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Programme & Abstracts



were used to formulate hypotheses on how H<sub>2</sub> oxidation can be coupled with sulfur reduction. Supported by experimental work, these data will help to understand the interconnection between carbon fixation and respiratory pathways in this chemosynthetic-driven environment.

### **B53. The occurrence of mycorrhizal fungi in *Betula aetnensis* Raf. roots: from ecological role to conservation strategies**

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*Betula aetnensis* Raf. is an endemic tree species of particular conservation value. It only thrives in the north-eastern slopes of Mount Etna (Sicily), from 1200 to 2100 m a.s.l. This pioneer plant is able to begin primary succession on nutrient-poor and water-limited soils (C = 0.17%; N = 0.05 %; P<sub>2</sub>O<sub>5</sub> = 4.1 ppm), where beneficial mycorrhizal fungi (MF) may play a crucial role. In order to investigate MF role in *B. aetnensis*, plant roots from natural sites and nursery grown specimens were analyzed for both ectomycorrhizal and endomycorrhizal structures. Typical structures of both symbiosis were detected by root staining and morphological observations. Ectomycorrhizae (EM) were more abundant in natural sites (≈88%) than in nursery (≈77%). Clear morphological differences in the EM root tips suggest the occurrence of different fungal species. About 50% of roots had arbuscular structures, both in natural habitats and nursery. The community structure of EM and AM fungal symbionts was characterized by DGGE analysis.

Mycorrhizal dependence trials are in progress to elucidate the relative importance of ecto- and endomycorrhizal symbionts for this endemism, whose conservation could be strongly linked to mutualistic associations established at root level.

### **B54. Chemical and microbiological characterization of a complex contaminated industrial area**

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The management and the remediation of large contaminated areas with multiple pollutant sources represent a big challenge to site owners. Therefore, a detailed chemical and microbiological site characterization is crucial to assess, at first, the potential of intrinsic remediation of the contaminated area and, then the feasibility to enhance specific biodegradation processes.

This study aimed at gathering data from a complex contaminated industrial area to evaluate the presence of potential degraders of chlorinated compounds and, thus to design an effective bioremediation strategy.

Contaminated groundwater was collected from a restricted area of the site. Chemical analyses of chlorinated ethenes, 1,2-dichloroethane (1,2-DCA), benzene, toluene, xylenes, ethylbenzene and chlorinated benzenes were performed. The structure of the microbial community was determined by Illumina Next-Generation Sequencing, whereas its functional profile was assessed by quantitative PCR of key genes encoding for enzymes involved in specific metabolisms.

Vinyl chloride (VC) and 1,2-DCA were found in most of the water samples at high