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Effects of Crop Residues Management on Soil Bacteria Community Structure

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Understanding the response of soils to agricultural management practices over the time helps to evaluate whether the investigated practices maintain or improve soil quality. Soil quality depends on a large number of chemical, physical, biological and biochemical properties, and its characterization requires the selection of properties sensitive to changes in management practices. Soil management affects soil microbial communities, which mediate many processes essential to the productivity and sustainability of soil. With the advent of modern molecular methods, in recent years, a number of culture-independent methods have been adopted to correlate changes in bacterial community structure and function in complex natural ecosystems with natural or artificially imposed environmental perturbations. Ploughing in of crop residues is a conventional practice to recycle uncropped material and to limit the loss of soil organic matter due to intensive and long-term cultivation.

This study reports the effects of wheat residues ploughing in or burning in a long-term field trial on the community structure of eubacteria, actinomycetes and ammonia-oxidizing bacteria. A field experiment was began in 1977 on a clay soil cultivated with durum wheat. Randomised blocks with three replicates were subjected to ploughing, ploughing + 100 kg/ha NH_4^+, burning of crop residues. Composite bulk soil samples were randomly collected from the surface layer ;rhizospheric soil was obtained by sonication of roots. A direct method was used to extract DNA from soil, using a bead beater system. Two sets of universal primers were used for Bacteria rDNA to amplify a $\cong$500 bp region of the 16S rDNA and a population of fragments relative to the 16-23S intergenic region; PCR amplicons were analysed, respectively, by ARDRA and RISA. DNA fragments of about 1.2 kb relative to the ammonia oxidizer 16S rDNA were amplified and analysed by ARDRA. Specific primers were also used to amplify

a $\cong$250 bp region of the actinomycetes 16S rDNA and PCR amplicons were analysed by DGGE. PCR products were separated onto urea-formamide denaturing gradients by polyacrylamide gels (DGGE) or on non-denaturing polyacrylamide gels (RISA). In the case of ARDRA amplified rDNA products were digested at 37 ^{O}C for 2 h with 5 U of restriction enzymes and separated by horizontal electrophoresis with agarose gels. Silver stained gels were recorded and profiles were compared and clustered. The similarities of the banding patterns was evaluated calculating the dice coefficients and using the unweighted pair group method with average linkage (UPGMA).

The cluster analysis of the genetic fingerprints, performed acquiring the presence/absence and the relative intensity of banding, and the relative Dice's coefficients of similarity among lanes (mostly $>$ 0.85) indicated that i) the fingerprints of different samples were quite similar and in many cases almost identical i) the differences among treatments were always less significant than the very low variability among replicates. This was even more evident when cluster analyses were performed by considering only the presence/absence of bands without weighting their relative intensity. In those cases Dice's coefficients were almost 1.0 and, of course, no clustering was detected. So, the long-term burning or ploughing of plant residues did not affect significantly the composition of eubacterial community, as well as of two relevant groups (actinomycetes and ammonia oxidizers) of bulk and rhizospheric soil. The analysis of metabolically active components of soil bacteria ,by rRNA-based fingerprinting, is in progress.