



## **Metabolic and genetic fingerprint of microbial communities in Mediterranean soils under different plant covers**

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Substrate-use abilities and genetic structure of microbial communities were investigated through three semi-arid Mediterranean soils of SE Spain. The profiles under study comprised a gradient of disturbance in their plant cover structure and composition, including a native woodland, a semi-natural grass steppe and an artificial pine plantation. Seven samples in 10 cm depth increments were taken in triplicate along each soil profile. Community level physiological profiles (CLPPs) based on sole-C-source use were determined to characterise the metabolic abilities. A 16S rDNA PCR-DGGE analysis was performed to investigate the genetic structure. Plant cover and land-use were history major determinants of microbial fingerprints. Microbial communities residing in soils under a native pinewood, the most diverse and stable plant cover, were the most complex both metabolically and genetically. The microbial community structure distinctly changed with depth, related to the quantity and quality of total organic carbon. Soils under a mature woodland and a grass steppe showed falling gradients of metabolic and genetic complexity. In the planted pinewood, however, the substrate-use diversity increased with depth, apparently a response to the depleted metabolic abilities within its upper layer (0-30 cm). Tilling and plant cover removal might be responsible for such a perturbation. In the same profile, molecular fingerprint patterns of the topsoil layer (0-10 cm) indicated a disturbed genetic structure that might underlie the loss of metabolic abilities. However, the genetic structure of the deeper layers of the planted and native pinewoods was not dissimilar, revealing that equivalent genetic resources perform different environmental functions under chang-

ing soil scenarios.