

## Exploring taxonomic and functional diversity of forest soil fungi in central Italy by metagenomic analyses.

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Fungi have a fundamental role in biogeochemical cycles and are one of the major pools of living biomass in forest soil ecosystems. Besides their fundamental role in organic matter degradation and recycling, fungi represent an important source of ecosystem services. Fungal assemblages in forest environments are influenced by several factors such as climate, soil characteristics and interaction with host plants and other microorganisms such as bacteria and archaea. In turn, the fungi may influence plant health, stress response and can either act as pathogens or as a defense against pathogens. Furthermore, several fungi (especially macro-fungi) are harvested and/or cultivated as edible mushrooms and as species with medicinal or biotechnological applications (1). Moreover, composition of fungal macro- and micro-communities and their variation through the years may represent valid bioindicators to study the effect of climate changes on terrestrial environments (2). Fungal biodiversity studies are typically performed by long term surveys of fruit bodies production and their taxonomic characterization based on morphological and/or molecular techniques. More recently the development of next generation sequencing technologies has allowed performing studies based on DNA metabarcoding by analyzing target metabarcodes such as the ITS region of rDNA, or by shotgun metagenomic sequencing. Several studies revealed that the fungal species producing fruit bodies or those that are culturable in vitro represent only a small fraction of the total biodiversity. Thus sequence-based studies have been revealed much more informative in disclosing the true species diversity. Metagenomics has revealed also a great potential for bioprospecting new enzymes and bioactive molecules directly from sequencing, without the necessity of isolation (3). Here, we analyze the taxonomic and functional diversity of fungal and bacterial communities present in two representative forest biomes in central Italy: beech forests (*Fagus sylvatica*) and oak forests (*Quercus cerris*). Ion Torrent PGM technology was used to sequence metabarcoding libraries based on ITS and 16S markers for fungi and bacteria, respectively. Functional diversity was also assessed by performing shotgun metagenome sequencing of total soil DNA using the Oxford Nanopore Minion technology. The main aims of this work were to study the fungal taxonomic and functional diversity in forest ecosystems of central Italy and find correlations between fungal and bacterial assemblages. Metagenomic sequence data were also explored to retrieve fungal and bacterial sequences of potential biotechnological interest such as lectins, cellulases, lipases.

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