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RESPONSE OF SOIL BACTERIAL COMMUNITY TO AGRICULTURAL LAND USES AND SEASONAL CHANGES

Patrizia Paganin[1], Maite Sampedro Pellicer[1], Luigi Ledda[2], Maria Cristiana Papaleo[3], Renato Fani[3], Anna Benedetti[4], Claudia Dalmastri[1], Annamaria Bevivino[1]*

[1]Technical Unit for Sustainable Development and Innovation of Agro-Industrial System, ENEA Casaccia Research Center, Rome, Italy; [2]Dept of Agronomy and Crop Genetics, University of Sassari, Italy; [3]Laboratory of Microbial and Molecular Evolution, Dept of Evolutionary Biology, University of Florence, Italy; [4]Research Centre for Plant and Soil System RPS–CRA, Rome, Italy

Abstract

Microbial communities play a critical role in the functioning of soil and represent a very susceptible index of soil quality. Among the factors driving differences in soil bacterial community structure, anthropogenic activities and seasonal temperature changes are very important. In this work, we aimed at determining the effects of land use intensification along with seasonal variations on soil bacterial community. Five different land-use units, characterized by different use and management with growing human impact, were chosen in Sardinia (Italy): cork-oak forest (coded Su), hayland-pasture rotation (Pa), semi-natural grassland (Er), and ploughed (VL) and grass covered vineyard (Vi). The sampling sites were selected inside the same environmental unit, with neutro-acidophylous cork-oak forest as potential vegetation. At each site, five separate sub-samples were collected from the top 20 cm depth of soil in spring and autumn. Along this land-use gradient, soil physic-chemical properties and bacterial communities were analyzed. All the soils resulted to be sandy-loam, presented pH reaction sub-acid and very low organic matter content that showed the highest values in soils with a lower human impact. Cluster analysis of the banding patterns obtained by culture-dependent denaturing gradient gel electrophoresis (CD-DGGE) revealed that soil bacterial communities clearly differed depending on season. Within each season, subgroups including bacterial communities associated to different land uses with increasing level of intensification were observed. All these data are in agreement with those resulting from Terminal Restriction Fragment Length Polymorphism (T-RFLP, cultivation-independent method). Phylogenetic analysis of 16S ribosomal RNA gene revealed that cultivable bacteria included members of *Proteobacteria*, *Actinobacteria, Bacteroidetes* and *Firmicutes* groups, with a prevalence of certain taxonomic units in a defined season (i.e. *Burkholderiales* in Autumn). Investigation of the relationships between soil physic-chemical properties and microbial biodiversity is in progress. In conclusion, different microbial biodiversity among samples and shifts in soil microbial community structure can be ascribed to seasonal changes, even if anthropogenic activity can also affect soil microbial community. The positive selection of *Proteobacteria* and the absence of *Acidobacteria* indicates a good state of health for the soils examined in the present study. The high prevalence of *Proteobacteria* could be used as an indicator of soil health.

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