



Methods for determining the abundance, diversity and activity of soil microbial communities

Lily Pereg

University of New England, School of Science and Technology, Armidale, Australia (lily.pereg@une.edu.au, 61 2 6773 3267)

The diversity and abundance of soil microbial communities play important roles in determining soil structure, quality and productivity. The past decade has seen an increase in the number and efficiency of methods for determining microbial diversity, abundance and function. Recognising that only a very small proportion of the soil microbial community can be cultured, most current studies use molecular techniques based on the 16S and 18S rRNA encoding sequences (DGGE, TRFLP, OFRG, ARISA, SSCP) as well as techniques based on the cellular composition of the microbes (PLFA composition). Recent developments include high-throughput sequencing and microarrays, representing major advances in microbial community analysis. While the diversity of microbes can be determined using DNA-based techniques, microbial activity changes under various conditions. Therefore, the analysis of soil function at any given time requires the analysis of gene expression using RNA-based techniques. Molecular techniques have tremendously advanced our knowledge in the field of soil microbiology, however, the limitations should not be underestimated. This presentation will critically review both the advantages and the limitations of techniques used in soil microbial analysis.