Responses of Soil Micro-Food Web to Land Use Change from Upland to Paddy Fields with Different Years of Rice Cultivation

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ABSTRACT

Land use changes affect belowground ecosystems. During the past few decades, land use in Northeast China has changed considerably, and the area of paddy fields has increased rapidly from upland. In this study, soil characteristics and soil biotic community in paddy fields with different years of rice cultivation were measured to examine the effects of land use change from upland to paddy fields on soil micro-food web. The upland maize fields were selected as control and the microbial community composition was characterized using phospholipid fatty acids (PLFAs) analysis. The microbial biomass (total PLFA), bacteria biomass, and fungi biomass were higher in the 20–40-year (late-stage) than 1–10-year (early-stage) paddy fields. The abundances of total nematodes and bacterivores were lower in the early-stage than late-stage paddy fields. The abundance of herbivores was the highest in the early-stage paddy fields but that of omnivore-predators was the highest in the late-stage paddy fields. Structural equation model indicated that soil food web was developed and structured after 20 years of paddy cultivation. Our results suggested that soil micro-food web may be a good indicator for soil development and stabilization of paddy fields following land use change.

Key Words: belowground ecosystem, microbial community composition, phospholipid fatty acids, soil nematodes, structural equation model

INTRODUCTION

Land use changes are one of the major global environmental change drivers, which can cause long-lasting and large-scale variations in land cover types, soil organic matter (SOM) turnover, and biogeochemical cycles (Wu *et al.*, 2003; Sheng *et al.*, 2013). A growing number of studies have investigated the impacts of land use changes on ecosystem processes (Wu *et al.*, 2003). Soil organisms are important components of agroecosystems, which are essential for nutrient cycling and offer multiple ecosystem services (Barrios, 2007). Land use changes can influence soil biota through the changes in nutrient availability and habitat loss (Doran and Zeiss, 2000). Insight into the soil communities and their relationships with soil abiotic characteristics is crucial to reveal structure and functioning of soil ecosystems following land use changes.

Land use change from upland (such as maize field, wheat field, and soybean field) to paddy fields is an important type of land use resulting from agricultural restructuring in China. Recently, a number of studies have focused on the changes of soil characteristics after initiating rice cultivation in the subtropical region of China (Li *et al.*, 2005; Zou *et al.*, 2011; Liu *et al.*, 2013). However, relatively little is known about the impact of land use change from upland to paddy fields on soil biota in temperate regions so far. In Heilongjiang Province, Northeast China, the reclamation area has sufficient water sources with great potential for rice production. Paddy fields are more productive and provide greater economic benefit to farmers than upland fields (Gao *et al.*, 1996). In the past few decades, vast areas cultivated with maize have been converted for rice cultivation (Gao *et al.*, 1996). This land use transition provides an opportunity to examine the responses of soil biota to these land use changes in temperate region.

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In this study we examined the structure and composition of soil micro-food webs, *i.e.*, microorganisms (bacteria and fungi), microbivores (protozoa and nematode), and predators (nematode), in the paddy fields with different years of rice cultivation. Maize fields were chosen as the control upland. Phospholipid fatty acids (PLFAs) analysis was used to investigate microbial community, which could reveal detailed information on soil microbial activities and community structure (Zhang *et al.*, 2005). The objectives of this study were to examine the responses of soil micro-food webs to land use change from upland to paddy fields with different years of rice cultivation, and to determine the relationship between soil biota and abiotic characteristics under these land use changes.

MATERIALS AND METHODS

Study area and experimental design

This study was conducted in Suihua, Heilongjiang Province of China ($46°49.64'$–$46°53.49'$ E, $127°5.48'$–$127°6.67'$ N). The study area was located in a continental temperate zone, with mean annual temperature of 2.4 °C, non-frost period of 120–140 d, and mean annual precipitation of 523 mm, more than 60% of which occurs from June to August. The soil is a black soil, classified as a Typic Hapludoll according to USDA Soil Taxonomy. Before the fields were used as paddy fields they had been planted with maize with a conventional tillage management for more than 100 years.

Six paddy plots with different years of rice cultivation were divided into two groups: the plots in use as paddy field for 1 to 10 years were classified as "early-stage" and those in use for 20 to 40 years were classified as "late-stage", with 3 replicate plots for each group. Maize plots were chosen as the control upland, which had been planted with maize with a conventional tillage management for more than 100 years. Area of each plot was at least 1 ha and the plots were located

less than 2 km apart. All plots were similar in soil type, topography level, climate, and irrigation and fertilizer use practices (except the control upland). Within each plot, 5 subplots were randomly selected. Soil samples were collected by scoop at 0–20 and 20–40 cm depths after the fall harvest in October 2012.

Analyses of soil samples

Soil inorganic N (NO_3^--N and NH_4^+-N) concentrations were measured using the methods of Robertson *et al.* (1999). Soil total N (TN) and total organic C (TOC) were determined using a FlashEA 1112 elemental analyzer (ThermoFinnigan, Italy). Soil pH was determined with a glass electrode in 1:2.5 (weight:volume) soil:water solution.

The microbial community composition was characterized using PLFAs analysis (Bossio and Scow, 1998; Briar *et al.*, 2011). All identified PLFAs (from C14 to C20) are listed in Table I.

Nematodes were extracted from 100-g soil samples (fresh weight) by a modified cotton-wool filter method (Liang *et al.*, 2009). The nematodes were identified to genus level and assigned to the following trophic groups characterized by feeding habits: bacterivores, fungivores, omnivores-predators, and herbivores (Yeates *et al.*, 1993; Ahmad and Jairajpuri, 2010). For diversity measurement of nematode, Shannon index (H') was used (Shannon and Weaver, 1949).

Statistical analysis

Linear mixed model was used to examine the differences in nematode and microbial community among different stages of paddy field with paddy field stage and soil depth as fixed factors and sampling plot as random factor. All subplots were used to fit the model. The model was fit by using nlme-R package. *P* values of < 0.05 were considered significant. Principal component analysis (PCA) was used to explore the composition of soil microbial and nematode communi-

TABLE I

Phospholipid fatty acids analysis for characterization of soil microbial community composition

Microbial community	Phospholipid fatty acids
Bacteria	14:0, 16:0, 17:0, 18:0, 20:0, i14:0, i15:0, a15:0, i16:0, i17:0, i17:1, a17:0, i15:1 G, cy19:0, cy17:0, 16:1ω7c, i17:1ω9c, i17:1 I, 17:1ω8c, 14:0 2OH, 16:1 2OH, 18:1ω7c[a]
Saprophytic fungi	18:2ω6,9c, 18:1ω9c[b]
Actinomycetes	10Me 17:0, 10Me 18:0[c]
Arbuscular mycorrhizal fungi	16:1ω5c[d]

[a] Aciego Pietri and Brookes (2009) and Bach *et al.* (2010).
[b] Bach *et al.* (2010) and Briar *et al.* (2011).
[c] Frostegård *et al.* (1993) and Joergensen and Potthoff (2005).
[d] McKinley *et al.* (2005) and Bach *et al.* (2010).