NJF Report • Vol 4 • No 3 • Year 2008

Nordic Association of Agricultural Scientists

# NJF Seminar 418

## New insights into sustainable cultivation methods in agriculture

**Piikkiö, Finland, 17-19 September 2008**

NJF
Nordic Association of Agricultural Scientists

# Genomic methods in analyzing the communities of soil bacteria

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Soil microorganisms play an important role in maintaining the health and sustainability of soil ecosystem. Development of effective methods for studying the composition, diversity, and behaviour of microorganism in soil habitats is essential for a broader understanding of soil quality. Classical microbiology involves the enrichment and isolation of pure microbial cultures, but it has been estimated that less than one percent of all microorganisms can be cultured (Tsai and Rochelle, 2001). Culture-independent examination of complex microbial communities has been made possible by recent advances in molecular biology. Terminal restriction fragment length polymorphism (T-RFLP) is one of such techniques that allow rapid assessment of the diversity of microbial community. This technique includes polymerase chain reaction (PCR) amplification of 16S rDNA, in which the forward primer is 5'-labeled with a fluorochrome. The fluorescently labeled amplicon is digested with a restriction endonuclease and resolved by automated DNA sequencer. This results in the detection of only the fluorescently labeled fragments (i.e., the terminal restriction fragments). This banding pattern is a fingerprint of the sample's microbial diversity. T-RFLP fingerprints are often used to track spatial and temporal changes in microbial diversity. The objective of this study was to develop a T-RFLP protocol suitable to analyze microbial communities such as soil bacteria from rhizosphere.