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Clary sage cultivation and mycorrhizal inoculation influence rhizosphere fungal community structure over time in a trace-element polluted site

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Fungal community in the soil plays a central role in natural systems and agroecosystems, therefore it attracted much research interests. However, the fungal microbiota of aromatic plants, such as *Salvia sclarea* L., especially in trace-element (TE) polluted conditions and within the framework of phytomanagement approaches, remains unexplored. The presence of high concentrations of TE in the soil is likely to negatively affect not only microbial diversity and community structures, but also plant establishment and growth. The objective of this study is to investigate the soil fungal and arbuscular mycorrhizal fungi (AMF) community structure and their changes over time in TE-polluted soils in the vicinity of a former lead smelter and under the cultivation of clary sage. We used Illumina MiSeq amplicon sequencing to evaluate the effects of in situ clary sage cultivation during two successive years, combined or not with an exogenous AMF inoculation, on the rhizospheric soil and root fungal communities. We obtained 1239 and 569 fungal amplicon sequence variants (ASV) respectively in the rhizospheric soil and roots of *S. sclarea* in TE-polluted conditions. Remarkably, 69 AMF species were detected in our experimental site, belonging to 12 AMF genera. Besides, the inoculation treatment significantly shaped the fungal communities in soil, and increased the number of AMF ASVs in clary sage roots. In addition, successive years of clary sage cultivation also significantly shaped both fungal and AMF communities in the soil and root biotopes. Our data provide new insights on fungal and AMF communities in the rhizospheric soil and roots of clary sage grown in TE-polluted agricultural soil.

Keywords: Trace Elements-polluted soils, fungal microbiota, *Salvia sclarea*, arbuscular mycorrhizal fungi