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Relationships between soil water repellency and microbial community composition under different plant species in a Mediterranean semiarid forest

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It is generally well accepted that soil water repellency (SWR) can greatly influence the hydrology and the ecology of the forest soils (Doerr et al., 2000). However, little is known whether SWR may influence the soil microbial community. Its appearance is mainly influence by many soil physic- chemical parameters like: SOM content and its quality, pH, moisture, texture etc. However, it might also be influence by the presence or activity of microorganisms. Early studies suggest that SWR might be caused by substances produced by the activity of certain fungi species (Savage et al., 1969). Soil WR is normally characterized by a high spatial variability in persistence, with wettable and water repellent patches (Lozano et al., 2013). Changes at the microsite scale (such as the presence of soil water repellent patches) might be reflected in the microbial community structure).
In the current study we have analysed how SWR influence the microbial community in soil samples with a range of water repellency persistence under different plant species (P. halepensis, Q. rotundifolia, C. albidus and R officinalis) in a Mediterranean forest. The microbial community was determined through phospholipids fatty acids (PLFA). The relationships between microbiological community structure and other different soil properties like pH, Glomalin Related Soil Protein and Soil Organic Matter content were also studied. Different statistical analyses were used: Principal Component Analysis (PCA), ANOVA, Redundancy Analysis (RA) and Pearson correlations. The highest concentrations of PLFA were found in water repellent samples. PCA showed that microorganism composition was more dependent of the severity of SWR than the type of plant species. In the RA, SWR was the only significant factor ($p<0.05$) to explain PLFA data distribution. The biomarker of Actinobacteria microbial group was the only biomarker directly related to SWR, therefore it can be concluded that this particular group is mainly associated with the mineralization of the hydrophobic compounds (Roper 2004). However, any specific microbial group has been related to be a factor in the occurrence of SWR and its persistence through about their activity or metabolic products. All the results suggest that SWR may be an important factor controlling the microbial community composition and not vice-versa.
Keywords: Soil Water Repellency; Phospholipids Fatty Acids; Microbial Community Structure; actinobacteria; Glomalin Related Soil Protein.
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