



Effects of organic amendments and mulches on soil microbial communities in quarry restoration under semiarid climate

Lourdes Luna Ramos (1), Roberta Pastorelli (2), Isabel Miralles Mellado (1), Arturo Fabiani (2), Felipe Bastida López (3), María Teresa Hernández Fernández (3), Carlos García Izquierdo (1), and Albert Solé Benet (1)

(1) Estación Experimental de Zonas Áridas (CSIC), La Cañada de San Urbano, 04120, Almería. Spain (lourdes@eeza.csic.es), (2) Agricultural Research Council, Research Centre for Agrobiology and Pedology, 50121 Florence, Italy, (3) Centro de Edafología y Biología Aplicada del Segura (CSIC), Espinardo, 30100, Murcia, Spain.

Mining activities generate loss of the quality of the environment and landscape specially in arid and semiarid Mediterranean regions. A precondition for ecosystem reclamation in such highly disturbed mining areas is the development of functional soils with appropriate levels of organic matter. In an experimental soil restoration in limestone quarries from Sierra de Gádor (Almería), SE Spain, 9 plots 15 x 5 m were prepared to test organic amendments (compost from solid urban residues-DOW-, sludge from urban water treatment-SS-, control-NA-) and different mulches (fine gravel-GM-, wood chips-WM-, control-NM-) with the aim to improve soil/substrate properties and to reduce evaporation and erosion. In each experimental plot, 75 native plants (*Macrochloa tenacissima*, *Anthyllis terniflora* and *Anthyllis cytisoides*) were planted. After 5 years from the start of the experiment, we evaluated how microbial community composition responded to the organic amendments and mulches. Microbial community composition of both bacteria and fungi was determined by phospholipid fatty acid (PLFA) and polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE) fingerprinting. The results of the two-way ANOVA showed that PLFAs were significantly affected by organic amendments but not by the mulches or interaction of both factors. Experimental plots with DOW showed significantly higher level of fungal PLFAs than those with SS and NA, even higher than the reference undisturbed soil. However, any plot with organic amendments did not reach the content of bacterial PLFAs of the reference soils. The bacterial diversity (evaluated by diversity indices calculated from DGGE profiles) was greater in soil samples taken under NA and GM. Comparing these indices in fungal DGGE, we found greater values for soil samples taken under DOW and without mulches. Results from UPGMA analysis showed significant differences in the structure of soil bacterial communities from the different treatments respect to that of reference soil. Fungal communities could be divided into main groups according to the organic amendment. Within each group, GM amendment generated fungal community structures with lower similarities with respect to the other mulch treatments. In contrast to PLFA results, DGGE fingerprints revealed significant influence of the combination of organic amendments and mulches on diversity and composition of soil microbial communities.