

1.5 = The soil mycobiome in an strict nature Reserve threatened by invasive species *Ailanthus altissima* (Mill.) Swingle

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The study of biodiversity in unmanaged forests is pivotal, because they are considered as reference systems for ecosystem restoration according to the Nature Restoration Law (Reg. EU 2024/1991). The forest biodiversity includes also the soil mycobiome, since fungi are a major component of forest ecosystem, with their role as organic substance degraders, mutualistic symbionts and parasites. The Strict Nature Reserve “Bosco Siro Negri” represents one of the rare examples of preserved forest vegetation of the Po valley, classified as a riparian mixed forest (Habitat 91F0), dominated by trees species such as pedunculate oak (*Quercus robur* L.), poplar (*Populus alba* L., *P. nigra* L.), elm (*Ulmus minor* L.), field maple (*Acer campestre* L.) and the alien black locust (*Robinia pseudoacacia* L.), including hazelnut (*Corylus avellana* L.), eldelberry (*Sambucus nigra* L.), hawthorn (*Crataegus monogyna* Jacq.), and bird cherry (*Prunus padus* L.), among the shrubs. Unfortunately, at the moment, the conservation of this Strict Nature Reserve is threatened by both oak decline and the widespread of *Ailanthus altissima* (Mill.) Swingle, an extremely invasive species native of Eastern Asia. The aim of this work was to assess the soil fungal biodiversity inside the “Bosco Siro Negri”, both near healthy oak trees, without *A. altissima* (SNA), and near declining oaks where *A. altissima* is abundant (SNB). Soil samples were also collected from two areas immediately adjacent to the “Bosco Siro Negri”, characterised by two different kinds of revegetation: one was a former poplar plantation, now colonised by ruderal vegetations, with the dominance of *Solidago gigantea* Aiton (R), the other was the result of a recent afforestation activity (established in 2015), now dominated by elm (*Ulmus minor* L.), field maple (*Acer campestre* L.), and dogwood (*Cornus sanguinea* L.) (MS). Five bulk soil samples were collected in each area for ITS-based fungal community analysis. The ITS2 region was amplified and sequenced using NGS illumina sequencing. Bioinformatic processing of the sequencing data was performed using QIIME2 and the statistical analyses were conducted using R. Moreover, metabolic profiling of soil microorganisms was performed by Biolog EcoPlates. The results showed a significant difference in the soil fungal community composition of each site. The metabarcoding of soil samples revealed a general dominance of *Ascomycota* in all sampled soils, but inside the “Bosco Siro Negri” *Basidiomycota* were more abundant than in the other areas. The SNA samples hosted a very high concentration of *Metarhizium*, a fungus known for its entomopathogenic potential against harmful insects, while the genus *Mortierella* was more abundant in SNB. The difference between the high ecological integrity area (SNA) and the degraded one (SNB) was also underlined by an increased ability of the SNA microbial communities to degrade amines, an indicator of a more functional nitrogen cycling. In conclusion, this study highlights how the introduction of invasive species like *A. altissima* can potentially entail profound modifications not only in the plant composition of old-growth forests, but also in the soil biodiversity and nutrient cycling.