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Responses of microbial community structure to land-use conversion and fertilization in southern China

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ABSTRACT

A short-term experiment was carried out in southern China to investigate the effects of land-use conversion from rice paddies to vegetable fields and fertilization on soil microbial community structure by analyzing soil phospholipid fatty acid (PLFA) profiles. A split-plot design with four replicates was adopted, in which land use (paddy and vegetable field) was the first-level treatment and fertilization (conventional fertilization and no fertilization) was nested as the second level. Our results showed that both land-use conversion and fertilization had significant effects on microbial community structure. After 2 years of land-use conversion, the total amount of PLFAs were 3.54 and 2.97 nmol g^{-1} for fertilized (V–F) and unfertilized (V–NF) vegetable fields, respectively, and 3.19 and 2.32 nmol g^{-1} for fertilized (R–F) and unfertilized (R–NF) rice paddies, respectively. Soil fungal PLFAs were 1.04 and 0.87 nmol g^{-1} for V–F and V–NF, respectively, which were significantly increased by 13.9 and 11.4 times compared with those of R–F and R–NF, respectively. The ratio of fungal to bacterial PLFAs significantly increased in vegetable fields compared with rice paddies. No significant differences were found in the total, bacterial, and actinomycetic PLFAs between vegetable fields and rice paddies. The application of fertilizer significantly increased the amount of total PLFAs and bacterial PLFAs. With land-use conversion and fertilization, soil physicochemical properties also changed, and microbial community structure showed a significant relationship with soil water content, NH_4^+-N, and pH, which explained the land-use conversion and fertilization effects on soil microbial community composition.

1. Introduction

Soil microorganisms play a unique role in the processes of nutrient cycling [1], carbon and nitrogen turnover [2,3], and greenhouse gas emissions [4]. Agricultural management practices, such as cropping rotation, irrigation, and fertilization are known to have significant effects on microbial community structure in soils [5–9], which thereby influence the overall agroecosystem functions [10–12]. Land-use conversion, such as the conversion of rice paddies to uplands or vice versa, can significantly affect soil microbial communities [13,14]. Bossio et al. [15] found that flooded paddy soils had higher abundance of branched fatty acids, lower abundance of monounsaturated fatty acids, and lower abundance of fungi and actinomycetes than upland tomato fields. Sun et al. [16] found that land-use change from paddy to vegetables decreased bacterial diversity and soil microbial biomass despite an increase in the abundance of culturable microorganisms.

Although previous studies have reported that land-use conversion could alter soil microbial communities [17,18], the mechanisms of the effects of land-use conversion on soil microbial communities are poorly understood. It is commonly believed that the land-use-conversion-induced changes in soil physical and chemical properties result in the transformation of soil microbial communities, but no consistent relationships have been observed among various

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studies. Soil water content has been shown to influence soil microbial communities directly and indirectly through impacts on soil aeration and nutrient availability [19]. Yang et al. [20] found that total phospholipid fatty acids (PLFAs) decreased significantly after land-use change from paddy to orchard, and soil moisture, organic matter, and nitrogen (N) were found to be the most important environmental factors affecting the variations in microbial community structure. Soil pH is another important factor that regulates soil microbial communities [21,22]. In the process of land-use conversion from paddy to upland, pH was one of the most important factors affecting soil microbial community structure [20].

Changes in fertilization often come with land-use change because different crops have different nutrient demands. The application of N fertilizer has been shown to have a significant influence on soil microbial community [23]. Yevdokimov et al. [24] found that N addition could increase the ratio of fungal to bacterial biomass and decrease the ratio of Gram-positive to Gram-negative bacteria using the PLFA technique. Li et al. [9] also found that the application of N fertilizer significantly increased soil microbial biomass, including bacteria, fungi, actinomycetes, Gram-positive bacteria, and Gram-negative bacteria. Fertilization can affect soil microbial communities through changing soil physicochemical properties. Fertilization changes the soil C/N ratio, which further affects the microbial community and the decomposition rate [25]. Fertilization has been shown to be one of the drivers of soil acidification [26,27] and could affect microbial community structure indirectly by changing soil pH [28].

In southern China, large areas of rice paddies have been converted to upland vegetable cultivation with the acceleration of urbanization and economic interests in the past decades. The vegetable cultivation area in China has grown from 3.5 to 17.9 million hectares, while the rice cultivation area has decreased from 33.3 to 26.5 million hectares since the 1980s [16]. Understanding the effects of land-use conversion on soil microbial communities is critical to elucidate the mechanisms and processes of greenhouse gas emissions and the potential for greenhouse gas management in China and beyond. And the influence of land-use conversion on soil conditions was undergoing a dynamic change. For example, Sun et al. [16] found that soil microbial community structure differed significantly between paddy and vegetable fields, and the soil microbial community structure of the new vegetable fields (10 years) was significantly different from that of the old vegetable fields (100 years). Thus, short-term, long-term and longer-term studies would give the findings a stronger underpinning. However, few studies have paid attention to the changes of microbial community structure in the early stage of land-use conversion. We hypothesize that two years of land-use conversion from paddy to vegetables and fertilization would significantly alter the soil microbial community structure and soil water content and pH could be important factors in shaping the soil microbial community structure. The current study used the PLFA method to examine: (1) the effects of land-use conversion from rice paddies to vegetable fields on soil microbial community structure; (2) the effects of fertilization on the soil microbial community structure; and (3) the environmental factors related to the changes in soil microbial community structure.

2. Materials and methods

2.1. Site description

The experimental fields were located at the Qianyanzhou Ecological Research Station (QYZ, 26°44′46″ N, 115°04′05″ E) in Jiangxi Province, southern China. The site is a typical, red soil hilly region with a subtropical monsoon climate. According to meteorological observations from 1989 to 2010 at QYZ, the mean air temperature is 18.0 °C with the coldest and warmest months in January and July, respectively. This area has abundant precipitation with an average annual precipitation of 1509.0 mm. Double cropping of paddy rice is the main cropping system in this area, but large areas of rice paddies have been converted to upland vegetable fields in past decades. Soil texture was sandy loam with 58% sand, 31% silt, and 11% clay. The topsoil (0–10 cm) has an organic carbon content of 9.40 g kg^{-1} and total N content of 1.00 g kg^{-1}. The soil pH was 4.99 and the bulk density was 1.30 g cm^{-3}.

2.2. Experimental design

The experimental fields had been continuously cultivating paddy rice for about 10 years. In July 2012, we converted a portion of the rice paddies to upland vegetable fields by draining the fields, with the remaining land continuing with rice cultivation. Each cropping system had two fertilization levels, e.g., conventional fertilization and no fertilization. Thus, the experiment included four treatments with four replicates in a split-plot design, in which the main plots were the cropping systems and each cropping system was split into subplots with and without fertilization. The treatments included vegetable fields with fertilization (V–F) and without fertilization (V–NF), and rice fields with fertilization (R–F) and without fertilization (R–NF). Each plot had an area of 120 m^2 (10 m × 12 m). In rice fields, rice was planted twice a year, with a fallow period in winter. In vegetable fields, vegetables were planted three times a year. The spacing was 17 cm × 25 cm for rice cultivation and 20 cm × 35 cm for vegetable cultivation. Compound fertilizer ($N:P_2O_5:K_2O$ = 15%:15%:15%) and urea were applied at a rate of 358 kg N ha^{-1} per year to the fertilized fields. The corresponding amount of phosphorus (P) and potassium (K) applied were 63 kg P ha^{-1} and 119 kg K ha^{-1} per year for paddy fields and 133 kg P ha^{-1} and 254 kg K ha^{-1} per year for vegetable fields, respectively. Conventional tillage was carried out at the beginning of each growing season.

2.3. Soil sampling

Soil samples were collected across the field at a depth of 0–20 cm using a corer device (diameter, 3 cm) in July 2014. In each plot, five soil cores were collected and pooled together as a composite sample. Composite samples were taken to the laboratory and plant residues and stones were removed from the soil samples. Each sample was sieved through 2-mm mesh and separated into three parts: one part was air dried for measurements of soil organic carbon (SOC), total N (TN), and pH, another part was preserved at −20 °C as fresh soil for measurements of soil NH_4^+-N and NO_3^--N, and the third part was freeze-dried and preserved at −80 °C for determination of PLFAs.

2.4. Soil property measurements

Soil water content was automatically recorded by an automatic data logging system through wireless technology. The soil NH_4^+-N and NO_3^--N were extracted from 20 g fresh soil with 1 mol L^{-1} KCL (soil:extract, 1:5) and analyzed using a flow-injection autoanalyzer ((CFA)-AA3, SEAL, Germany). Soil pH was measured at a soil:water ratio of 1:2.5 using a pH meter. SOC and TN were measured using a C/N analyzer (Elementar, Vario Max CN, Germany) with the combustion temperature of 900 °C.

2.5. PLFA analysis

PLFAs were analyzed using the method described by Bååth and Anderson [29]. Lipids were extracted from freeze-dried soil (8 g) in