



# Parent materials have stronger effects than land use types on microbial biomass, activity and diversity in red soil in subtropical China

Huan Deng<sup>a,b</sup>, Yong-Jie Yu<sup>a,b</sup>, Jin-E. Sun<sup>a,b</sup>, Jin-Bo Zhang<sup>a,b</sup>, Zu-Cong Cai<sup>a,b</sup>,  
Guang-Xia Guo<sup>c</sup>, Wen-Hui Zhong<sup>a,b,\*</sup>

<sup>a</sup> Jiangsu Provincial Key Laboratory of Materials Cycling and Pollution Control, School of Geography Science, Nanjing Normal University, Nanjing 210023, China

<sup>b</sup> Jiangsu Center for Collaborative Innovation in Geographical Information Resource Development and Application, Nanjing 210023, China

<sup>c</sup> Key Laboratory of Alpine Ecology and Biodiversity, Institute of Tibetan Plateau Research, Chinese Academy of Sciences, Beijing 100085, China

## ARTICLE INFO

### Article history:

Received 27 August 2014

Received in revised form 5 February 2015

Accepted 5 February 2015

### Keywords:

CLPP

PLFA

Redundancy analysis

Soil texture

## ABSTRACT

To examine the effect of parent materials and land use types on micro-organisms of red soil, we sampled soils from the combination of three land use types including coniferous forest, shrub and farmland, and three parent materials including granite, tertiary red sandstone and quaternary red earth. Soil microbial biomass and diversity was estimated using phospholipid fatty acids (PLFA) while microbial activity and functional diversity were determined using community level physiological profiles (CLPP) with Biolog® Eco-plates. In addition, a series of soil physicochemical properties were established. Results showed that parent materials explained a larger part of total variance of microbial biomass, activity and diversity than land use types, though both parent materials and land use types had a significant effect. The PLFA amount and microbial activity was highest in granite but lowest in quaternary red earth. Redundant analysis (RDA) showed that sand and clay content, which were determined by parent materials, significantly influenced both PLFAs and CLPP. Our study suggests that soil parent material may be a more important driver of soil microbial communities than land use type in the red soils of the region sampled here. Therefore, researchers should explicitly account for soil origin in studies seeking to understand the effects of land use on microbial community structure and function.

© 2015 Elsevier GmbH. All rights reserved.

## Introduction

Red soil (Ultisols and Oxisols in US Soil Taxonomy), one of the typical subtropical soils, is widely distributed in southern China. The red soil region covers about two million km<sup>2</sup> or 21% of China's land area, and supports 40% of the nation's population (Huang et al. 2012). However, mainly due to the wet climate and hilly landscape, red soils are heavily weathered and leached soils, and are characterized by low pH and deficiencies in available nutrients, particularly N and P (Zhong and Cai 2007). The nutrient limitation and acidic stress not only restrict the production of plants and crops, but also lead to relatively low microbial biomass, activity and diversity (Yin et al. 2014). The degradation of red soil has largely been due to

inappropriate practices such as deforestation (Zhang et al. 2010). As a result, it is urgent to find sustainable means to reduce red soil degradation and improve soil quality (Ma et al. 2014).

Land use types have significant influence on red soil quality. Since soil micro-organisms play a crucial role in nutrient cycling and are sensitive to environmental change, microbial properties including microbial biomass, activity and diversity have been widely used as diagnostic indicators to evaluate the effect of land use types on soil quality (Bending et al. 2004). Deng et al. (2010) studied the effect of vegetative restoration on microbial biomass and diversity of degraded red soil. Ying et al. (2013) compared the effect of restoration, degradation (logging), cropland, and pine plantation on soil microbial community by using DNA- and PLFA-based methods. Yin et al. (2014) evaluated soil microbial functional diversity of degraded red soil restored with different vegetation types. In these studies, the effect of land use type was attributed to soil physicochemical properties, which however, were not solely determined by land use types.

\* Corresponding author at: School of Geography Science, Nanjing Normal University, Nanjing 210023, China. +86 25 85891352.

E-mail address: [zhongwenhui@njnu.edu.cn](mailto:zhongwenhui@njnu.edu.cn) (W.-H. Zhong).

Parent materials largely affect the soil formation process and soil physicochemical properties (Miller and Donahue 1990) and have a dramatic influence on soil micro-organisms (Steven et al. 2013). In subtropical region of China, red soil is typically derived from quaternary red earth, tertiary red sandstone or granite (Zhao et al. 1988). Only a few studies have addressed the effect of parent materials on specific characteristics of red soil. Lou et al. (2004) studied CO<sub>2</sub> emission from soil, which was derived from granite, tertiary red sandstone and quaternary red clay. Results exhibited an emission order of granite > tertiary red sandstone > quaternary red clay. Xu and Cai (2007) showed that red soil denitrification capacity was significantly affected by parent materials and land use types. However, denitrification is a specific function and carried out by only a small group of micro-organisms. Thus, our knowledge about the effect of parent materials on soil microbial community and their functions in red soil is still limited. The severe degradation and relatively low microbial activity in the red soil region have been attributed to the rainy climate, hilly landscape and inappropriate land use, yet the significance of parent materials is seldom studied and little understood. Comparisons between the effect of parent materials and other factors, e.g. land use types, would help understand its significance.

Phospholipid fatty acids (PLFA) analysis has been widely accepted as a reliable method to evaluate the microbial community diversity and biomass (Deng et al. 2009). In addition, the relative amount of specific groups of micro-organisms can be addressed by their 'signature' PLFAs. Soil micro-organisms and their functions can be linked by community level physiological profile (CLPP), which was intensively employed to study soil microbial activity and functional diversity (Liu et al. 2010). Combining PLFA and CLPP methods was adequate to make an integrated evaluation of microbial community (Chodak and Niklińska 2010). In this study, soil samples were collected from three land use types including coniferous forest, shrub and farmland derived from three parent materials including granite, tertiary red sandstone and quaternary red earth. To minimize the effect of climate and landscape on the study, the sampling sites were selected in a plain with similar annual average temperature and precipitation. Because there is one sampling area for each parent material, researchers may argue that this type of experiment has pseudoreplication. However, the nature of landscape-scale studies precludes replications in the way they are constructed in lab experimentation. Concerns about pseudoreplication in ecological studies may cause 'unwarranted stigmatization of a reasonable way to test predictions referring to large-scale systems' (Oksanen 2001). Therefore, some studies on large-scale ecosystem have been carried out with pseudoreplication when true replication is not available under natural condition (Chauvat et al. 2007). Consequently, our experimental strategy allowed us to distinguish between the effect of parent materials and land use types, though we are aware of the possible bias caused by pseudoreplication. We hypothesize that parent materials may have a more profound effect than land use types on microbial biomass, activity and diversity of red soil through soil physicochemical properties. By using CLPP and PLFA methods, we aimed to determine the effects of parent materials and land use types on integrated microbial properties including microbial biomass, activity, community diversity and functional diversity.

## Materials and methods

### Site description and soil sampling

Sampling sites were located in Yingtan City (27°52'–28°17' N, 116°56'–117°30' E), Jiangxi Province, and a typical subtropical region of southern China (Fig. 1). The average annual temperature and precipitation of the city is 18.4 °C and 1785 mm, respectively.

Granite, quaternary red earth and tertiary red sandstone derived soil were mainly located at N 28° 18', E 117° 12'; N 28° 13', E 116° 49' and N 28° 4', E 116° 48', respectively. In sampling sites, the major land use types include natural secondary coniferous *Pinus massoniana* forest, shrub with diverse species dominated by *Lespedeza bicolor* and peanut (*Arachis hypogaea*) farmland that had been converted from bush forest that was clear-cut for at least thirty years.

### Soil sampling

Three sites where soil was derived from granite (Gran), quaternary red earth (Earth) or tertiary red sandstone (Sand) were selected for soil sampling in May 2009. Each site covers an area of more than 12 km<sup>2</sup>. The climate and landscape over the three sampling sites is nearly the same since the distance between sites is less than 51 km and the sites are located in a plain. The average annual temperature and precipitation between the three sites varied within 0.4 °C and 100 mm. In each site, soil was sampled from three land use types including a natural secondary coniferous forest (Conif), a shrub and a peanut farmland (Farm). As a result, there are nine soil groups combining three parent materials and three land use types, namely, Gran-Conif, Gran-Shrub, Gran-Farm, Earth-Conif, Earth-Shrub, Earth-Farm, Sand-Conif, Sand-Shrub and Sand-Farm. In each site, three plots with slopes less than 10° and a distance of more than 200 m between plots were selected to represent a soil group. In each plot, surface soil samples (0–20 cm) at three randomly selected points (0.5 m × 0.5 m) were collected and mixed to represent the plot. Therefore, a total of 27 soil samples were collected. Soil samples were sieved through a 2 mm diameter mesh, and subsequently either stored at 4 °C for less than two weeks before PLFA and CLPP measurements or air dried for physicochemical analysis. Prior to PLFA and CLPP analyses, the soil was adjusted to 50% of the maximum water holding capacity (WHC), which was determined using the gravimetric method (Allen 1989) and pre-incubated at room temperature for seven days.

### Soil physicochemical analysis

Soil chemical properties were analyzed according to Lu (2000). Briefly, soil pH was established using a pH glass electrode at a soil water ratio of 1:2.5 (w/v). Soil organic C was determined by dichromate oxidation and total N by Kjeldahl digestion; hydrolysable N by alkali-hydrolyzed diffusing method; total P by alkali-melting-molybdenum-blue method; available K by ammonium acetate extraction and atomic absorption spectrometry; soil total Al by atomic absorption spectrometry; cation exchange capacity (CEC) by saturation with ammonium acetate; soil texture by the sieve and pipette method.

### Community-level physiological profiles (CLPP)

CLPPs of soil microbial communities were assessed by using BIOLOG Eco-plates (Biolog Inc., Hayward, CA) according to Garland (1997). Ten grams of fresh soil samples was suspended in 100 ml of sterile phosphate buffer (0.05 M, pH 7.0) and shaken for 30 min. One milliliter of the soil suspension was then diluted tenfold in sterile phosphate buffer (0.05 M, pH 7.0). Subsequently, 150 μl of this dilution was added to each well of an Eco-plate. Plates were incubated at 25 °C and measured at 590 nm using an Emax precision micro plate reader (Biolog Inc., Hayward, CA) every 12 h for one week.

### Phospholipid fatty acid (PLFA) analysis

Soil microbial PLFA was determined with a modified Bligh-Dyer method (Bligh and Dyer 1959; Deng et al. 2009).

Download English Version:

<https://daneshyari.com/en/article/2061008>

Download Persian Version:

<https://daneshyari.com/article/2061008>

[Daneshyari.com](https://daneshyari.com)