



# Changes of anaerobic to aerobic conditions but not of crop type induced bulk soil microbial community variation in the initial conversion of paddy soils to drained soils



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## ABSTRACT

Soil microorganisms are the main drivers of all of the biochemical processes that occur in soils. Land-use conversion, a common occurrence driven by market economy, changes plant species and the associated management strategies, thus significantly influences soil microbial communities. However, few studies have been conducted to disentangle the effect of the alteration of plant species from that of soil environment during the initial years of conversion. In this study, the effect of land-use conversion from double rice cropping (RR) to maize-maize (MM) and soybean-peanut (SP) double cropping systems on soil physical and chemical properties and microbial communities was studied two years after the conversion in southern China. The results showed that land use conversion significantly changed the soil properties, microbial communities and microbial biomass. The soil water content decreased significantly by 26.3%, and the pH decreased by 0.50 and 0.52 for MM and SP, respectively, compared with RR. Soil inorganic N also decreased significantly by 55% after the conversion to drained fields. The total phospholipid fatty acids (PLFAs), and bacterial, G<sup>+</sup>, G<sup>−</sup> and actinomycetic PLFAs decreased significantly after the conversion. No significant differences were found in the soil properties, microbial communities and microbial biomass between the converted MM and SP. Our results indicated that the changes of anaerobic to aerobic conditions, rather than of crop type, induced the variations in the soil properties and microbial communities during the initial years after conversion from paddy soils to drained soils. In particular, soil pH was the key factor that regulated the variations in the soil microbial communities after conversion.

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## 1. Introduction

Soil is an important component of terrestrial ecosystems and plays a crucial role in plant productivity and ecosystem services. Soil microorganisms are involved in all of the biochemical processes that occur in soils, and play an important role in organic matter decomposition, nutrient transformation and cycling, and trace gas emission (Creamer et al., 2015). Land use conversion, particularly within cropland, is a common occurrence driven by market economy (Houghton et al., 1999). The alteration of land use changes plant species, the associated management strategies and disturbance intensity, and thus strongly influences soil physicochemical properties, soil microbial biomass and community composition (Bossio et al., 2005; Lauber et al., 2008; Nishimura et al., 2008; Wang et al., 2014). However, few studies have been conducted to identify the effects of the changes in plant species and in soil environment.

Previous studies have shown that shifts in the soil microbial community structure can be associated with changes in a number of soil properties, including the soil water content (Yang and Zhang, 2014; Yuan et al., 2015), the soil total phosphorus, available phosphorus (Sheng et al., 2013), NO<sub>3</sub>-N, and soil organic carbon contents, pH (Sheng et al., 2013; Yang and Zhang, 2014; Yuan et al., 2015), and so on. The different relationships between microbial communities and soil properties are mainly affected by land use type and land use history (Lisboa et al., 2014) and has been shown to be site-specific (Williams et al., 2013). The development of different plant species associated with land use conversion would have different influences on soil microbial communities in the rhizosphere, which depends on the differences in the quantity and quality of carbon resources different plant species produce (Sanon et al., 2009). It is crucial to differentiate the effects of plant species from soil environment for carbon and nitrogen cycle modeling and agriculture production management. However, there is conflicting evidence of plant influences on bulk soil across individual fields (Jangid et al., 2011).

Land use conversion results in dynamic changes in soil processes (Arevalo et al., 2011). For example, Alberti et al. (2010) showed that there was a net loss of carbon in terms of net biome production

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2 years after conversion from corn to alfalfa, but this difference decreased over the next few years (Robertson et al., 2000). Sun et al. (2011) suggest an initial increase in soil nutrients (SOC and total N) within 10 years after rice conversion to vegetables, followed by stability in the nutritional status during an extended period of vegetable cultivation between 10 and 100 years. Land use conversion can have significant and long-lasting effects on soil properties and microbial communities (Murty et al., 2002). Consequently, the understanding of the conversion effects at different timescales is important and urgently required. However, little research has been conducted to understand the effect on soil properties and microbial communities during the initial years after land conversion.

Rice is the second most important crop in the world after wheat and is the most important crop in China. The rice area in China accounts for approximately 19% of the global rice area and plays an important role in China's food security and agricultural production (Zhang et al., 2005). However, in recent years, a considerable quantity of rice fields has been converted to maize, soybean and vegetable fields due to water shortages and economic benefits (Nishimura et al., 2008; Sun et al., 2011; Yuan et al., 2016). For example, in the Huai river basin in northern China, the main crops approximately 20 years ago were winter wheat and lowland rice (in summer); however, farmers started replacing lowland rice with crops such as maize, soybean, and cotton because of increasing water shortages (Tong et al., 2003). However, few studies have been carried out to compare the soil properties and microbial community composition between double rice paddies and maize or soybean fields, especially for newly established drained fields. After land use conversion from a paddy to a drained field, the soil environment changes from anaerobic to aerobic; this significantly influences the soil water content and soil pH, which have profound effects on the soil microbial community (Wang et al., 2014). Moreover, converted drained fields have been planted to many different types of crops (Nishimura et al., 2008), which would also influence the soil microbial community. However, few studies have focused on converted crop types to determine how they influence the soil microbial community. It is important to distinguish between the effects of the changes of anaerobic to aerobic conditions and of crop type conversion on the soil microbial community to develop sustainable agriculture.

Accordingly, in this study, we compared the soil properties and microbial communities of double rice (RR) paddies and newly converted maize-maize (MM) or soybean-peanut (SP) fields. The objectives were 1) to identify the variation in the soil properties and soil microbial community structure 2 years after land conversion from RR to MM or SP; and 2) to compare the difference in soil properties and microbial community structure between MM and SP. We hypothesized that 1) recent conversion from paddy fields to drained fields would change the soil properties and microbial communities; 2) conversion to MM and SP would have similar effects on the soil microbial communities in the initial years after land conversion; and 3) pH is the main driver of the variation in the soil microbial communities.

## 2. Materials and methods

### 2.1. Site description

An experimental site was set up at the Qianyanzhou Ecological Station (26°44' N, 115°03' E) of the Chinese Academy of Sciences (CAS), located in Jiangxi Province, southern China. The site is a typical red soil, hilly region with a subtropical monsoon climate. The average annual temperature varies between 17.4 and 18.9 °C. Annual precipitation varies between 945 and 2144 mm, with 24%, 41%, 23% and 12% of the total precipitation occurring in the four respective quarters of the year. The soils (equivalent to Plinthudults in the US Soil Taxonomy) are predominantly sand and loam and were formed from alluvial fans of nearby rivers. The soils contain 53.4% sand, 37.8% silt and 8% clay. The topsoil (0–20 cm) has an organic content of 15.8 g kg<sup>-1</sup> and a total nitrogen

content of 1.35 g kg<sup>-1</sup>, and the soil pH was 5.35 and the bulk density was 1.30 g cm<sup>-3</sup> before land conversion.

### 2.2. Experimental design

The experimental fields were continuously cultivated with paddy rice for approximately 30 years. In April 2011, we converted a portion of the rice paddies to drained fields by draining the fields, and the remaining land continued to be cropped with rice. The treatments included 3 rotation systems, i.e., early rice-late rice-fallow (RR), maize-maize-fallow (MM) and soybean-peanut-fallow (SP). Each treatment had three replications and the experiment was designed as a randomized complete block. The plot area was 7.6 m × 6.3 m. In the drained fields, the crops were planted on beds that were 1.2 m wide and 7.6 m long, with a 0.3-m wide and 7.6-m long furrow between the beds. All crops had a broad range of fertilizer rate according to the local farmers' practices. To control other influencing factors except treatments, all of the plots received 120 kg N ha<sup>-1</sup>, 120 kg P<sub>2</sub>O<sub>5</sub> ha<sup>-1</sup> and 210 kg K<sub>2</sub>O ha<sup>-1</sup> in each growing season. The fertilizers used were urea (46% N), fused calcium/magnesium phosphate (13% P<sub>2</sub>O<sub>5</sub>), and potassium chloride (60% K<sub>2</sub>O). The fertilizer was broadcast for the rice and hole-applied for the other crops. Within a growing season, the crop varieties chosen had a similar planting date and growing period. Following the local farmers' practices, both of the early rice and late rice was transplanted at spacing of 20 × 17 cm. Forty percent of the total N was applied as a basal dressing during land preparation, and other remainder was top-dressed seven days after the rice was transplanted. Herbicide was applied in the third day after transplanting in each growing season and hand-weeding in the later growing stage. Maize was sowed with a spacing of 60 × 27 cm, and 40% of the total N was basal-dressed during land preparation and other remainder was top-dressed at the elongation stage. Soybean and peanut was sowed with a spacing of 30 × 20 cm, and 40% of the total N was applied as a basal dressing and other remainder was top-dressed at the fourth trifoliolate development stage. The phosphate and potassium chloride was applied before transplantation or sowing and incorporated during land preparation. The drained fields were sprayed with herbicide 2 days after seeding to prevent the emergence and growth of grass and hand-weeding after crop establishment.

### 2.3. Soil sampling and analysis

Soil samples were collected after crop harvest according to a systematic sampling design along S-shaped transects in July 2013. Five soil cores (0–20 cm) were collected from every plot, composited and mixed thoroughly. The mulch layer was removed before collecting the cores. Each soil sample was placed in a cooler plastic bag in the field and transported to the laboratory. The soil samples were passed through a 2-mm sieve, mixed and divided into three parts, i.e., for the determination of soil water content; immediate storage at –20 °C for phospholipid fatty acid (PLFA) and inorganic N (NH<sub>4</sub>-N and NO<sub>3</sub>-N) determination; and air-dried to determine pH and continued to pass through a 0.149-mm sieve for SOC and TN analyses.

### 2.4. Soil physical and chemical properties analysis

The soil water content was determined using gravimetric methods. The soil pH was determined in a 1:2.5 soil to water solution using a digital pH meter. The total organic carbon (SOC) and total soil nitrogen (TN) contents of the dried samples were measured using an elemental analyzer (Elementar, Vario-Max, Germany). The inorganic N (NO<sub>3</sub>-N and NH<sub>4</sub>-N) concentration was quantified colorimetrically using a flow injection autoanalyzer (AutoAnalyzer 3, Bran + Luebbe, Germany).

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