soil fungal composition differed across a chronosequence after fire and was correlated with soil fertility conditions and the changes would be explained partially by the edaphic conditions. Contrary to our expectation, root-associated symbiotic fungi like that of the mycorrhizal fungi were not lacking in fire-affected stands. We assume that mycorrhizal fungi present in the spore bank were able to colonize the roots of plants that survived the fire. In the fire-affected forests, we also found fungi that are known to form ectomycorrhizal associations with several host tree species. This key ecological role could provide support for the importance of fungal conservation in the dry Afromontane forest systems in Ethiopia. Similarly, vital edaphic variables such as OM and K also appear to be important in shaping the composition of mycorrhizal soil fungi in different ways. Thus, the effect of forest management practices such as thinning and harvesting on soil fertility should be taken into consideration owing to the important relationship between these ecological parameters and the soil fungal composition in the dry Afromontane forests of Ethiopia.

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Supplementary material -1

Table S1: Summary of similarity percentage (SIMPER) results showing contrasts between the cumulative total contribution (50% cut-off) and the contribution (%) of the most influential fungal operational taxonomic units (OTUs) to the dissimilarity between the three types of stand in the study area, Wondo Genet, Ethiopia.

Species	Individual contribution to the dissimilarity	Cumulative contribution to the dissimilarity
One- and 10-year-old burned stands		
Agaricus campestroides	10.95	10.95
Gymnopilus ochraceus	6.69	17.65
Hypocreales sp.	4.57	22.22
Onygenales sp.	3.02	28.71
Mortierella sp.	2.67	31.38
Mortierella sp.	2.11	33.49
Postia sp.	1.82	35.31
Penicillium pimiteouiense	1.36	36.68
Alternaria sp.	1.34	38.02
Geastrum sp.	1.24	39.26
Onygenaceae sp.	1.04	40.3
Fusarium sp.	0.87	44.02
Dactylonectria macrodidyma	0.85	44.87
Metarhizium marquandii	0.70	46.31
Helotiales sp.	0.68	46.99
Capnodiales sp.	0.68	47.68
Cylindrocarpon sp.	0.68	48.36
Lecanicillium fungicola	0.67	49.04
Chaetothyriales sp.	0.63	49.68
One-year-old burned stands and unburned stands		
Agaricus campestroides	10.92	10.92
Gymnopilus ochraceus	9.52	20.45
Hypocreales sp.	4.83	25.29
Onygenales sp.	3.03	28.31
Mortierella sp.	2.84	34.17
Mortierella sp.	2.04	36.21
Alternaria sp.	1.87	38.08

Species	Individual contribution to the dissimilarity	Cumulative contribution to the dissimilarity
Penicillium pimiteouiense	1.57	39.65
Postia sp.	1.48	41.13
Geastrum sp.	1.25	43.70
Vanrija humicola	1.19	44.89
Dactylonectria macrodidyma	1.05	47.01
Fusarium sp.	0.97	49.01
Ascomycota sp.	0.77	50.58
10-year-old burned stands and unburned stands		
Gymnopilus ochraceus	13.23	13.23
Dothideomycetes sp.	2.73	15.97
Vanrija humicola	2.43	18.4
Postia sp.	2.19	23.00
Alternaria sp.	1.98	24.98
Hypocreales sp.	1.82	26.80
Onygenaceae sp.	1.50	28.30
Psathyrellaceae sp.	1.29	29.59
Agaricales sp.	1.19	30.79
Onygenales sp.	1.15	33.11
Dactylonectria macrodidyma	1.13	34.25
Pseudaleuria sp.	1.12	35.38
Chaetothyriales sp.	1.09	36.48
Fusarium buharicum	1.09	37.57
Coprinopsis igarashii	0.91	39.44
Archaeorhizomyces sp.	0.84	40.29
Dothideomycetes sp.	0.80	41.09
Penicillium pimiteouiense	0.75	41.84
Mortierella sp.	0.69	42.53
Agaricus campestroides	0.60	43.14
Xylariales sp.	0.59	43.73
Geoglossum difforme	0.56	44.29
Fusarium sp.	0.56	44.86
Onygenales sp.	0.55	45.41
Fusarium brasiliense	0.53	46.48
Onygenales sp.	0.51	47.00
Herpotrichiellaceae sp.	0.51	47.51
Eurotiales sp.	0.48	47.99
Onygenaceae sp.	0.46	48.45
Dothideomycetes sp.	0.46	48.91
Chaetomium homopilatum	0.45	49.36
Pyronemataceae sp.	0.44	49.81
Eurotiales sp.	0.44	50.25

Supplementary material -2

Table S2: List of the most abundant mycorrhizal species used in the canonical correspondence analysis. Abbreviations: UB, unburned stands; Y1B, one-year-old burned stands; Y10B, ten-year-old burned stands; OTUs, operational taxonomic units.

OTUs	Mycorrhizal species	Species abbreviation	UB-1	UB-2	UB-3	Y1B-1	Y1B-2	Y1B-3	Y10B-1	Y10B-2	Y10B-3
OTU_3067	*Cenococcum*	*Cenococc*	6	0	0	0	2	0	0	0	0
OTU_70	*Wilcoxina mikolae*	*WilcMikl*	0	15	0	0	196	0	0	0	0
OTU_103	*Tomentella*	*Tomentel*	0	0	0	0	2	0	0	0	0
OTU_124	*Rhizopogon pseudoroseolus*	*RhizPseu*	0	0	2	0	13	0	0	0	0
OTU_1307	*Scleroderma*	*Sclerodr*	0	0	0	2	0	0	0	0	0
OTU_1596	*Rhizopogon mohelnensis*	*RhizMohl*	3	0	0	0	3	0	0	0	0
OTU_1690	*Phaeoclavulina abietina*	*PhaeAbie*	0	0	0	0	0	13	0	0	0
OTU_2511	*Laccaria*	*Laccaria*	0	0	0	0	0	0	0	0	0
OTU_2558	*Sebacina*	*Sebacina*	0	0	0	0	0	3	0	0	8
OTU_2591	*Austropaxillus squarrosus*	*AustSqua*	0	0	0	2	0	0	0	0	2
OTU_2678	*Cortinarius walkeri*	*CortWalk*	2	0	0	0	0	0	0	0	0
OTU_2680	*Cortinarius croceocoeruleus*	*CortCroc*	0	0	0	2	0	0	0	0	0
OTU_2967	*Tricholoma*	*Tricoholm*	0	0	0	0	0	0	0	0	4
OTU_2985	*Naucoria tantilla*	*NaucTant*	0	7	0	0	0	0	0	0	0
OTU_313	*Tomentella lateritia*	*TomnLatr*	11	8	0	40	11	4	10	3	186
OTU_3443	*Tomentella*	*Tomentel*	0	0	0	4	2	0	2	0	13
OTU_3455	*Sebacina*	*Sebacina*	0	0	0	0	0	0	0	0	3
OTU_3502	*Xerocomellus cisalpinus*	*XercCisl*	0	0	0	0	0	0	0	0	3
OTU_3945	*Piloderma*	*Piloderm*	0	0	0	0	0	3	0	0	0
OTU_4	*Scleroderma albidum*	*SclrAlbd*	0	0	0	0	5	0	0	0	0
OTU_40	*Descomyces albellus*	*DescAlbl*	0	0	0	0	0	0	0	2	0
OTU_4244	*Pisolithus arhizus*	*PislArhz*	0	2	0	0	0	0	0	0	0
OTU_4697	*Inocybe*	*Inocybe*	0	0	0	0	0	0	0	0	2
OTU_5053	*Laccaria*	*Laccaria*	0	0	0	0	0	2	0	0	0

OTUs	Mycorrhizal species	Species abbreviation	UB-1	UB-2	UB-3	Y1B-1	Y1B-2	Y1B-3	Y10B-1	Y10B-2	Y10B-3
OTU_5162	*Amanita nauseosa*	*AmanNaus*	2	0	0	0	0	0	0	0	0
OTU_5181	*Hebeloma cavipes*	*HebelCav*	2	0	0	0	0	0	0	0	0
OTU_5185	*Thelephora*	*Thelephr*	2	0	0	0	0	0	0	0	0
OTU_566	*Cortinarius helobius*	*CortHelb*	0	0	77	0	2	0	11	0	0
OTU_646	*Cortinarius violaceipes*	*CortViol*	0	0	0	19	3	44	0	0	7
OTU_654	*Ramaria eumorpha*	*RamrEumr*	0	0	0	35	3	0	2	0	0
OTU_842	*Inocybe*	*Inocyne*	0	0	0	9	23	0	0	35	0
OTU_936	*Tricholoma*	*Tricholm*	0	0	0	0	30	0	0	0	0