



Erosion barriers act as potential reservoirs for soil fungal species key for restoring areas affected by high-severity wildfire in Sierra de la Culebra (NW Spain)

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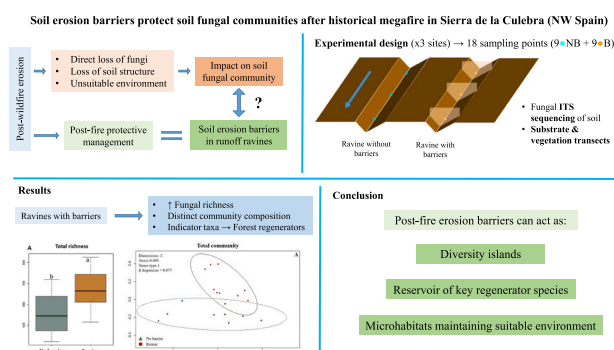
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HIGHLIGHTS

- Barriers create a microenvironment that supports greater fungal species richness.
- Fungal community composition differed between areas with and without barriers.
- Barriers act as reservoirs for potential fungal facilitators of forest regeneration.

GRAPHICAL ABSTRACT



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ABSTRACT

A short-term consequence of increasingly frequent and severe wildfires in the Mediterranean Basin is runoff-induced soil erosion in areas where vegetation has been removed by high-intensity fires. To mitigate this problem, erosion control barriers are often installed in gullies to reduce runoff velocity. The potential impact of these barriers on soil fungal diversity and community composition has not been commonly studied. To assess this effect, we collected soil samples from plots with barriers and plots without barriers in an area affected by the 2022 megafire in the Sierra de la Culebra, Spain. Fungal operational taxonomic units were identified by sequencing the ITS1 region of fungal DNA in soil samples. Vegetation cover and substrate type were also recorded via transects at each sampling point.

Our findings suggest that barriers create a microenvironment that supports greater fungal species richness. This may contribute positively to broader-scale diversity if these localized islands of richness serve as sources of soil fungi for the recolonization of surrounding areas. Fungal communities in plots with barriers were significantly different from those in plots without barriers and were enriched with animal endosymbionts, mycoparasites, and plant pathogens—functional guilds whose role in postfire recovery remains uncertain. However, certain species associated with barrier plots, such as *Mortierella elongata* and *Mortierella alpina*, may play a role in promoting vegetation recovery. This research highlights the adequacy of the use of soil erosion barriers as a

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postfire management tool that can have a positive impact both on direct preservation of soil fungal diversity and subsequent vegetation recovery of burned areas.

1. Introduction

Wildfires are a frequent, natural disturbance within Mediterranean ecosystems (Pausas et al., 2008; Shakesby, 2011), playing a crucial role in the cycling of nutrients and in the renewal and transition of ecosystems (Caon et al., 2014). However, due to changes in land use and climate change, Mediterranean fire regimes are increasing in frequency and intensity (Pausas et al., 2008). Factors such as rising temperatures, anthropogenic wildfires, and longer fire seasons have led to conditions that enhance the susceptibility of forests to ignition and increase the spread and intensity of fires (Jones et al., 2022). However, an increase in fire intensity has negative feedback on the postfire regeneration of an ecosystem (Debano, 2000; Reynard-Callanan et al., 2010).

Following a fire, one of the most severe ecological impacts of the fire and one of the most significant factors affecting postfire recovery is the increased risk of soil erosion (Girona-García et al., 2021; Shakesby, 2011). The loss of the vegetative layer and humus cover exposes the soil to wind and water erosion (Debano, 2000). Furthermore, the high temperatures that occur during an intense forest fire reduce soil cohesion and often lead to the formation of a hydrophobic soil layer that prevents water infiltration, which increases water run-off during precipitation (Debano, 2000). On steep slopes, a sharp increase in soil erosion can be observed after forest fires, at times even exceeding those observed over millennial timescales (Ellett et al., 2019; Tang et al., 2019). Most post-fire erosion occurs in the first one or two years following a fire, before the vegetation has had sufficient time to reestablish a cohesive cover over the soil (Badía et al., 2015; Shakesby, 2011). Therefore, erosion control measures need to be implemented in the period immediately following a fire. One of the most expedient measures that can be implemented is the construction of log erosion barriers to reduce water run-off and to capture eroding ash and soil. This soil protection measure is a standard part of the postfire management strategy used in Spain following a wildfire (Vallejo et al., 2012). However, little is known about the ecological impact of erecting these barriers.

Soil hosts a highly diverse community of organisms, including soil fungi (Van Der Heijden et al., 2008). When a wildfire occurs, not only the direct impact of fire can deplete the soil fungal community, but also the associated negative effects such as the already mentioned post-fire soil erosion. Anyways, this impact is concerning, since soil fungi are a crucial part of the ecosystem because of their central role in many soil processes, influencing decomposition, nutrient cycling and plant health, diversity, and composition and, thus, soil fertility (Finlay and Thorn, 2019; Went and Stark, 1968), among others. Additionally, mycorrhizal fungi also help to maintain soil structure (Burri et al., 2013), which plays an essential role in providing ecosystem services such as carbon sequestration, water filtration, and nutrient retention (Gianinazzi et al., 2010). Therefore, without a healthy mycorrhizal network, the natural regeneration of vegetation may be delayed or inhibited, prolonging the vulnerable period of the ecosystem following a wildfire (MacColl and Maherli, 2024). In general, the loss of a healthy soil community can ultimately reduce ecosystem resilience and make the ecosystem more vulnerable to external disturbances (Figueiredo et al., 2021).

The main objective of this study is to gain a deeper understanding of the impact of log erosion barriers on the soil fungal community and assess how critical is their implementation in postfire regeneration. To this end, on ravines located on slopes with or without erosion barriers in an area affected by a megafire we: 1) Gathered data of vegetation and substrate surface cover and natural tree regeneration; 2) Genetically identified fungi present in soil samples to calculate and compare OTU richness and evenness in plots with and without barriers; 3) Compared

the community composition (in terms of OTUs and of fungal trophic guilds) of the managed and unmanaged plots cover.

Our working hypothesis regarding our specific objectives are: 1) We expect to find differences in surface cover and tree regeneration between plots with and without barriers, due to harder impact of erosion in plots without barriers. 2) Plots that were managed using barriers will preserve more fungal taxa, since we expect that barriers will actively protect soil fungi from being dragged away by erosion. 3) Community composition of plots with and without barriers will be different, because we expect that barriers will trap mineral soil and soil organic matter, hence creating small microhabitats behind the log erosion barriers suitable for maintaining a less disturbed fungal community.

This way, catchment areas behind barriers may act as fungal diversity islands and may also work in the long term as a source of fungal diversity for the surrounding areas, favoring the restoration of the soil fungal community. Soil erosion barriers may also have a positive impact on vegetation recovery. If vegetation cover regenerates better, the wildfire site would be less susceptible to erosion, mitigating part of the damage caused by the wildfire. In addition, higher species richness and balanced dominance could lead to the development of more robust ecosystems. If our working hypotheses are correct, our findings could lead to further research aimed at increasing the efficiency of log erosion barriers and the development of more effective postfire management strategies. Given the increasing frequency and intensity of forest fires in the Mediterranean region, this knowledge may prove valuable in mitigating the damage caused by future wildfires.

2. Materials and methods

2.1. Study area

To study the ecological effect of log erosion barriers on the fungal community, three sites were selected in Sierra de la Culebra, north-western Spain. This study area is located within the Mediterranean climate zone and is continentally influenced. Most precipitation occurs during the spring and autumn months, with comparatively lower levels in the winter and severe droughts during the summer months (Rodríguez-Jiménez et al., 2024). The forest fire season starts in early June and, depending on the meteorological conditions of the year, can last until early autumn.

During the summer of 2022, two of the most destructive wildfires in Spain's history occurred in Sierra de la Culebra. Although the wildfires started nearly one month apart, the burned areas were directly adjacent to each other. The first fire ignited on June 15th, 2022, and resulted in the burning of 29,670 ha of land before it could be extinguished. The second fire started on July 17th, 2022, and resulted in the burning of 35,960 ha (Rodríguez-Jiménez et al., 2024). Before the forest fires, the area was primarily composed of forests dominated by *Pinus sylvestris* and *Pinus pinaster* (Consejería de Medio Ambiente, 2023a, 2023b). The post-fire management included salvage logging to remove dead and damaged trees from most of the burned forest area. In addition, to protect waterways and rivers from being contaminated with ash in water, runoff erosion barriers were erected along naturally formed ravines on the slopes. Log erosion barriers were created using local tree stumps and branches and were erected in the months following the fire. These barriers were 1.0 m to 1.5 m in height, and their length was adjusted to the width of the gully or ravine (Consejería de Medio Ambiente, 2023a, 2023b).

2.2. Sampling

Sampling was carried out on October 24th, 2024, at three different sites that had been directly impacted by the megafires of 2022. Before the fire, all three sites were forested with a mixture of *Pinus pinaster* and *Pinus sylvestris*. At each site, two ravines were selected for sampling: one ravine had been managed postfire by erecting log erosion barriers and the other ravine had not received any postfire management. Soil sampling and surface cover data were collected at three different altitudes per ravine (i.e., 18 plots in total), on the uphill side of the log erosion barriers in the case of the managed ravines, and at similar altitudes in each of the site-analogous non-managed ravines.

In each sample plot, a 5 m transect line was established, oriented parallel to the slope and located at the lowest point in the ravine, where we expected greatest erosion. Along this transect, five soil cores were extracted from the first 10 cm of the topsoil while attempting to avoid direct contact with plant root systems. The five cores were then mixed to form one composite sample of about 500 mL. This approach was used to account for the spatial variability of the soil fungal community, minimizing the possibility of biased results due to the presence of a small-scale disturbance or irregularity in the soil. Samples were frozen to preserve them and subsequently taken to the laboratory where the soil was dried and sieved.

The same 5 m linear transects established for soil sampling were used for surface cover data collection. Surface cover of different types of vegetation and substrates (e.g., grasses, bushes, bare fine soil, stones, and litter) was recorded by measuring the length of the segments of each type of substrate in contact with the transect line. Lastly, the number of newly grown *Pinus* seedlings at 1.5 m on both sides of the linear transect (inside a rectangle of 5x3m) was also recorded.

2.3. Genomic DNA amplicon sequencing and taxa identification

DNA was extracted from 0.25 g of each of the collected soil samples using the commercial DNeasy PowerSoil Kit from Qiagen and following the manufacturer's instructions. The extracted DNA was quantified using a Qubit 4 Fluorometer from ThermoFisher and diluted to adjust the initial DNA concentration to 5 ng μL^{-1} when necessary. The library was prepared by amplifying the ITS1 region using a limited cycle PCR as described in the Fungal Metagenomic Sequencing Demonstrated Protocol (Illumina, 2019). The ITS1 region was amplified using a pool of forward and reverse primers. The forward primer set comprised:

ITS_fwd_1 with the sequence CTTGGTCATTAGAGGAAGTAA;
ITS_fwd_2 with the sequence CTCGGTCATTAGAGGAAGTAA;
ITS_fwd_3 with the sequence CTTGGTCATTAGAGGAAGTAA;
ITS_fwd_4 with the sequence CCCGGTCATTAGAGGAAGTAA;
ITS_fwd_5 with the sequence CTAGGCTATTAGAGGAAGTAA;
ITS_fwd_6 with the sequence CTTAGTTATTAGAGGAAGTAA;
ITS_fwd_7 with the sequence CTACGTCATTAGAGGAAGTAA;
ITS_fwd_8 with the sequence CTTGGTATTAGAGGTCGTAA.

The reverse primer set comprised:

ITS_rev_1 with the sequence GCTGCGTTCCTCATCGATGC;
ITS_rev_2 with the sequence GCTGCGTTCATCGATGG;
ITS_rev_3 with the sequence GCTAGTCTTCATCGATGC;
ITS_rev_4 with the sequence GCTGCGTTCCTCATCGATGT;
ITS_rev_5 with the sequence ACTGTGTTCTTCATCGATGC;
ITS_rev_6 with the sequence GCTGCGTTCCTCATCGTTGC;
ITS_rev_7 with the sequence GCGTTCCTCATCGATGC.

AMPure XP beads were used to purify the amplicon PCR products. An Index PCR was then performed to add Illumina sequencing adapters and dual-index barcodes to the amplicon target using a Nextera XT Index Kit v2. Index PCR products were purified as described for the previous step and then the library was quantified, normalized, and pooled. The library was sequenced using the Illumina iSeq100 System using a 2 × 150 bp run and following the manufacturer's instructions.

2.4. Taxa identification

Sequencing data were processed using the Illumina BaseSpace 16S Metagenomics App, which performs a taxonomic classification at all taxonomic levels using the UNITE database (Abarenkov et al., 2024). Pairwise similarity searches were performed against the meticulously curated UNITE Fungal ITS Database (version 7.2) to classify sequences into taxonomic groups. This database assigns identified fungal sequences to species hypothesis (SH) groups, which are based on fluctuating sequence similarity thresholds (Köljalg et al., 2020). We used the PlutoF web workbench to assign sequences (Abarenkov et al., 2010). Operational taxonomic units (OTUs) with more than 90 % similarity to a fungal SH group with a recognized ecological function were assigned to functional groups in accordance with FungalTraits (Pölme et al., 2020).

2.5. Data analysis

We performed all statistical analyses using the sequence count for each OTU as an abundance value of nonsingleton fungal communities. We excluded from the raw data all the OTUs whose highest read count in its most represented plot was lower than 3 reads.

Shannon's diversity index and Pielou Evenness were calculated using the *diversity* function in the *vegan* package of R. Data used for statistical analyses did not need to be transformed because they achieved the parametric criteria of normality and homoscedasticity. We assessed differences in fungal and surface cover variables in plots with or without barriers using linear mixed-effects (*lme*) models, where the plot was defined as random and the presence of barriers was defined as a fixed factor. We determined the adequacy of the mixed models by verifying the normality and homoscedasticity of residuals through graphical inspections and by conducting a Shapiro–Wilk test. Data were analyzed using R, version 4.4.3 (R Core Team, 2025).

The composition of fungal communities was analyzed by performing a permutational multivariate analysis of variance (PERMANOVA) based on Bray–Curtis dissimilarity using the *adonis2* function in R to reveal potential differences in the soil fungal community composition between plots with or without barriers. The homogeneity of group dispersion was checked to avoid the misinterpretation of potential differences observed using the function *betadis* in the R *vegan* package. We used a Hellinger transformed community matrix and environmental scaled data for the analysis. The ordination technique used for assessing community composition was non-metric multidimensional scaling (NMDS), and the *multipatt* function was used to perform multilevel pattern analysis to identify indicator taxa that were significantly associated with plots with or without barriers.

3. Results

3.1. Plot surface cover description

Analysis of the surface cover revealed minimal variances between plots with barriers or without barriers in terms of vegetation cover and substrate types. There was a significantly higher abundance of stones in plots without barriers ($F = 38.161$; $p < 0.001$), which was anticipated and was attributed to the higher erosion levels observed in these plots. The remaining disparities between plots were deemed to be of a circumstantial nature and were not statistically significant. Mean surface cover data in managed and unmanaged plots can be found in Table 1.

3.2. Fungal diversity

We obtained 870,256 high-quality sequences from the collected soil samples (455,077 sequences from plots with barriers and 415,179 from plots without barriers), which were grouped into 2972 OTUs. Of these, 2698 OTUs were identified down to genus level and 2125 were identified down to species level. Between 23,682 and 97,439 high-quality

Table 1

Mean values and standard deviation of: Proportion of each substrate or vegetation type assessed with surface cover transects; Number of newly established *Pinus* seedlings counted in 3x5m surface, in ravines managed using erosion barriers and unmanaged ravines.

Treatment	Type of substrate or vegetation (%)							Num of seedlings
	Stones	Soil	Litter	Moss	Sprout	Grass	Shrub	
Ravines with barriers	12.73 ± 10.51	14.64 ± 15.36	40.87 ± 24.99	4.04 ± 12.13	11.78 ± 18.15	9.40 ± 8.40	6.53 ± 10.35	6.22 ± 10.12
Ravines without barriers	14.76 ± 7.38	29.38 ± 32.78	34.27 ± 26.55	1.13 ± 3.40	0.00 ± 0.00	13.29 ± 10.19	6.80 ± 8.51	16.78 ± 23.23

reads were obtained from each sample.

As expected, most OTUs belonged to Ascomycota (81.9 % of reads) or Basidiomycota (14.4 %). The most abundant genera were *Calypotryma* (26.4 % of the genus-identified reads), *Penicillium* (21.1 %), *Oidiodendron* (7.7 %), *Naganishia* (5.5 %), *Kabatiella* (3.4 %), *Venturia* (2.8 %), and *Microidium* (2.6 %).

The OTU richness analysis revealed significant differences between plots with or without log erosion barriers ($F = 9.620$; $p = 0.009$). Higher richness values were found in barrier-managed plots (Fig. 1A).

In terms of relative abundance and dominance-dependent indexes, there were no significant differences in either Shannon diversity ($F = 0.441$; $p = 0.519$) or the Pielou evenness ($F = 0.288$; $p = 0.602$) index between plots with or without barriers (Fig. 1B and C). Both diversity index values were very similar for ravines with or without barriers and did not show any observable trends.

3.3. Community composition

NMDS of species provided a good representation (stress = 0.090) of the structure of the fungal community (Fig. 2A). The presence of log erosion barriers had a significant influence on community composition ($F = 2.407$; $R^2 = 0.147$; $p = 0.009$). The *betadispersion* analysis value was not significant, which indicates homogeneity of dispersion within the analyzed groups.

NMDS of guild community composition (stress = 0.119) revealed that the composition of trophic functional groups in plots with barriers overlapped with the community composition of plots without barriers (Fig. 2B). PERMANOVA revealed significant differences in fungal guild composition between treatments ($F = 2.407$, $R^2 = 0.147$, $p = 0.010$). The *betadispersion* analysis value was not significant, which indicated that differences between barrier-managed and unmanaged plots were not affected by the dispersion within the analyzed groups ($F = 0.085$; $p = 0.775$).

In total, 84 OTUs were significantly associated with plots with barriers, whereas only 44 OTUs were associated with plots with no barriers (Supplementary Table 1). Species associated with plots with barriers included the mycorrhizosphere-inhabiting *Mortierella elongata* and

Mortierella alpina and the mycoparasitic *Trichoderma martiale*.

The indicator taxa analysis of trophic fungal guilds revealed several functional trophic groups associated with either plots with barriers or with plots without barriers. Specifically, mycoparasites ($p = 0.006$), plant pathogens ($p = 0.016$), and animal endosymbionts ($p = 0.017$) were significantly associated with plots with barriers, whereas nectar saprotrophs ($p = 0.002$) and soil saprotrophs ($p = 0.010$) were significantly associated with plots without barriers.

4. Discussion

4.1. Barriers act as a reservoir of soil fungal richness

Significantly higher levels of species richness were observed behind erosion barriers than in ravines without barriers. One of the reasons for this may be that erosion in plots without barriers was more severe, which agrees with the surface cover analysis data. A significantly higher cover of stones was found in plots without barriers, which is an indicator that fine soil particles have been lost through erosion (Lowdermilk and Sundling, 1950; Verheijen et al., 2024).

Erosion damages the soil fungal community because it washes away both soil fungi and organic material, reducing the potential for soils to harbor fungal inoculum (Carpenter et al., 2001) and, hence, there is a reduction in the general fungal richness of the soil (Cho et al., 2017; Du et al., 2021; Huang et al., 2013). A decrease in erosion through the implementation of erosion barriers is expected to actively protect the soil fungal community. In addition, the catchment area behind barriers seems to accumulate soil organic matter after forest fires (López-Vicente et al., 2021). The accumulation of these deposits and their associated soil resources, such as organic matter, has been reported to enhance fungal richness (Du et al., 2021).

The retention of a wider range of fungal taxa in plots with barriers than in plots without barriers is a positive outcome given that species richness is an important aspect of biodiversity (Gotelli and Colwell, 2001). Furthermore, the presence of a broader array of taxa in plots with barriers enhances the probability of taxa occupying ecological niches that are pivotal for ecosystem regeneration (Grubb, 1977) and, thus,

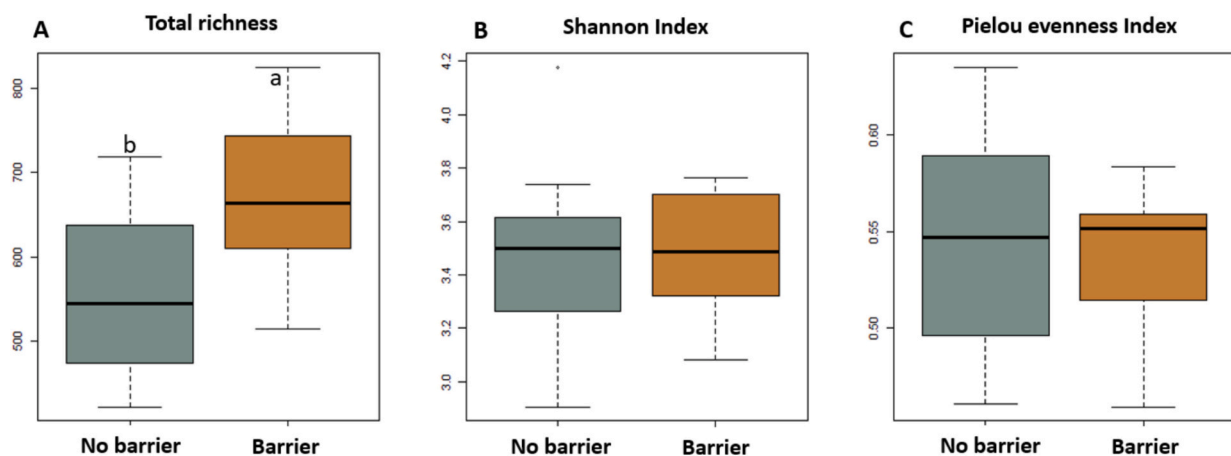


Fig. 1. Effect of log erosion barriers on fungal diversity indexes. A, Total richness; B, Shannon diversity index; C, Pielou evenness index. Different letters indicate a significant difference between plots with or without log erosion barriers ($p < 0.05$).

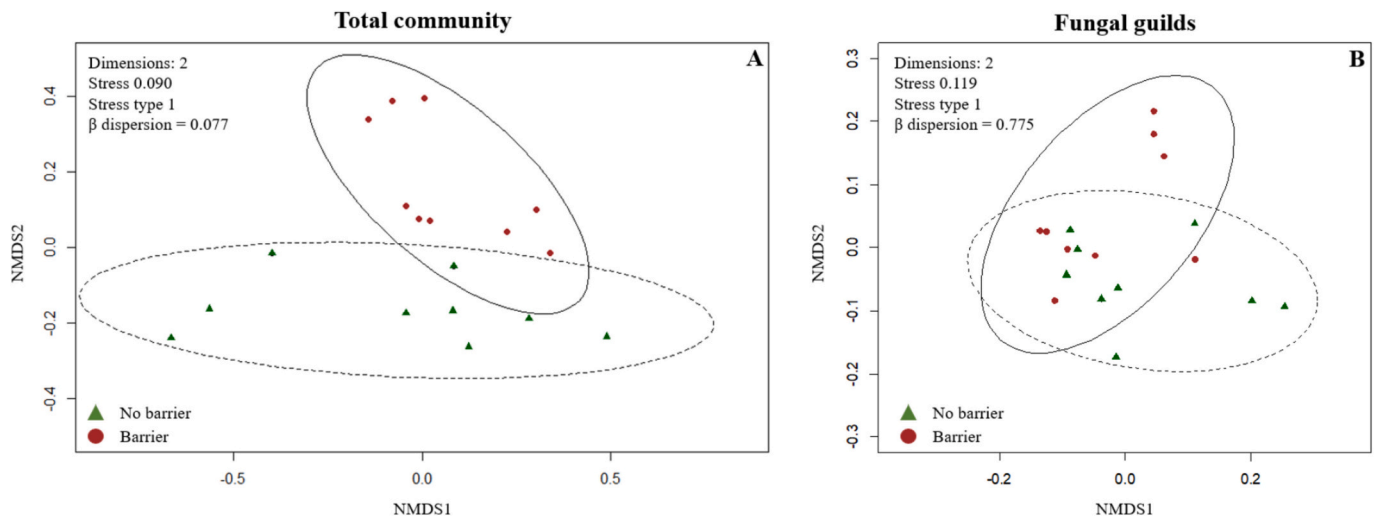


Fig. 2. Non-metric multidimensional scaling (NMDS) of fungal community composition showing the influence of log erosion barriers. A, Total operational taxonomic units; B, fungal guilds.

increasing the likelihood of reestablishing a robust ecosystem. Erosion barriers erected following a high-intensity forest fire create catchment areas that function as reservoirs of fungal species, thereby preserving a broader range of fungal taxa in the burned area.

4.2. Erection of postfire barriers homogenizes community composition and may act as a potential source of diversity

The analysis of fungal community composition in plots with or without barriers revealed differences between them in terms of the presence and abundance of identified fungal OTUs. This finding is consistent with conclusions of previous studies that reported significant differences in soil communities between eroding and deposition zones (Helgason et al., 2014; Sun et al., 2018).

Fungal community dispersion was greater in plots without barriers, indicating a higher degree of variability in species composition among plots without barriers. This suggests that the environmental conditions influencing the composition of the fungal community behind the barriers were largely similar (Kivlin et al., 2014). Although the study did not assess soil characteristics, previous studies have observed that erosion barriers in close proximity exhibited comparable moisture levels (Stavi and Lal, 2011) and frequently had higher organic matter content levels than more eroded plots (Huang et al., 2013). Studies by Du et al. (2021) and Huang et al. (2013) identified moisture levels in the soil as a primary factor influencing fungal community composition, followed by the availability of soil organic matter. Although this could explain the observed homogeneity of fungal communities located behind erosion barriers, it also raises the question of whether fungal communities situated behind barriers could directly expand into the broader environment or if conditions in the catchment area would be too dissimilar to those in adjacent areas. If deposition zones behind the barrier could act not only as a reservoir but also as a source of fungal organisms, postfire barrier management could be an interesting option for boosting fungal diversity restoration in wildfire-affected areas.

4.3. Postfire management can determine community functionality and ecosystem recovery

The indicator taxa analysis indicated that *Mortierella elongata* and *Mortierella alpina* were significantly associated with barrier-managed plots. These are mycorrhizosphere-inhabiting fungi that have been shown to strengthen the growth, improve the health, and increase the seed production of several herbaceous and woody plant species,

including pines (Ozimek and Hanaka, 2020; Li et al., 2018). Therefore, given that the vast majority of natural tree regeneration observed in the studied area comprised pine seedlings, the presence of these fungi may favor vegetation reestablishment. In addition, *M. elongata* has been shown to have a positive impact on nutrient cycling and soil formation (Li et al., 2018).

When community composition was analyzed by guilds, the community composition of plots with barriers showed a greater overlap with the community composition of plots without barriers than when analyzed by OTUs. Nevertheless, some functional groups were identified as significantly associated with either plots with barriers or with plots without barriers. Specifically, plant pathogens, animal endosymbionts, and mycoparasites were associated with barrier-managed plots, whereas nectar saprotrophs and soil saprotrophs were associated with plots without barriers.

Although we had assumed that saprotrophic fungi would be more prevalent behind erosion barriers owing to the accumulation of soil organic matter (López-Vicente et al., 2021), the accumulation of debris behind the barrier seems to have benefited other fungi that outcompeted saprotrophs. Similar outcomes have been reported by other studies, including Du et al. (2021), who found a greater number of plant pathogenic fungi in the topsoil of deposition zones and concluded that greater soil resources favor pathogenic fungi over saprotrophic fungi. Similarly, Shi et al. (2019) observed a decline in saprotrophic fungi that was correlated with an increase in pathogenic fungal taxa. Plant pathogenic fungi are known to reduce plant growth and productivity, which could slow down vegetation reestablishment or change the species composition (Van Der Heijden et al., 2008), particularly given that ecosystems may be particularly vulnerable to soil pathogens in early succession stages (Kardol et al., 2006).

However, some species of mycoparasites, which were found to be significantly associated with plots with barriers, act as biocontrol agents against other fungi, particularly plant pathogens (Ram et al., 2018; Waqar et al., 2024). Indeed, species such as the mycoparasite *Trichoderma martiale*, which has been reported as a biocontrol agent, was an indicator species of plots with barriers. However, there are also many mycoparasites that infect beneficial soil fungi, including those that favor vegetation recovery. The critical factor that determines which mycoparasites occur in a plot is the presence of their host fungi. Thus, the significant association between plots with barriers and this fungal guild may stem from the greater species richness of soil fungal communities in catchment areas behind barriers. Nevertheless, as the presence of mycoparasites is a normal component of an ecosystem, their presence is

not a cause for concern (Baker, 1987).

5. Conclusions

When we initiated this study, we hypothesized that the fungal community retained behind erosion barriers may act in the long term as a source of soil fungi and comprise organisms that could potentially recolonize slopes affected by intense wildfires. Our analyses confirmed our expectations that the soil fungal community behind the barriers is richer than the community found on unmanaged erosion-affected slopes. This result underscores the potential of these diverse islands to act initially as a reservoir and then as a source of fungi if they are able to colonize the wider area.

However, community composition of managed and unmanaged ravines are different. These distinct fungi, which thrive in the wetter and more stable environment behind the barriers, may not be able to adapt to the wider area and, hence, further research is necessary to reach a definitive conclusion regarding the capacity of these fungi to repopulate the wider burned area.

Our findings also suggest that log erosion barriers may mitigate the loss of key fungal taxa due to erosion in areas that have experienced high-intensity forest fires. Given that a significant correlation was identified between fungal taxa conducive to the regeneration process and the erosion barrier treatment, we propose that the use of soil erosion barriers as a postfire management tool may have a positive impact both in preserving the soil fungal community and key taxa that can lead to vegetation recovery of burned areas.

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CRediT authorship contribution statement

Marlene Spiong: Writing – original draft, Investigation, Data curation. **Claudia Prada-Polo:** Writing – review & editing, Investigation, Formal analysis, Data curation. **Pablo Martín-Pinto:** Writing – review & editing, Supervision, Methodology, Investigation, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Data availability

Data will be made available on request.

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