



Soil-inhabiting fungal community composition as qualitative indicator of C metabolism processes

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Although fungi represent the greater part of soil microbial biomass, they play an important role in macro-aggregate formation and their carbon (C) assimilation efficiency is markedly higher than that of bacteria (Bailey et al., 2002), they have not yet been widely used as soil biological indicators. The reason is mainly due to the difficulties in application of molecular analysis tools due to limited availability of reference sequence of fungal strains in DNA database and to the low concentration of fungal DNA in soil and in isolating, enumerating and identifying groups of fungi differing for their functioning in soil and for biological characteristics.

The presence of Ascomycetes and Basidiomycetes as the two main groups of soil-inhabiting fungi were investigated in four different cropping systems. The soil DNA of soil samples coming from twenty sites (five sites for each system), collected in two cropping systems in northern (soil organic matter - SOM content varying from 0.8 to 1.4 %) and two in southern Italy (SOM from 1.4 to 2.3%), was amplified using Ascomycete-specific primer ITS1F – ITS4A (Larena et al., 1999) and Basidiomycete-specific primer ITS1F –ITS4B (Gardes and Bruns, 1993). On the basis of soil DNA amplified with specific primers, Ascomycetes were much more represented than Basidiomycetes in the cultivated top soil. Basidiomycetes are usually reported to account for more than half of the fungal biomass in undisturbed soils. However the low ratio of Basidiomycete DNA to soil fungal DNA observed in this study could be a feature of soil fungal communities in arable soil affected by desertification problems as those of some Italian cropping systems mainly in Mediterranean area. This phenomenon could be due to soil tillage, which is well known to deeply reduce fungal biomass and to continuous incorporation into the soil of herbaceous crop residues. In fact, Ascomycetes decompose holocellulose in preference to lignin (Oslo & Takeda, 2002) and their growth may depend on readily available energy sources, such as soluble carbohydrates (Hudson, 1968). The high ratio of Ascomycetes in the top layer where crop residues of the recurrent had represented the main substrate for saprophytic fungi could explain these results. On the contrary, Basidiomycetes are the most important synthesizing biomass organisms in forest soils as well as the most effective organisms in lignin decomposition with an important role in humic substances processes (Hurst et al., 1963; Cook and Rayner, 1986).

Preliminary results of this study suggest that the composition of soil-inhabiting fungal communities, which are the organisms most involved in C metabolism processes, could represents an useful indicator in programs aimed to increase the quality of organic matter in arable soils.

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