



Long lasting effects of the conversion from natural forest to poplar plantation on soil microbial communities



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ABSTRACT

In this study, we evaluate the long-lasting effects on soil microbial communities of a change within a single land-use category, specifically the conversion from natural forest to forest plantation. To minimize the effects of impacts other than land-use (i.e., climatic and anthropogenic), we chose three sites within a Natural Park, with homogeneous orographic and soil texture characteristics. We compared microbial diversity in a total of 156 soil samples from two natural mixed forests and a similar forest converted to poplar plantation about thirty years ago. The diversity and structure of bacterial and fungal communities were investigated by terminal restriction fragments length polymorphism (T-RFLP) analysis of the 16S-rRNA gene and the ITS-rDNA regions, respectively. Bacterial and fungal communities from the forest plantation, compared to those from natural forest soils, showed different community structure and lower α -diversity values, consistently with the significantly higher pH values and lower organic matter content of those soils. β -diversity values, the number of measured and estimated dominant OTUs, and their distribution among the three sites showed that microbial communities from the two natural forests were much more similar to each other than they were to communities from the poplar plantation, suggesting an effect of the forest conversion on the composition and diversity of soil microbial communities. α -diversity in cultivated forest soils had narrower temporal fluctuations than in natural forest soils, suggesting higher temporal stability of microbial communities. Overall, we demonstrated that the conversion from natural forest to forest plantation altered soil microbial communities, changing their structure, lowering their diversity, and causing a spatial and temporal homogenization.

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1. Introduction

Soil microbial communities are a key component of the forest ecosystem; they are involved in fundamental processes, like decomposition and nutrient cycling, and perform a link role between plants and ecosystem functions (Zak et al., 2003; Van der Heijden et al., 2008; Bardgett and Wardle 2010). The influence of the tree type on microbial community structure and function was supported by a number of different reports (Myers et al., 2001; Hackl et al., 2004; Bastias et al., 2007; Schweitzer et al., 2008; Berg and Smalla 2009; Wubet et al., 2012; Wang et al., 2013). In turn, belowground-living microorganisms have been demonstrated to influence, directly or indirectly, the productivity, diversity and composition of plant communities (Van der Heijden et al., 2008; Wagg et al., 2011).

With 200 million ha (10 million of which in Italy), forests represent the major natural vegetation cover in West Europe (31.5% of the land area, 5% of the world's forests); a quarter of these forests are of the mixed type. Despite a positive reforestation trend, risks for European forest health and vitality seem on the increase, mainly due to anthropic impact (MCPFE, 2007). Despite the fundamental issue of nature conservation and biodiversity preservation of forest sites and the recognized important role that microbial communities play in the functioning of forestry ecosystems, very few studies have investigated the effects on microbial diversity of forest management and forest conversion in a preserved natural environment (Nacke et al., 2011). Recently, the deforestation of Amazon rainforests (Da C Jesus et al., 2009; Rodrigues et al., 2013) or of pristine forests in the Pampa biome (Suleiman et al., 2013) to obtain pasture sites has been reported to alter microbial diversity and community structure of soil microorganisms. Far less attention has been spent on the effect that a change within a single land-use category, such as the conversion from natural forest to planted forest, have on soil microbial communities; with the result that this special case

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of forest land-use change is still poorly understood (Nacke et al., 2011), especially with respect to fungi. Very recently, two studies reported that conversion from natural forest to plantation forest, in the Pampa biome (Lupatini et al., 2013) and in Southeast Asian tropical forest (McGuire et al., 2014), alter the below-ground ecosystem, and ultimately affect the microbial communities resident in the soil. The conversion of natural forests to oil palm plantation is reported to affect the composition of both bacterial and fungal communities (Lee-Cruz et al., 2013; Kerfahi et al., 2014). As plantation forests in the world accounted for around 7% of global forest cover, and are projected to continue to increase in the foreseeable future; a wealth of soil microbial diversity, as well as the enormous and still untapped pool of biological resources they constitute, could be at risk; especially in hot spot of plant diversity, such as the Mediterranean area (Myers et al., 2001).

The main objective of the present work was to study the effects that a change within a single category of soil land-use, specifically a long-term (about 30 years old) conversion from natural mixed forest to poplar plantation, had on soil inhabiting microbial communities. Due to the long time since the conversion took place, we expect to detect long lasting, and almost permanent, effects. With this aim, the structure, and α -diversity (inside each study site) and β -diversity (between different study sites) of bacterial and fungal communities from the soil of a converted poplar plantation and two natural forests were compared. The three forest sites were located within a natural park (Migliarino–San Rossore–Massaciuccoli Regional Park, Tuscany, Italy), not far from each other, in a climatic, orographic and soil texture homogeneous landscape. In this way natural and anthropic effects, other than those linked to the conversion, were minimized. To characterize microbial communities, we used a cost-effective and rapid technique of DNA fingerprinting, the terminal restriction fragment length polymorphism (T-RFLP) analysis. T-RFLP has been widely used for studying microbial community structure and dynamics (Osborn et al., 2000), and has been recently re-evaluated for the estimation of microbial community diversity (Van Dorst et al., 2014). Secondly, the relationships that microbial community structure and diversity had with the physicochemical properties of the soils and with seasonality was analyzed to recognize the contribution that other factors had beyond land-use conversion.

2. Materials and methods

2.1. Site description and soil sampling

The study area is located inside the Migliarino–San Rossore–Massaciuccoli Regional Park (latitude 43°35′–43°51′,

longitude 10°15′–10°22′, approximately; mean altitude 4 m), which ranges along the Tyrrhenian Sea between the cities of Viareggio and Livorno (Tuscany, Italy), and belongs to the Mediterranean climate type. The study was conducted in three different field sites within the Park (Table 1). Sites 1 (an approximately 7000 m² large meso-hygrophilic/hygrophilic deciduous forest) and site 3 (an approximately 118,000 m² meso-hygrophilic deciduous forest) were old natural mixed-deciduous forests that until mid-1970's were subjected to controlled logging, after that they were left undisturbed. Site 1 and 3 are 8300 m apart each other, in the north and south of the Park, respectively. Site 2 (a 28,000 m² planted forest) was a mature 15 years old (in 2010) poplar plantation never subject to any agricultural practice; it is 325 m apart from site 1 toward north. Site 2 was originally a natural hygrophilic mixed-deciduous forest, converted to poplar plantation; aerial photos of this site (including also site 1) placed the first establishment of a poplar plantation between 1978 and 1982 (Fig. 1). Plants in the three sites were identified and georeferenced. Individual soil samples were seasonally collected from georeferenced trees, using a bulb planter (10 cm wide × 15 cm depth), at about 20 cm from the trunk; for each tree, samples at different seasons were collected at spots not disturbed by previous sampling activities. A total of 156 soil samples were collected from soils associated with different trees: seven natural poplars (5 *Populus alba* and 2 *Populus canescens*) in site 1, from Autumn 2010 to Summer 2012; four cultivated poplars (hybrid Triplo clone *Populus nigra* × *Populus deltoids*) in site 2, from Spring 2011 to Summer 2012; and eleven maples (*Acer campestre*) in site 3, from Winter 2011 to Summer 2012. Individual soil samples were placed separately in sterile plastic bags and immediately stored at 5 °C; the same day the samples were brought to the lab. Each individual sample was sequentially sieved through 5 mm and 2 mm pores size stainless steel sieves. The sieved soil from each sample was split into four aliquots that were stored at 4 °C, for total microbial counts, moisture content, pH determination and loss on ignition measure; a further aliquot was stored at –80 °C for molecular analysis.

Rain and air temperature values, measured by two meteorological stations placed as part of the LIFE08 NAT/IT/00342-DEMETRA project, have been averaged over a 7 days period before the sampling dates.

2.2. Analysis of soil chemistry

Sampling sites were classified as follow: site 1, Humic Eutrudepts, coarse sand, mixed, thermic; site 2, coarse sand, mixed, thermic; site 3, Fragic Hapludalfs, fine, mixed, thermic. Data for site

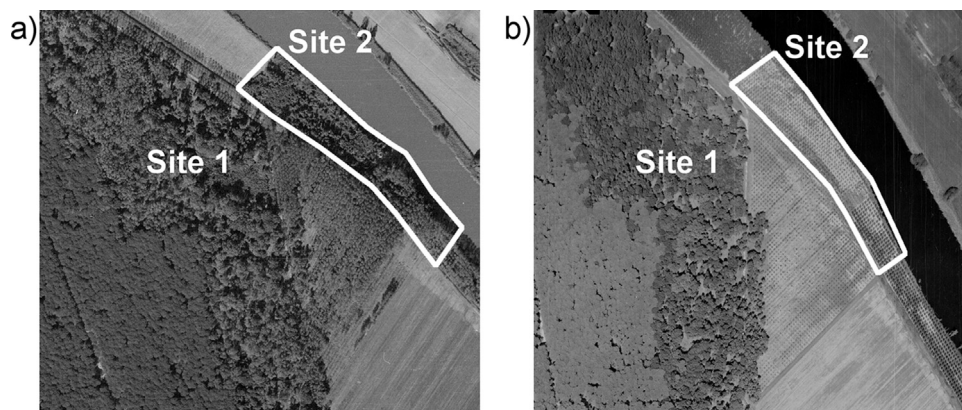


Fig. 1. Aerial photography, executed by Rossi–Brescia (Italy), of Site 2 in (a) 1978 (folder c0117, swipe 29, frame 412), and (b) 1982 (folder c0233, swipe 3a, frame 335). Images Courtesy of the General Cartographic archive of the Tuscany Region.

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