

Abstract:

Microbes are the main agents of biogeochemical cycles in soil and affect their development and fertility. Nucleic acid second generation sequencing technologies of the collective microbial genomes (metagenomes) now allow analysing the diversity and function of these communities, independent of cultivation. Directed towards specific taxonomic marker genes (e.g. small subunit ribosomal RNA; rRNA), metagenomic sequencing is frequently used to demonstrate and compare microbial community composition in different soils or to investigate effects of experimental treatment or environmental change. Ultimately, metagenomic shotgun sequencing approaches aim at analysing the total genomic content and at predictions of physiological functions. The advent of second generation sequencing technologies in the last few years has revealed a staggering microbial diversity and functional complexity. Advantages and limitations resulting from these technologies will be discussed.