

THE SOIL MICROBIAL ECOLOGY AND SUSTAINABILITY OF ORGANICALLY AND CONVENTIONALLY MANAGED VINEYARDS

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Microorganisms are involved in many important processes in soil, as nutrient cycling and organic matter decomposition and transformation, which contribute to soil quality and are essential for long-term sustainability of agricultural systems. Recent studies have demonstrated the impacts of organic and conventional production systems on the soil microbial and chemical characteristics. The principal input of conventional agriculture is the large dependence on intensive chemicals, characterized by extensive application of synthetic fertilizers, insecticides, fungicides and herbicides. These agricultural practices have been associated with loss of soil fertility, ground water and environmental pollution, as well as with the loss of soil microbial diversity. On the other hand, organic agriculture eliminates the use of synthetic fertilizers and pesticides, animal drugs and food additives and attempt to close nutrient cycle. The adverse effects of conventional farming system on soil productivity and environmental quality have led to an increasing interest in organic farming that is gaining worldwide acceptance and has been expanding in the last decade. We investigated the effects of conventional and biodynamic management on microbial communities in vineyards soil to establish if agriculture practices affect microbial biodiversity and composition on soil. Another important objective was to identify microbial species or model groups that would be indicative of the organic farming soil status. Three different agricultural practices were evaluated: conventional, organic (biodynamic) and biodynamic with green manure's application. Genomic DNA from soil was extracted and amplified by PCR using 16S rDNA and ITS fragments, respectively to bacteria and fungi, and analysing by DGGE to assess diversity indices, identify shared similarities and compute statistical differences between communities. First results indicate that microbial communities respond sensitively to management practices. Majority of fungal and bacteria species were common to all the analyzed soils, whereas some of them were restricted to different agricultural practices. The presence of specific groups correlate with the management agricultural systems will be investigated a matter using the 454 sequencing method.