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Original article

Effects of land-use conversion from paddy field to orchard farm on soil microbial genetic diversity and community structure

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ABSTRACT

Studies of the effects of land-use conversion on soil microbial genetic diversity and community structure may provide essential information for assessing the quality and sustainability of soil. Land-use conversion from paddy fields to orchard farms has occurred widely in southern China over the last two decades. To understand the effects of this conversion on soil microbial structure and diversity, which is an integral part of soil quality, a study was conducted on surface soils (0–15 cm), using combined methods of denaturing gradient gel electrophoresis (DGGE) and phospholipid fatty acid (PLFA) analyses. The results showed that after land-use conversion from paddy field to orchard farm, microbial biomass carbon and soil respiration rate decreased significantly ($P < 0.01$) alongside shifts in physical and chemical properties. Moreover, PLFA analysis indicated that the total amount of PLFAs declined significantly ($P < 0.01$), soil microbial community structure changed, and nutritional stress in microbial communities enhanced significantly ($P < 0.05$). Redundancy analysis (RDA) indicated that soil moisture, organic matter and nitrogen were the most important environmental factors in affecting microbial community structure ($p < 0.01$). Multivariate analyses of DGGE and PLFA data were in agreement with each other, indicating that shifts in soil microbial genetic diversity and community structure were primarily attributable to land-use conversion rather than orchard age. This study concludes that after the land-use conversion, certain soil physical and chemical properties deteriorated, nutritional stress was significantly exacerbated, and soil microbial quantity declined, however, a diverse microbial community could be achieved and maintained in paddy soil systems, hence it is suggested that land-use conversion from paddy field to orchard farm is not an effective way to maintain the microbial diversity and sustainability of soil.

1. Introduction

Paddy fields are the production bases of the World's most important staple food crop (rice), and they also comprise an important artificial wetland ecosystem, which may have great significance in regional ecological (e.g. hydrological, thermal, and biotic) balance and material circulation [1]. Approximately 50% of the World population and 65% of the Chinese population depend on rice as a staple food [2]. In Zhejiang Province of southern China, the area planted in rice has been gradually declining over the last two decades. For instance, the area planted in rice was approximately 0.89 million hectares in 2011, which represents a decrease of approximately 1.19 million hectares from the area planted in rice in 1997. Moreover, approximately 31.0 thousand hectares of paddy fields were converted to forests, orchard farms, mulberry gardens and tea gardens from 1997 to 2007 [3]. The main reasons for the land-use conversion from paddy fields to orchards were related to water shortage or to higher income by planting fruit trees.

Soil quality, a measure of the sustainability of land use and soil management practices, can be assessed through the measurement of soil physical, chemical and biological indicators [4]. Soil organisms contribute to the maintenance of soil quality by controlling the decomposition of plant and animal materials, biogeochemical cycling and the formation of soil structure [5]. Land-use conversion is a common and direct factor that affects soil quality [6]. Land-use conversion from paddy field to upland has led to declines in soil moisture, pH, organic carbon, nitrogen, microbial biomass and activity, as well as changes in soil structure, aeration and nutrient status [7–9], which has had important effects on soil microbial community structure [10,11].

The soil microbial community and its diversity, which are important bio-indicators of soil health and quality, can be affected by land-use conversions [12]. PLFA technique was a convenient way

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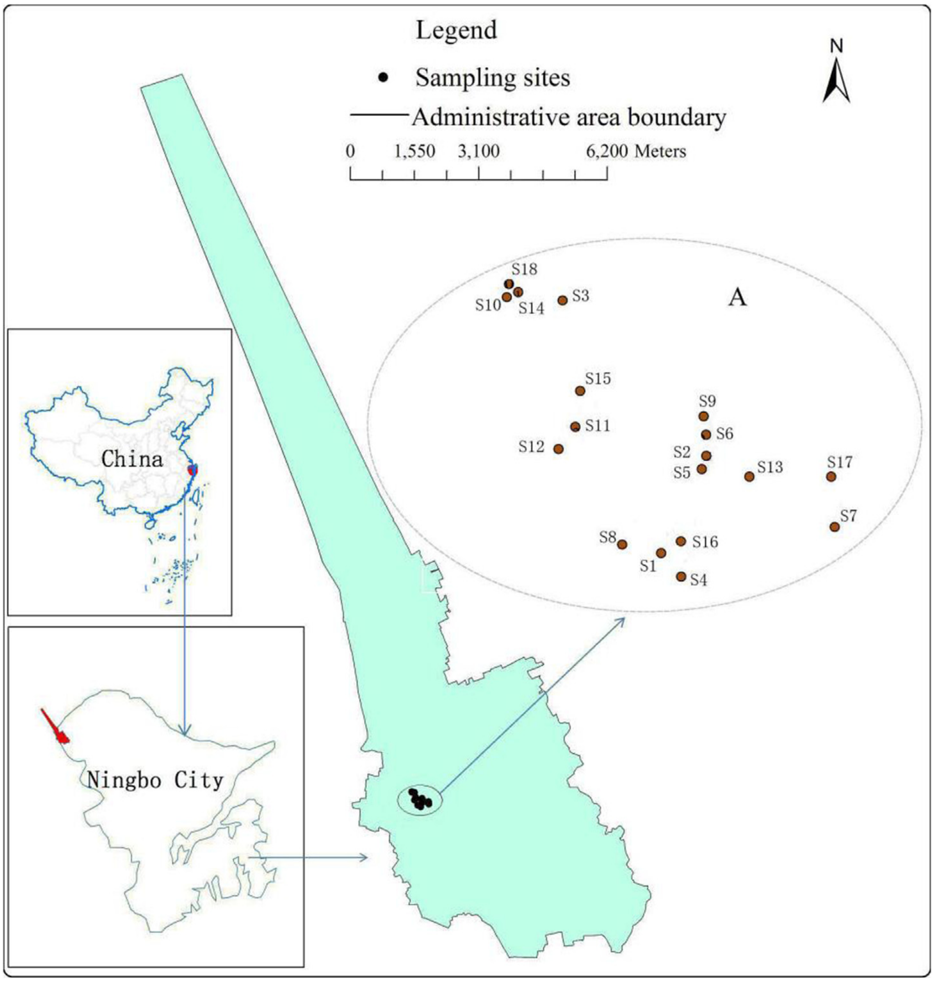

Fig. 1. Map showing the location of study area and sampling sites. The symbols of S1 to S18 represent 18 soil sample locations. The study area (zone A) covers approximately 25 ha, the major axis of the ellipse (zone A) is approximately 680 m long, and the minor axis is approximately 480 m long.

to assess soil microbial physiological, stress state and communities in response to land-use conversions [13–16]. In addition, McKinley et al. divided soil samples into groups according to their overall similarity of their PLFA profiles using redundancy analysis (RDA), and related the differences between the groups to environmental parameters and land uses [16]. However, the application of PLFA analysis to microbial classification at the species level has been limited. To overcome this limitation, PLFA studies have been complemented by nucleic acid analyses [17]. Muyzer et al. described the microbial genetic diversity in different samples and changes in microbial communities over time and space using DGGE analysis [18]. Subsequently, several studies successfully monitored pronounced shifts in the microbial diversity and community structure following land-use conversions in agricultural environments, using combined methods of PCR-DGGE and PLFA analyses [19,20]. In addition, Xue et al., using PLFA biomarkers and DGGE analyses in parallel, found that land-use conversion had a greater effect than tea garden age on microbial community structure [21].

Previous studies about the effects of land use on soil quality have primarily focused on differences in soil properties, however, with less focus on the response and dynamic shifts of soil microbial diversity in response to land-use conversion of paddy field into orchard farm over time. In this study, we compare typical paddy soils with a chronosequence of orchard soils that were converted from the paddy soils for various years. We hypothesized that land-use conversion from paddy fields to orchard farms and land-use history with their associated management may produce a unique soil environment, in which microbes with specific environmental requirements may be selected and supported. The purposes of this study were to gain insights into the changes in soil microbial genetic diversity and community structure in response to land-use conversion over time using a space-for-time substitution methodology, and to discuss the interactions between soil microorganisms and environmental factors. We hope to assess soil quality and nutrient status by monitoring the shifts of soil microbial genetic diversity and community structure, and to provide theoretical guidance for maintaining soil sustainability.

2. Materials and methods

2.1. Study area

The study site was located in Huangjiabu town, west of Ningbo city, in the Ningshao plain of Zhejiang province in southern China (Fig. 1). The study area covered 25 ha, and its geographic coordinates are 30°7′13″–30°7′25″ N and 120°56′25″–120°56′40″ E. The area is characterized by a subtropical wet monsoon climate with a mean annual temperature of 14 °C and a mean annual precipitation of approximately 1800 mm [22]. Physiognomy in the area is flat, and all studied soils originated from homogeneous