ЗАХИСТ ЛІСУ

UDK 630.182.49:630.43

https://doi.org/10.33220/1026-3365.137.2020.110

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EARLY EFFECTS OF A FOREST FIRE ON THE DIVERSITY OF FUNGAL COMMUNITIES IN PINE FORESTS IN LEFT-BANK UKRAINE WITH SPECIAL EMPHASIS ON MYCORRHIZAL FUNGI

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Forest fires constitute widespread and potentially destructive disturbances in forest ecosystems, particularly negative impact on soil mycorrhizal fungi which are major players of the belowground plant. This study investigated the short-term effects of wildfire on fungal communities in Left-Bank Ukraine with special emphasis on mycorrhizal fungi. During the fourteen months after autumn wildfire, fruiting bodies found in the plots were identified, and their mycological richness, diversity and production in both burned and unburnt areas were measured. Total fungal diversity decreased in burned plots, where fungal richness and diversity of mycorrhizal species were significantly lower. Our results also confirmed the data on a rather destructive influence of post-fire forest management on fungal diversity. Only three mycorrhizal fungi associated with *Pinus sylvestris* L. were common to both sites while pyrophilic species were in close association with burned sites.
K e y w o r d s : mycorrhiza, pine plantation, post-fire erosion, wildfire.

Introduction. Due to a high significance of *Pinus sylvestris* L. for the environment and Ukrainian forest economy, pine stands are among the most important in Ukrainian forests, and occupy vast areas of poor sandy soil and degraded habitats. Since this species is tolerant of poor soil, drought, wind and frost, a pine breeding programme was initiated in the middle 1950s (Los et al. 2015) where plus pine trees were carefully selected taking into account their growth rate and form traits. Given that plus trees are proven to have a higher capacity of resistance to many forest diseases and unfavourable conditions, they should be considered for reforestation purposes. However, primarily because of its high fuel content, pine stands are highly flammable and prone to wildfires, although this species is considered one of the most resistant to low and moderate severity burns (Fernandes et al. 2014). Nevertheless, forest fires are common in Ukraine, and a lack of rainfall and increasing drought in Left-Bank Ukraine (Lyalko et al. 2014) have also increased the frequency and severity of wildfires, which may potentially increase soil degradation (Moody et al. 2013, Fernandes et al. 2014) and contaminate streams with toxic compounds in ashes (Bodí et al. 2014). The post-fire erosion could still have an important impact on soil degradation due to the loss of organic matter and soil microorganisms (Vieira et al. 2015), although it has also been difficult to quantify how forest soil is affected by spatial fire patterns and vegetation recovery (Moody et al. 2013). The extent of these consequences is defined by the fire severity, climate, surrounding vegetation, topography, and soil moisture content (Sousa 2011). Post-fire forest lands are often managed in many countries using different reforestation projects. The common practice of post-fire management includes salvage logging and reforestation. These methods often strengthen the forest disturbance and can potentially result in long-term effects on the woodland fungal community (Wang et al. 2006, Kutorga et al. 2012). Pre-fire fungal communities including mycorrhizal fungi are largely eradicated after a wildfire and a post-fire succession of fungi is initiated. Parasitic, saprophytic and mycorrhizal fungi play a fundamental role in ecosystem functioning and are in occasions a high value forest resource (Martín-Pinto et al. 2006). Forest fires constitute potentially destructive disturbances in forest ecosystems, particularly negative impact on soil mycorrhizal fungi which are major players of the root system. Mycorrhizal species are significant component of the soil community, providing plant with enhanced water and nutrients, extending root volume (Martín-Pinto et al. 2006) and protecting against pathogens. However, there is generally a lack of information about mycorrhizal fungi associated with pine trees in Ukraine in pre-fire and post-fire stands as previous studies were mainly conducted in other regions of Europe (Sousa et al. 2011, Kutorga et al. 2012, Hagenbo et al. 2019). As post-fire reforestation projects are increasingly

observed, the investigation of seedling mycorrhization impact on growth and survival of host plants is of particular interest. Such investigations in Ukraine are still fragmentary (Danilenko 2013; Ugarov et al. 2013), although this information can be of particular practical importance for forest health. Reforestation projects after wildfires require healthy and high-quality seedlings with the containerized root system (Recommendations 2010, Recommendations 2019). Moreover, physiological condition of seedlings, their demand for water and nutrients could be carefully monitored. Also, controlled mycorrhization and biological and chemical protective treatments are applied, and pests and pathogens are actively eliminated (Recommendations 2014).

Seedlings of *P. sylvestris* form belowground mutualistic symbiosis called ectomycorrhiza which commonly have significant effects on nutrient uptake, growth and plant survival and are, therefore, important components (Sousa et al. 2011, Hagenbo et al. 2019). Ectomycorrhizal (ECM) fungi are integral part of a tree's life history and operate as the tree's primary nutrient-absorbing organ (Teste & Simard 2008). Ectomycorrhizal fungi can determine the structure and dynamics of plant communities and are major component of belowground plant interactions (Sousa et al. 2011). There is a wealth of scientific information confirming fire-impacted fungal communities strongly focused on the natural regeneration of the ecosystem (Sousa et al. 2011) although reforestation processes in drought steppe are often required to mitigate consequences of severe burns. Therefore, many studies show that seedlings inoculated with ECM fungi could strongly enhance plant development in the field (Martín-Pinto et al. 2006). Moreover, numerous studies confirm that ectomycorrhizal mycelial networks can enhance aeration and water infiltration into deeper soil layers for post-fire site (Sousa et al. 2011, Kutorga et al. 2012, Hagenbo et al. 2019).

The destructive wildfire which occurred in planted pine stands in Krasnograd State Forest Enterprise in Kharkiv Region resulted in the death of all trees as well as a significant burn of the litter cover in an area of ca. 70 ha. Therefore, *the aim of the study* was to assess diversity and functional community structure of fungi during early stage of succession in differently managed post-fire areas with special emphasis on changes in species richness and a composition of soil-associated fungi in burnt pine stands.

Material and Methods. The study was carried out in two forest ecosystems dominated by *P. sylvestris* in Kharkiv Region of Ukraine (compartments 126–127, Natalinske forestry, Krasnograd State Forest Enterprise). This region has a temperate-continental climate with a dry season of three months in the summer and an annual precipitation of about 563 mm, average temperatures ranging from +19.7°C in summer to 5.1°C below zero in winter. A large wildfire burned 70 ha in September 2017. The fungal production and diversity in the forest from October 2017 through late December 2018 were observed during our study.

Since forest management of the burnt sites differed in different areas, three permanent sampling plots were established for each of two practice variants: burnt, not managed (BNM) and burnt, clear-cut (BC). Additionally, three control plots of the same size were established in one unburnt site (UB). Plots of 2 m × 50 m were established in accordance with previous studies (Dahlberg et al. 2001, Martín-Pinto et al. 2006). Field sampling was performed from October 2017 until December 2018, the period corresponding to an early post-fire succession stage of fungal communities (Kutorga et al. 2012). The study sites were monitored four times per year during one visit in autumn 2017 (October) and three visits in 2018 (May, August, and November) in accordance with other studies (Dahlberg et al. 2001, Martín-Pinto et al. 2006).

To analyse fungal community, all fruiting bodies were collected on all substrates (soil, litter, wood samples, mosses, etc.), with the aim of finding as many species as possible for all habitats. Fungal fruiting bodies were taken to the laboratory, where they were stored at 4–8°C and processed within 24 h after collection for identification. The search for soil-associated fungi was performed by a collection of soil layer for the preparation of moist chamber cultures and molecular analyses. The fungi were classified into the following functional groups according Dix and Webster (1995): saprotrophic (on soil, forest litter/wood), biotrophic, mycorrhizal and pathogenic fungi for further statistical analysis. The samples that could only be identified to the genus level were grouped into a

genus taxon. Both frequency of occurrence and abundance of the different fungal species on each site were used to test for differences in the fungal community in the three sample plots. Frequency was estimated from the presence/absence data matrix of each fungal species. Relative abundance was calculated for each area as a number of samples colonized by a taxon divided by the total number of samples collected in that site.

Fungal identification. Morphological identification was based on macro- and microscopic characteristics of the isolates. Specimens were observed both under a stereomicroscope and a light microscope, after anamorph fruiting structures were mounted on glass slides in cotton blue (Davydenko et al. 2019). The fruit bodies were identified at species level whenever possible according to the mycological keys. For molecular identification DNA was extracted from the unidentified fruit bodies/fungal cultures of the isolates representing morphological groups. Approximate DNA concentrations were determined at 260 nm using the Nano-drop 2000 spectrophotometer (Nano-drop Technologies, Wilmington, DE, USA), and extracts were diluted to 10 ng μl−1 in double-distilled water (Sigma-Aldrich, St. Louis, MO, USA). Internal transcribed spacer (ITS) regions 1 and 2, including the ribosomal 5.8S gene, were amplified using the primers pairs ITS1-F and ITS4 F (Gardes & Bruns 1993). The reaction mixture contained, in a total volume of 15 μl, 200 μM deoxyribonucleotide triphosphates, 0.2 μM of each primer, 0.03 U/μl Thermo Green Taq polymerase with reaction buffer Green, and 2.75 mM final concentration of $MgCl_2$. The thermal cycling was carried out using an Applied Biosystems GeneAmp PCR System 2700 thermal cycler (Foster City, CA, USA). An initial denaturation step at 95°C for 5 min was followed by 35 amplification cycles of denaturation at 95°C for 30 s, annealing at 55°C for 30 s, and extension at 72°C for 30 s. The thermal cycling was ended by a final extension step at 72°C for 7 min. PCR products were size separated on 1 % agarose gels and visualized under UV light. The PCR products were purified with Qiagen DNA extraction PCR M kit (Qiagen, Hilden, Germany). Sequencing was carried out by Macrogen Inc., Korea. Raw sequence data were analysed using the SeqMan Pro version 10.0 software from DNASTAR package (DNASTAR, Madison, WI, USA). Databases at GenBank (Altschul et al. 1997) and at the Department of Forest Mycology and Plant Pathology, Swedish University of Agricultural Sciences, were used to determine the identity of ITS rRNA sequences. The criteria used for identification were: sequence coverage > 80%; similarity to taxon level 98–100%, similarity to genus level 92–97 %.

Statistical analyses. Two-dimensional non-metric multidimensional scaling (NMDS) and the Jaccard's similarity index for presence-absence data and Bray – Curtis dissimilarity were employed to compare fungal species compositions in different study sites. Shannon's H0 diversity index (Mead 2017) was used for the analysis.

Two-way analysis of similarity (ANOVA) was used to test the differences in fungal species compositions or community structures. Non-parametric Kruskal – Wallis and Mann – Whitney U-tests were used to compare species frequency and abundance in the three areas, followed by the Bonferroni – Holm's procedure for controlling experiment wise error rates for multiple independent tests. Species that occurred too rarely to apply statistical tests were left out. Pair wise comparison for a fire effect on a number of soil associated fungi species was made using a *t*-test of the Shannon diversities. Statistical data analysis was performed using the statistical software package PAST: Paleontological Statistics Software Package for Education and Data Analysis (Hammer et al. 2001).

Results and Discussion. Generally, forty-nine fungal species were identified from the collected samples. The phylogenetic analysis showed that 24 species belonged to the Basidiomycota phylum while 16 species were Ascomycota (Fig. 1), and 9 species remain unidentified. 81.6% of the obtained sequences could be identified up to genus or species level. Some of the sequences (18.4%) that could not be properly designated to a species clustered closely together with other sequences (see Fig. 1) and were therefore considered as ECM fungal species or unidentified species (depends on similarity rate).

Among them, a total of 24 mycorrhizal fungal species was identified. Basidiomycetes and ascomycetes respectively accounted for 75% and 25% of the identified mycorrhizal fungal species.

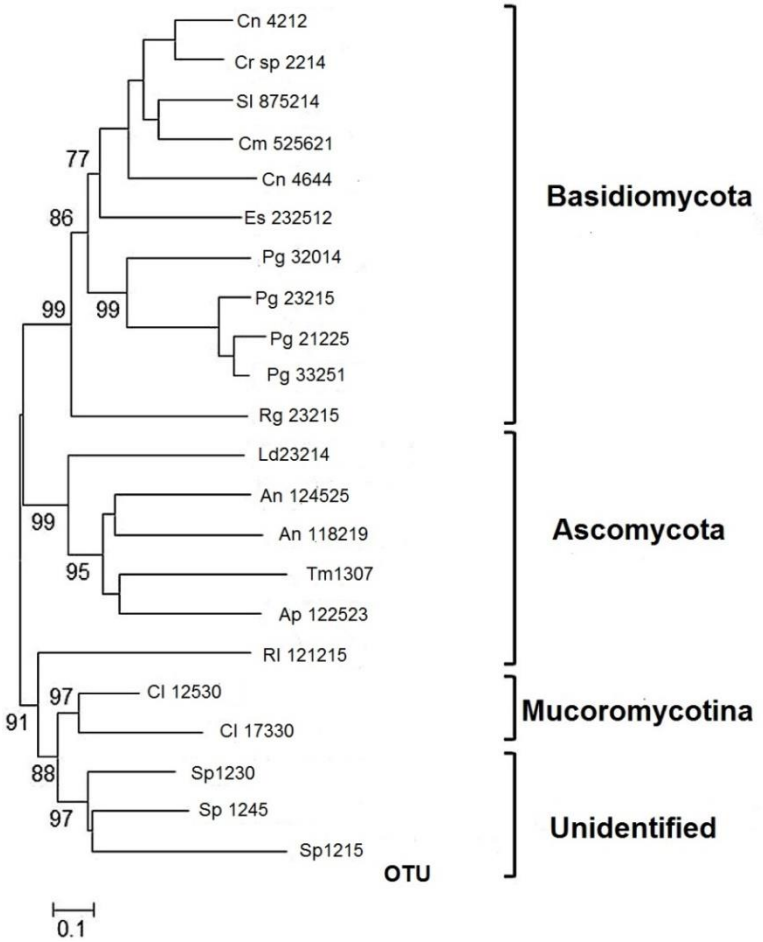

Fig. 1 – Maximum likelihood tree based on ITS sequences obtained from field-collected samples (wood, forest litter, soil) in this study and reference related sequences obtained from Genbank. Numbers at the nodes are values for branch support estimated using the SH-like approximate likelihood ratio test (1,000 resamplings); values below 0.1 are not shown. The scale bar indicates a number of substitutions per site

Most sequences (51.1%) corresponded to mycorrhizal fungal species (Table 1), 43.1% to saprotrophic species, but 6.12% (3 species) of all fungal species corresponded to non-mycorrhizal root inhabiting fungi (see Table 1).

The most frequent and abundant mycorrhizal taxa across the whole area were *Pholiota highlandensis, Russula* sp., *Tricholoma* sp, *Hyphoderma setigerum* and *Hebeloma cistophilum* with the frequency of occurrence 11.09; 5.06; 7.13; 4.56, and 4.16% respectively. According to the obtained data, only 10 species were found exclusively in burnt sites and 26 ones exclusively in the unburnt sites. In total, only 13 species were present in both ones, among them only three taxa (*Rhizophoraceae* species, *Cryptococcus* sp, and *Mycena* sp) belongedto mycorrhizal fungi. Also, five species remained unidentified for burnt and six for unburnt sites.

The wildfire in *P. sylvestris* stands caused a significant decrease of fungal richness in all studied one-month-old and one-year-old burnt sites. Therefore, the number of species recorded for the non-managed burnt area was 2.1 times less of the numbers in the unburnt plots (19 vs 39 fungal species). In burnt, clear-cutting plots, the number of species recorded was 3.25 less than the numbers in the unburnt plots (12 vs 39 fungal species). Results are shown in Figure 2.

The results indicate that the species composition recorded after wildfire and in one-year-old burnt sites was quantitatively and qualitatively different from those of unburnt plots. Only four species were found and identified as fire-surviving species immediately following (October 2017): four and two species on non-managed and clear-cut burnt site respectively (see Fig. 1).

Table 1

Total taxa collected from *Pinus sylvestris* plots

#	Taxa	Phylum of fungi	Sample plots*			Functional groups**
			BNM	BC	UB	
1	*Agaricaceae Chevall* sp.	Basidiomycota	–	–	+	MY
2	*Agrocybe pediades* (Fr.) Fayod	Basidiomycota	–	–	+	MY
3	*Amanita phalloides* (Vaill. ex Fr.) Link	Basidiomycota	–	–	+	MY
4	*Atheliaceae* Jülich sp. 1	Basidiomycota	–	+	+	S
5	*Atheliaceae* Jülich sp. 2	Basidiomycota	+	–	–	S
6	*Collybia* cf. *butyracea* (Fr.) Kumm.	Basidiomycota	–	+	+	S
7	*Cortinarius sp.*	Basidiomycota	–	–	+	MY
8	*Hebeloma cistophilum* Maire	Basidiomycota	–	–	+	MY
9	*Hyaloscypha finlandica* (C.J.K. Wang & H.E. Wilcox) Vohník, Fehrer	Basidiomycota	–	–	+	MY
10	*Hygrophorus discoxanthus* (Fr.) Rea	Basidiomycota	–	–	+	S
11	*Hyphoderma setigerum* (Fr.) Donk	Basidiomycota	–	–	+	MY
12	*Inocybaceae* Jülich sp. 1	Basidiomycota	+	+	–	S
13	*Inocybaceae* Jülich sp. 2	Basidiomycota	–	–	+	S
14	*Myxomphalia maura* (Fr.) Hora,	Basidiomycota	–	–	+	MY
15	*Pholiota highlandensis* (Peck) Quadr. & Lunghini	Basidiomycota	–	–	+	MY
16	*Rhizopogonaceae* Gäum. & C.W. Dodge sp.	Basidiomycota	+	–	+	MY/S
17	*Russula* sp.	Basidiomycota	–	–	+	MY
18	*Terfezia* sp. 1	Basidiomycota	–	–	+	MY/S
19	*Tomentella terrestris* (Berk. & Broome) M.J. Larsen	Basidiomycota	–	–	+	MY
20	*Tomentellopsis* Hjortstam sp.	Basidiomycota	–	–	+	MY/S
21	*Tricholoma* sp.	Basidiomycota	–	–	+	MY
22	Uncultured *Cryptococcus* sp.	Basidiomycota	+	–	+	MY
23	Uncultured *Mycena* sp.	Basidiomycota	+	+	+	MY
24	Uncultured *Pezizaceae* sp.	Basidiomycota	+	–	–	MY
25	*Anthracobia* Boud sp.	Ascomycota	+	–	+	S
26	*Ascobolus furfuraceus* Pers.	Ascomycota	–	–	+	MY
27	*Cenococcum geophilum* Fr.	Ascomycota	–	–	+	MY
28	*Cladobotryum* sp.	Ascomycota	+	+	+	S
29	*Cladosporium* sp.	Ascomycota	+	+	+	S
30	*Geopyxis carbonaria* (Alb. & Schwein.) Sacc.	Ascomycota	–	+	+	S
31	*Pyronema omphalodes*	Ascomycota	+	–	+	S
32	*Rhizina undulata* Fr.	Ascomycota	+	+	+	P
33	*Rhizoscyphus* sp.	Ascomycota	–	–	+	S
34	Unidentified Helotiales HH79	Ascomycota	–	–	+	MY
35	Uncultured ECM (Ascomycota)	Ascomycota	–	–	+	MY

Continuation of Table 1

#	Taxa	Phylum of fungi	Sample plots*			Functional groups**
			BNM	BC	UB	
36	Uncultured ECM (Ascomycota)	Ascomycota	–	–	+	MY
37	*Mucor ramosissimus* Samouts	Mucoromycotina	+	+	+	S
38	*Mucor fragilis* Bainier	Mucoromycotina	+	+	–	S
39	*Glomus tenue*	Mucoromycotina	+	+	–	MY/S
40	*Umbelopsis isabellina* (Oudem.) W. Gams	Mucoromycotina	+	–	+	S
41	Unidentified sp. 22145	Unidentified	–	–	+	S
42	Uncultured Ascomycota 1230	Unidentified	–	–	+	S
43	Uncultured Ascomycota 5243	Unidentified	+	–	–	S
44	Uncultured Ascomycota 175243	Unidentified	+	+	+	S
45	Uncultured plant pathogenic Ascomycota 1245	Unidentified	–	–	+	P
46	Uncultured Ascomycota 11215	Unidentified	+	–	–	S
47	Uncultured plant pathogenic fungus 1256	Unidentified	–	–	+	P
48	Unidentified sp. 7523	Unidentified	+	+	–	S
49	Unidentified sp. 36214	Unidentified	+	+	–	S
Overall Shannon-Weaver diversity index			3.6	1.9	4.9	–
Overall Jaccard's index			0.67	0.49	0.73	–

* BNM – burnt, not managed; BC – burnt, clear-cut; UB – unburnt site.
** MY – mycorrhizal fungi; S – saprotrophic fungi; P – pathogenic fungi.

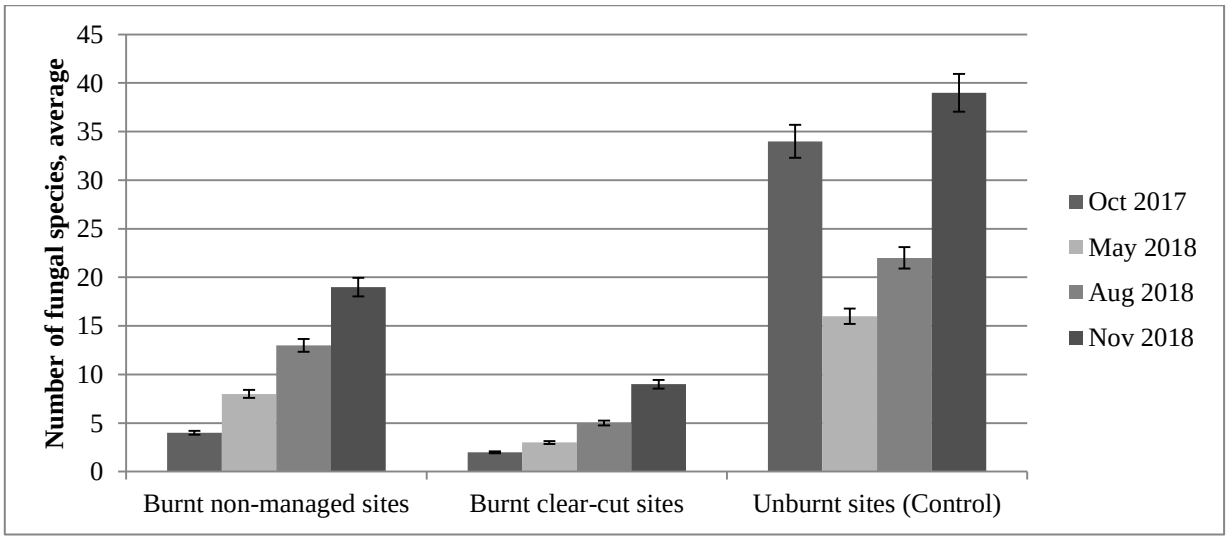

Fig. 2 – Number of fungal species in different treatment variants (2017-2018)

It could be explained by the fact that post-fire fungi normally form fruit bodies during the first significant rain event following disturbance because of spore bank left in the soil over time since the previous fructification. Since spores longevity in the soil has been studied and described for only a few species, in general, it is well-known that they retain viability for many years (Helgason et al. 2002, Claridge et al. 2009).

Some fire-surviving fungi also act as post-fire fungi because they can form fruit bodies only after the fire, even though they may have formed mycorrhizae with surviving trees prior to wildfire (Dahlberg et al. 2001, Claridge et al. 2009).

Moreover, some fungal species produce dormant spores that require heat treatment to germinate (Izzo et al. 2006, Claridge et al. 2009). It has been also studied that spores are carried over time to various depths in upper soil profiles through the run-off processes and rainfall. Therefore, a wildfire can kill spores near the surface, but at some depth, the soil temperature activates spore germination rather than kill them (Claridge et al. 2009). Thus, we could find only four fungal species a few months after the wildfire. In total, nineteen of the taxa were harvested in burned plots (only 36.8 % mycorrhizal, 57.9 % saprophytic and 5.3 % pathogenic) in fourteen months after wildfire while thirty-nine taxa were collected in unburnt sites (56.4 % mycorrhizal, 35.9 % saprophytic and 7.7 % pathogenic).

A dynamic accumulation of fungal species in burnt sites was observed during the following after fire year (2016–2017). In one year after wildfire, additional fungal species not detected previously were recorded in all sample plots (see Fig. 2); moreover, most species were identified next autumn. In burnt plots were 15 and 10 additional species for non-managed and clear-cutting sites respectively.

Five species, namely *Myxomphalia maura, Geopyxis carbonaria, Pyronema omphalodes, Pholiota highlandensis*, *Rhizina undulata* recorded in burnt plots are considered pyrophilic, i.e. dependent upon fire and the immediate post-fire conditions to complete their life cycles and secure their long-term survival (Dahlberg 2001), although these species have also been found on unburnt area but only sporadically (Fig. 3).

While these pyrophilic species also were found on the unburnt area, non-metric multidimensional scaling (NMDS) demonstrate a close association of pyrophilic species with burnt area (see Fig. 3). We have applied a non-metric multidimensional scaling (NMDS) to represent fungal communities (three habitats) in an ordination plot and to find the best representation of the most common species. The NMDS ordination (stress value = 0.0259) explained 89.8% of the variation in species composition between the sites (see Fig. 3). The ordination axis ($R2 = 0.623$) showed two clearly defined site groups: burnt (non-managed) and unburnt sites. In fact, no species were found in close association with burnt area where clear-cutting were applied after fire, indicating that recorded species after forest fire and clear cutting were retrieved by coincidence.

Moreover, overall fungal species compositions (all found species during whole sampling time) from the unburnt sites were similar (Jaccard's index range, 0.49–0.73, see Table 1), thus indicating rather stable fungal community and environmental conditions in the undisturbed pine forest during the study period (Mead 2017).

In contrast, according to the NMDS ordination and two-way ANOVA using Jaccard's index, the fungal species compositions in the burnt sites were dynamic and showed significant differences based on types of forest management ($F = 7.59$; p-value = 0.00001). The NMDS ordination also showed a significant shift of fungal communities from the burnt sites toward those of the unburnt sites.

F-test of Shannon's diversity index showed a significant difference between fungal communities from the burnt and unburnt sites ($F = 21.256$, p-value = 0.0009645). Analysis of the data by two-way ANOVA using the Jaccard's index showed that different management practices in the post-fire forest had an effect on the overall fungal species compositions, indicating the impact of clear-cut logging on fungi (Table 1). However, we consider that a fourteen-month period was too short to carry out a comprehensive assessment of how forest management impacts upon fungal species composition.

Differences in fungal communities can be used as a simple method to evaluate fungal response to fire. It is well known that fungal communities that have been assessed aboveground very rarely/or do not correspond to their belowground counterparts (Dahlberg et al. 2001) but may also reflect phenological differences in the fruiting frequencies of different fungal species and may differ depending on methods (Dove & Hart 2017). Therefore, assessment of the mycorrhizal colonization of plant roots after a fire may differ depending on sampling and evaluation methods.

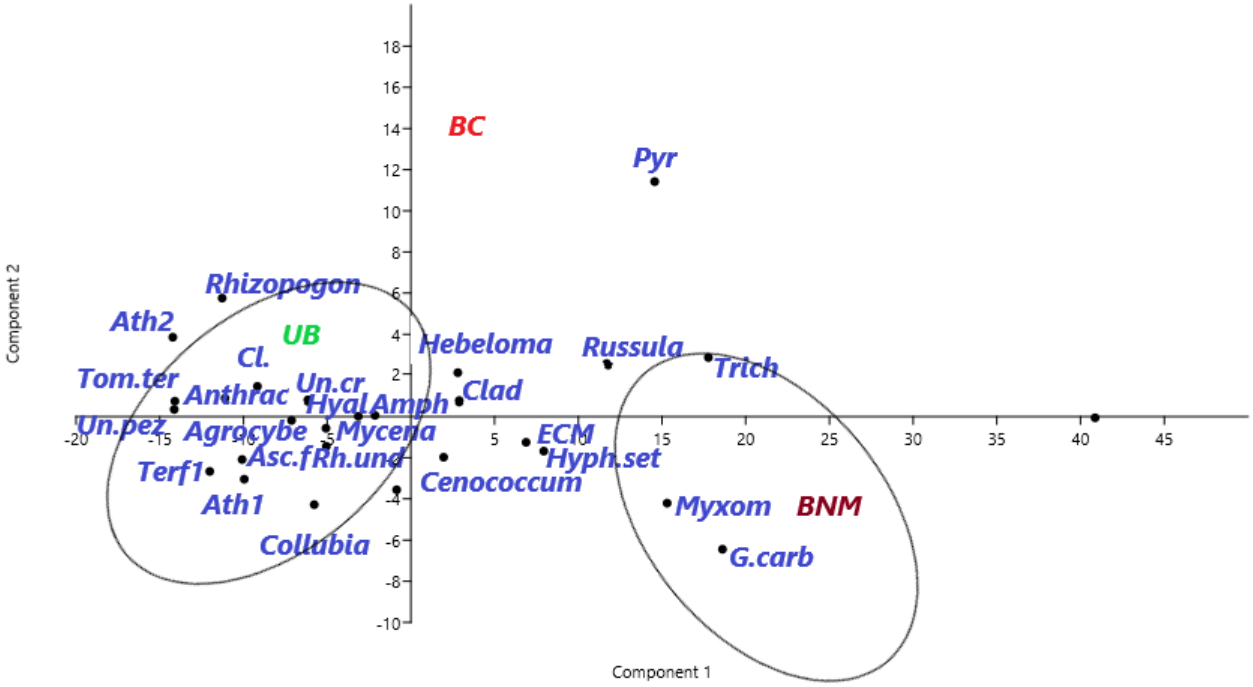

Fig. 3 – Results of NMDS ordination (2D) of all sampling plots performed on abundance data of fungal species in three areas: BNM (burnt, non-managed), BC (burnt, clear-cutting) and UB (unburnt area)

Eigen values of axis 1 and 2 are 0.115 and 0.208 and explain 73.5% of the variance of the species data for abundance (7.1% axis 1, 6.4 % axis 2). Specie abbreviations are: Agrocybe – *Agrocybe pediades* (Fr.) Fayod; Am.ph – *Amanita phalloides* (Vaill. ex Fr.) Link; Ath1 – *Atheliaceae* sp. 1; Ath2 – *Atheliaceae* sp. 2; Collybia –*Collybia* cf. *butyracea* (Fr.) Kumm.; Hebeloma – *Hebeloma cistophilum* Maire; Hyal. Fin – *Hyaloscypha finlandica* (C.J.K. Wang & H.E. Wilcox) Vohník, Fehrer & Réblová; Hygr. – Hygrophorus discoxanthus (Fr.) Rea; Hyph.set – *Hyphoderma setigerum* (Fr.) Donk; Myxom – *Myxomphalia maura* (Fr.) Hora; Pholiota – *Pholiota highlandensis* (Peck) Quadr. & Lunghini; Rhizopogon – *Rhizopogonaceae* Gäum. & C.W. Dodge sp.; Russula –*Russula* sp.; Terf1 – *Terfezia* sp. 1; Tom.ter – *Tomentella terrestris* (Berk. & Broome) M.J. Larsen; Trich. – *Tricholoma* sp; Un. Cr. – Uncultured *Cryptococcus* sp.; Mycena – Uncultured *Mycena* sp; Un. Pez. -– Uncultured *Pezizaceae* sp.; Anthrac. – *Anthracobia* Boud sp.; Asc.f. – *Ascobolus furfuraceus* Pers; Cenococcum – *Cenococcum geophilum* Fr; Clad. – *Cladobotryum* sp.; Cl. – *Cladosporium* sp.; G.carb. -– *Geopyxis carbonaria* (Alb. & Schwein.) Sacc; Pyr. – *Pyronema omphalodes* (Bull.) Fuckel; Rh.und. *Rhizina undulata* Fr.; ECM – Ectomycorrhizal fungi

Several anthropogenic influences are also well-known to decrease mycorrhizal diversity or at least cause significant changes in species composition. The effects of anthropogenic disturbances on mycorrhizal communities are reviewed by many researchers and these include forest logging, especially clear-cutting, wildfire (Dahlberg 2001), fertilization, atmospheric nitrogen deposition, acid rain, etc. (Egerton-Warburton & Allen 2000, Hagenbo et al. 2019, Jo et al. 2019). Microclimate and land relief may also influence mycorrhizal fungi, but it is likely indirectly, acting on plant community first. Unfortunately, in this research, we could not study how a diversity of bacteria species changes as mycorrhizal fungal communities are also influenced by interactions with other soil organisms. Mycorrhizal species may act as helper soil bacteria and enhance root colonization by mycorrhizal fungi (Munkvold et al. 2004). Therefore, further experimental research is necessary to provide reliable and updated information related to study mycorrhizal fungal communities as soil stabilizers and remediators for forest ecosystem after wildfire.

Therefore, our results confirmed data on a rather destructive influence of post-fire forest management on fungal diversity and community composition that has been the subject of a wide number of studies over the last two decades (Dahlberg et al. 2001, Hagenbo et al. 2019, Jo et al. 2019). The main findings of the effects of silvicultural practices indicated that the higher the management intensity, the lower the diversity of mycorrhizal and other fungal species (e.g. wood decay fungi), at least in the short term. Moreover, the found mycorrhizal fungi might use for

seedling mycorrhization for reforestation. Our data suggest that inoculation with selected (local) ectomycorrhizal fungi in containerized nurseries or during planting in forest can be an advantageous approach for the successful establishment of *P. sylvestris* in burned soil. Besides, obtained results give us a lot of data for further experiments with local strains. Given the different factors that can impact on obtained results significantly, the use of a reliable analysis of fire-fungal composition may help to identify specific fungal responses to fire and may help to predict associated changes in the forest ecosystem.

Conclusion. Our study confirms a destructive effect of wildfire on forest ecosystems, particularly its negative impact on mycorrhizal fungi. Generally, 49 fungal species were identified from the burnt and unburnt sites, among them 24 species belonged to the Basidiomycota phylum, while 16 species were Ascomycota and 9 species remain unidentified. According to obtained data, only 10 species were found exclusively in burnt sites and 26 ones exclusively in the unburnt sites.

The most frequent and abundant mycorrhizal taxa across the whole area were *Pholiota highlandensis*, *Russula* sp. *Tricholoma* sp, *Hyphoderma setigerum* and *Hebeloma cistophilum* with the frequency of occurrence 11.09; 5.06; 7.13; 4.56 and 4.16% respectively. All these species were collected in unburnt sites only. In total, only 13 species were present in both (burnt and unburnt sites), among them only three taxa (*Rhizophoraceae* species, *Cryptococcus* sp, *Mycena* sp) belong to mycorrhizal fungi. Moreover, non-metric multidimensional scaling showed that no close connection was found for fungi from the burned area where clear-cutting was applied after the fire, indicating that species after a forest fire and clear-cutting were found by coincidence. Therefore, our results also confirmed the data on a rather destructive influence of post-fire forest management (clear-cutting) on fungal diversity.

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РАННІ НАСЛІДКИ ВПЛИВУ ЛІСОВОЇ ПОЖЕЖІ НА РІЗНОМАНІТНІСТЬ ГРИБНИХ УГРУПОВАНЬ СОСНОВИХ ЛІСІВ ЛІВОБЕРЕЖНОЇ УКРАЇНИ З ОСОБЛИВИМ АКЦЕНТОМ НА МІКОРИЗНИХ ГРИБАХ

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Лісові пожежі мають значний руйнівний вплив на лісові екосистеми, особливо на ґрунтові мікоризні гриби, які утворюють симбіотичні асоціації з багатьма хвойними деревами. У цьому дослідженні ми вивчали ранні наслідки впливу верхової пожежі на угрупування грибів соснових лісів. Протягом чотирнадцяти місяців після осінньої пожежі збирали плодові тіла грибів на згарищах і на ділянках соснового лісу, не пошкоджених пожежею. Визначали видове різноманіття та частоту поширення грибів на всіх ділянках. Загальне різноманіття грибів на згарищах було значно меншим, ніж у не пошкоджених пожежею ділянках, особливо для мікоризних видів. Наші результати також підтвердили дані про сильний руйнівний вплив проведення суцільних санітарних рубок відразу після пожежі, що значно знижує різноманітність грибних угруповань. Так, лише три види мікоризних грибів знайдено на ділянках після проведення суцільних санітарних рубок, а пірофільні види були тісно пов’язані зі згарищами.

К л ю ч о в і с л о в а : мікориза, соснові культури, післяпожежена ерозія, природна пожежа,.

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Одержано редколегією 22.10.2020