



Effects of land use change on the composition of soil microbial communities in a managed subtropical forest



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ABSTRACT

Soil microbial communities play vital roles in nutrient cycling and ecosystem functioning but these communities could be affected by land use change. To understand the impacts of land use change on soil microbial communities, we assessed the relative abundance of soil microbial communities and soil physicochemical properties following stand conversion from native broadleaf forests to mixed and bamboo forests in Feng yang Mountain Nature Reserve, China. We used phospholipid fatty acid (PLFA) profiling analysis to determine the composition of microbial communities, quantified soil bulk density, pH, organic carbon, nitrogen, and phosphorus concentrations to determine soil physicochemical properties, and assessed species richness and evenness to determine vegetation structure. We found that the abundance of anaerobic bacteria was significantly higher in the bamboo forests than in broad-leaved or mixed forests, while the abundance of 16:1 ω5c was significantly lower in the mixed forests than other forests. The relative abundance of 16:1 ω5c was positively correlated with soil pH, while the abundance of anaerobic bacteria was negatively correlated with soil phosphorus concentration. Among the three different land use types, bamboo forest was characterized by significantly higher soil pH, while the broad-leaved forest had significantly higher nitrogen concentration, and mixed forest had significantly higher soil bulk density. Overall, the composition of microbial communities in native broad-leaved forest was distinct from converted forests in the relative abundance of anaerobic bacteria and 16:1 ω5c, underscoring the fact that land use change can have a profound impact on soil microbial composition.

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1. Introduction

Soil microbial communities play important roles in regulating soil nutrients and ecosystem processes that are critical for the growth and maintenance of plants (Simpson et al., 2007; Chaparro et al., 2012). However, composition and diversity of these communities are largely governed by soil environmental conditions, especially by soil physicochemical factors (Bass Becking, 1934). In the human-dominated landscapes, land use is a major determinant of soil environmental conditions, and as such, land use is a major driver of soil microbial communities (Bardgett and van der Putten, 2014; Lange et al., 2015). Deeper understanding of such change in microbial community structure in relation to land use change would greatly benefit land management or restoration.

Earlier studies, focused mainly on intensive land use such as agriculture, suggest that land use history or time elapsed since alternative land use shape the composition of microbial communities. Buckley and Schmidt (2001), for example, found striking similarity in microbial community structure for sites abandoned from agriculture 45 years ago versus sites still undergoing agriculture. Jangid et al. (2011) examined the effects of land use change in terms of cropland to native forest, or to mowed grasslands and found confirmatory evidence suggesting that land use history is a major determinant of microbial community composition, for both short (~17 years) and long-term (>50 years) settings and found significant changes in bacterial abundance due to conversion of tilled cropland to grasslands. Both of these studies, however, focused on intensive land use i.e. agriculture and tillage cropping, where soil nutrients are heavily deplete (Buckley and Schmidt, 2001), and land use history appeared to maintain its legacy effects on microbial community. In contrast, Krashevskaya et al. (2015) compared the short term (~13 years) consequences of land use change in terms of conversion of rainforests into rubber plantation and

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found significant decrease of bacterial abundance and an increase of arbuscular mycorrhizal fungi. However, it is still unclear whether such difference in microbial community structure associated with forest conversion, which is a modest form of land use, would still persist in the long term. This understanding is particularly important because conversion of natural forest to plantation forestry or to other forests is a common practice in the subtropics, with potential consequences for the microbial communities and ecosystem processes, including forest production.

Natural evergreen forest *versus* plantation forestry such as mixed species plantation or bamboo forests are examples of different types of land use in the subtropics. The quantity and quality of leaf-litters produced by a broadleaf forest is typically higher than a coniferous (Barbier et al., 2008), or a bamboo forest. Needles produced by conifer species have a lower decomposition rate than leaves produced by broad-leaved species (Prescott et al., 2000). In addition, near ground light regimes are expected to vary among broad-leaved, mixed or bamboo forest: a broadleaf forest will permit high level of light penetration through its canopy, while a mixed forest would permit slightly lower, and a bamboo forest would permit the lowest amount of light/solar radiation penetration through canopy. Together, soil physicochemical properties and light/temperature environment and in turn the composition of microbial communities are expected to vary between land use types. As a result, composition of soil microbial communities is expected to vary among broad-leaved, mixed- and bamboo forest.

Feng yang Mountain Nature Reserve, China offers an ideal setting to test the effects of alternative subtropical forest land uses on microbial community composition. The reserve was initially a broad-leaved evergreen forest, later sections of the reserve were converted to mixed plantations and bamboo forests only for a brief period of time (less than three years), and immediately after the conversion, the reserve enjoyed protection against any further disturbances. We studied the composition of microbial community ~40 years after forest conversion and pursued three questions: (i) Do microbial compositions vary between three different land use types? (ii) Do soil physicochemical characteristics and overstory vegetation characteristics vary between these land use types? (iii) Can we explain any variation in microbial composition through the variations in soil physicochemical and overstory vegetation characteristics? We anticipated that soil fungal composition would vary between land use types, as fungal communities are sensitive to long-term land use (Yu et al., 2013), and any such difference can be explained by differences in soil physicochemical properties especially, soil pH and carbon, nitrogen and phosphorus concentrations.

2. Materials and methods

2.1. Study area

This study was conducted at the Feng yang Mountain Nature Reserve, China (longitude: 119°06′–119°15′E, latitude: 27°46′–27°58′N). The reserve is located at an elevation of 600–1929 m a.s.l. and is characterized by a subtropical humid climate, with an annual mean temperature of 12.3 °C and annual rainfall of

approximately 2400 mm. Historically, the reserve was an evergreen broad-leaved forest, dominated by *Camellia japonica* Linn., *Cyclobalanopsis glauca* (Thunberg) Oersted, *Eurya japonica* Thunb., and *Rhododendron simsii* Planch. But in the year 1971, sections of the native evergreen broadleaf forest were converted into mixed forests by introducing conifer species *Pinus taiwanensis* Hayata. In parallel, and at a similar time frame, other sections of the native forest were converted into bamboo forest, or to tea garden. In 1975, the entire area was declared as nature reserve, and since then, has been protected against further land use change or anthropogenic disturbances, and the composition has not returned to pre-conversion communities. Currently, this reserve represents sections of different land uses including the native evergreen broad-leaved forest, the mixed forest, and the bamboo forest. An overview of general vegetation composition of the study area is presented in Table 1.

2.2. Sampling

In September 2013, stands from three different land uses (the native evergreen broad-leaved forest, the mixed forest and the bamboo forest) were randomly selected for this study. Each type of land use was replicated at five stands, for a total of 15 stands. Selected stands were well-drained, flat slope (slope less than 5%) and mesic.

In each stand, a 20 × 20 m² plot was established to assess the composition of soil microbial communities, together with soil physicochemical properties and overstory vegetation. First, for overstory vegetation, all trees >2 cm in diameter at breast height (DBH, 1.3 m above root collar) were identified up to species, and their height and DBH were recorded. This plot-level data are then represented as richness (*S*), defined as the number of species present in each sampling plot (Magurran, 2013), and evenness (*J*), defined as the relative dominance of individual species within a sampling plot, and quantified as:

$$J = -\left(\sum_{i=1}^S P_i \times \ln P_i\right) / \ln S \quad (1)$$

where *P_i* is the proportion of the individuals (No. of stems) of *i*th tree species in the plot, *S* is the tree richness index in the plot (Whittaker, 1972).

For soil microbial community and physicochemical properties, four separate sampling points were selected within each 20 m × 20 m plot, but ensured at least 8 m apart from each other. From each point, we first removed fallen leaf-litter, and then collected two soil samples for phospholipid fatty acid (PLFA) profile and physicochemical properties analysis (except for soil bulk density) using a sharp knife and a trowel at three different depths: 0–10, 10–20, 20–30 cm. At each sampling plot, 12 samples from four points and three depths were mixed to one sample and later assessed for phospholipid fatty acid (PLFA) profile. For physicochemical properties analysis, samples were stored without mixing resulted in 12 samples for each sampling plot. For soil bulk density analysis, we carefully extracted soil samples by using a metal corer (diameter: 5.5 cm, height: 5 cm) from four points and three depths (Laganriere et al., 2013b).

Table 1
Forest characteristics of stand samples.

Land use type	Stand age (years)	Density (stems/ha) ^a	Main species and composition (%) (mean and 1 SD)
Evergreen broad-leaved forest	Old-growth	2180 (487)	<i>Adinandra glischrol</i> [13 (1)], <i>Symplocos anomala</i> [15 (3)], <i>Schima superba</i> [4 (1)], and others [68 (11)]
Mixed forest	43	2260 (431)	<i>Pinus taiwanensis</i> [11 (1)], <i>Schima superba</i> [17 (2)], and others [72 (24)]
Bamboo forest	42	2160 (233)	<i>Pylostachys heterocycle</i> [75 (4)], <i>Schima superba</i> [5 (1)], and others [20 (2)]

^a Values in the parenthesis are standard deviations (SD).

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