Characterization of microbial communities and functional diversity associated to native plant species *Pistacia lentiscus* L. and *Helichrysum microphyllum* subsp. *tyrrhenicum* in abandoned mining areas

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Among phytoremediation approaches, phytostabilization occurs at the root-substrate interface, where excluder-type metallophytes and associated microorganisms mitigate metal mobility and bioavailability. This study presents an integrative analysis of microbial diversity associated to two native plants of Sardinian abandoned mining areas and candidate for revegetation and restoration programmes. Spontaneous plants were studies in a Zn-Pb mine tailing dump and its surrounding areas. To deepen our understanding of the interaction among mine substrates, metals, plants, and microbes under real field conditions, a multifactorial approach was employed evaluating dehydrogenase activity, Community Level Physiological Profiling, bacterial and fungal communities through high-throughput sequencing of ribosomal genes in mine tailings, rhizosphere and roots. The studied site exhibited significant heterogeneity in environmental parameters and metal concentrations. Analysis revealed differences between the two plant species in metabolic activities and highlighted distinct abiotic drivers shaping bacterial and fungal community structures. Bacterial communities associated with the rhizosphere and roots differed between plant species, while fungal communities of both plants were dominated by the same taxa. This study represents the first comprehensive characterization of microbial communities associated with *P. lentiscus* and *H. tyrrhenicum*. Our findings demonstrate that different plant species select different microbial communities, providing critical insights into the ecological roles of root-associated microbiomes and their potential for site-specific remediation strategies. This work has been developed within the framework of the project e.INS www.einsardinia.eu (Next Generation EU- PNRR-M4 C2 I1.5 CUP F53C22000430001).