Fungal functional diversity in trace element contaminated soils from the Guadiamar Green Corridor

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Introduction

Soil fungal communities are key in terrestrial ecosystems due to their role as organic matter decomposers and their multiple interactions with plants as symbionts. In degraded ecosystems, the establishment and succession of fungal communities are necessary for the recovery of important ecosystem services (supporting, provisioning, regulating, cultural services).

In a trace element contaminated area (due to a mine-spill), a phytoremediation strategy was carried out with tree afforestation as one of the main measures to restore the area into a novel ecosystem. Twenty years after tree planting and a successful tree growth, we evaluated how belowground communities have been established and developed thanks to this phytoremediation plan.

We conducted a study focused on soil fungal communities in order to compare the community evolution from a contaminated to a phytoremediated soil in terms of fungal community structure, diversity and function.

Methodology

• Study area
We sampled soils (0-5 cm depth) with different plant covers: Bare soil (not-restored), Grassland and three tree species: Wild olive (Olea europaea), White poplar (Populus alba) and Stone pine (Pinus pinea) in two sites with different contamination background: North and South, within the Guadiamar Green Corridor (Figure 1).

• Molecular Identification
We massively sequenced the fungal community in sampled soils (ITS2+ITS5 region using the Illuma MiSeq platform). The fungal taxonomy was inferred (UNITE) and the taxa classified by their ecological guild (FunGUILD).

Fungal OTUs
In the North site, White poplar and Stone pine species showed the highest number of exclusive OTUs, while in the South site was found Grassland soils. In both sites, Wild olive species presented a low exclusivity (Figure 2).

In general, in the South site a higher number of OTUs were shared among studied plant covers, specially between White poplar and Stone pine.

Species diversity of fungal communities

Plant growth enhanced fungal species richness and diversity in both sites. The highest abundance was found in White poplar and Stone pine soils, however diversity and evenness was higher in Grassland and Wild olive soils (Figure 3).

Bare soils presented a different trend to the rest as they showed a low species richness and diversity, and a higher beta diversity. Therefore, soil contamination reduced fungal development and maintained a different community to plant covered soils.

Functional diversity of fungal communities

In terms of functional diversity, we found three distinct community groups: White poplar and Stone pine communities which were predominantly formed by ectomycorrhizal and epiphyte fungal species; Wild olive and Grassland communities which were rich in guilds, with more saprophytic and arbuscular mycorrhizal fungal species, and Bare soils which were completely different due to the dominance of fungal pathogens (Figure 4).

Conclusions:

• Soil fungal communities seemed to establish and develop according to their aboveground vegetation. Tree afforestation increased fungal species abundance and diversity, especially in White poplar and Stone pine soils, however these soils presented a higher species dominance.

• The specific mycorrhizal symbioses among fungi and plant roots explained the different functionality of the communities, dividing ectomycorrhizal (White poplar and Stone pine) and arbuscular mycorrhizal (Grassland and Wild olive) fungal communities.

• Phytoremediation plan showed to be effective to recover soil fungal communities along with the growth of natural grassland and planted trees, and different vegetation engage different fungal communities.

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Resumen

Fungi play a key role in terrestrial ecosystems as organic matter decomposers and by interacting with plants as symbionts or pathogens. In trace element (e.g. heavy metal) contaminated soils, the effect of restoration measures, such as tree afforestation, in enhancing ecosystem services is of interest. In this study, we hypothesised that vegetation, through soil biotic and abiotic changes, is key in the establishment of soil fungal communities in terms of structure, diversity and function.

Twenty years after the accidental spill of the Aznalcóllar mine (April 1998), where acidic waters and pyrite sludge with high concentration of trace elements were released into the Guadiamar River basin, in SW Spain, we have evaluated the recovery of the soil fungal communities. Restoration measures included sludge removal followed by amendments addition and afforestation with native tree species. We selected restored soils within a plant cover gradient consisting of bare soil, grassland to tree (the latter with a comparison between three native species: white poplar, stone pine and wild olive). We also selected two sites, North and South, located at 15 and 30 km from the mine tailing, respectively. A total of 50 soil samples were analysed.

We massive sequenced the fungal community in the above-mentioned soils (ITS1F-ITS2 region using the Illumina MiSeq platform). The fungal taxonomy was inferred and the taxa classified by their ecological guild.

Interaction of site and plant cover fixed factors were found significant for soil abiotic C:N and P, but not to biotic variables (Table 1). Fungal diversity indices were lower in bare and stone pine soils. Species richness was significantly lower in bare soils. The composition and structure of fungal communities were significantly explained by the interaction of site and plant cover factors ($R^2 = 0.405$). Fungal functionality was assessed by ecological guild ordination (Figure 1). Bare soils were dominated by plant pathogen fungi, while grassland and wild olive soils presented a diversity of fungi dominated by saprotrophs. White poplar and stone pine in the South soils were dominated by ectomycorrhizal fungi, while the North presented diverse guilds such as epiphytes, ericoid mycorrhizal and ectomycorrhizal.

Palabras clave

Aznalcóllar, Fungal community, Fungal guild, Microbiome, Next Generation Sequencing
Table 1. The effects of site and plant cover factors on soil abiotic and biotic properties. Mean (SD) and two-way ANOVA. N = 50. Significant main and interaction effects in ANOVA are indicated by: * p < 0.05, ** p < 0.01, *** p < 0.001. Sites: N = North, S = South. Plant cover: BS = Bare soil, G = Grassland, OE = wild olive, PA = white poplar, PP = stone pine. Variables: DH = dehydrogenase activity, S = species richness, H = Shannon index, D = Simpson index.

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<th>Variable</th>
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<td>N</td>
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<td>5.32 (1.90)</td>
<td>6.56 (1.90)</td>
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<td>5.36 (1.48)</td>
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Figure 1. Nonmetric multidimensional scaling (NMDS) ordination of fungal communities from soil samples grouped by site and plant cover factors and relationship to functional guilds. AM: Arbuscular mycorrhizal, ECM: Ectomycorrhizal, ERM: Ericoid mycorrhizal, OM: Orchid mycorrhizal.