

RESEARCH ARTICLE

Effect of Different Vegetation Types on the Rhizosphere Soil Microbial Community Structure in the Loess Plateau of China

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Abstract

The Loess Plateau in China is one of the most eroded areas in the world. Accordingly, vegetation restoration has been implemented in this area over the past two decades to remedy the soil degradation problem. Understanding the microbial community structure is essential for the sustainability of ecosystems and for the reclamation of degraded arable land. This study aimed to determine the effect of different vegetation types on microbial processes and community structure in rhizosphere soils in the Loess Plateau. The six vegetation types were as follows: two natural grassland (*Artemisia capillaries* and *Heteropappus altaicus*), two artificial grassland (*Astragalus adsurgens* and *Panicum virgatum*), and two artificial shrubland (*Caragana korshinskii* and *Hippophae rhamnoides*) species. The microbial community structure and functional diversity were examined by analyzing the phospholipid fatty acids (PLFAs) and community-level physiological profiles. The results showed that rhizosphere soil sampled from the *H. altaicus* and *A. capillaries* plots had the highest values of microbial biomass C, average well color development of carbon resources, Gram-negative (G⁻) bacterial PLFA, bacterial PLFA, total PLFA, Shannon richness, and Shannon evenness, as well as the lowest metabolic quotient. Soil sampled from the *H. rhamnoides* plots had the highest metabolic quotient and Gram-positive (G⁺) bacterial PLFA, and soil sampled from the *A. adsurgens* and *A. capillaries* plots had the highest fungal PLFA and fungal:bacterial PLFA ratio. Correlation analysis indicated a significant positive relationship among the microbial biomass C, G⁻ bacterial PLFA, bacterial PLFA, and total PLFA. In conclusion, plant species under arid climatic conditions significantly affected the microbial community structure in rhizosphere soil. Among the studied plants, natural grassland species generated the most favorable microbial conditions.

Key words: soil microbial biomass, microbial community structure, PLFA, community-level physiological profiles, vegetation types

INTRODUCTION

Knowledge of natural variations in ecosystems is essential for the sustainability of ecosystems as well as for the reclamation of degraded arable land. Soil microorganisms contribute to soil quality and play

key roles in soil ecosystem processes, including nutrient cycling, organic matter decomposition, and bioremediation (Chen M M *et al.* 2007). Variations in soil microbial communities attributed to ecosystem management and global change can significantly affect the ecosystem balance (Bossio and Scow 1995). Soil microorganisms are closely related with

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their surroundings, rapidly responding to changes and environmental stresses. Thus, these microorganisms are used as sensitive indicators of soil stresses and of soil recovery (Winding *et al.* 2005).

Rhizosphere is defined as the soil adjacent to and influenced by plant roots; a zone of usually high microbial activity and clearly distinct from bulk soil in terms of nutrient availability, pH, and redox potential (Hinsinger *et al.* 2009). Plant roots release a high amount of exudates, such as sugars, amino acids, organic acids hormones, and enzymes (Grayston *et al.* 1997), most of which are available to the microbial community (Nguyen 2003). Consequently, numerous microorganisms are found in this zone. Many studies have investigated the microbial community structures in rhizospheres, ranging from a purely agricultural point of view to a more environmental perspective (Esperschütz *et al.* 2009; Hamer and Makeschin 2009). The most common methods of characterizing microbial communities in soil are the phospholipid fatty acid (PLFA) and community-level physiological profiles (CLPPs). For instance, Innes *et al.* (2004) assessed the effects of individual plant species on the microbial communities in rhizosphere soils of different fertility properties using a microcosm experiment in the semi-fertile temperate grasslands of northern England. A greenhouse pot experiment was conducted by Chen *et al.* (2007b) to investigate the influence of soil moisture content on the soil microbial community structure of white clover and ryegrass using PLFA and CLPP methods. Tschirko *et al.* (2004) quantified the effect of *Poa alpina* on the soil microbial community in a primary succession of alpine ecosystems, and determined whether these effects are controlled by the successional stage. The plant-specific growth of soil microbes can reportedly exert a positive or negative effect on a plant, thereby altering the relative performance of individual species within plant communities (Klironomos 2002).

The Loess Plateau in China, covering approximately 58×10^4 km², is known for its long agricultural history and serious soil erosion (Chen L D *et al.* 2007). Vegetation destruction resulting from long-term poor land use practices, such as deforestation, overgrazing, and over-reclamation, has accelerated soil erosion (Fu *et al.* 2009) and deteriorated the ecological

environment. In 1999, a project named Grain for Green was launched by the Chinese government to control soil erosion and improve land quality by converting large areas of sloping cropland to forestland and grassland in the loess hilly area of the Loess Plateau. These conversions have resulted in improved soil conditions, including physical properties (Zhu *et al.* 2010), nutrient status (Cao *et al.* 2008; Zhang *et al.* 2011a), and microbial properties (An *et al.* 2009; Zhang *et al.* 2012; Xiao *et al.* 2013). However, changes in soil microbial communities during the conversion of slope cropland to other land use in this region, particularly at the root-soil interface (rhizosphere) where microorganismal metabolic activities frequently develop, are rarely reported. Therefore, this study aimed to determine the effect of six revegetation types (two each of artificial shrublands, artificial grasslands, and natural grasslands) on the soil microbial communities in the Loess Plateau using PLFA profiles and CLPP analysis. We hypothesized that the vegetation type significantly affected the microbial community structure and functional diversity, and that soil sampled from the natural grassland plots had the highest PLFA biomass, microbial diversity, and functional diversity.

RESULTS

Soil microbial biomass C, basal respiration, and metabolic quotient

The content of microbial biomass C, basal respiration, metabolic quotient, and pH significantly differed among the vegetation types ($P < 0.05$, Table 1). The highest microbial biomass C was found in the soil of *Heteropappus altaicus* and *Artemisia capillaries*, followed by *Astragalus adsurgens*, *Panicum virgatum* and *Caragana Korshinskii* (Fig. 1-A). Similar basal respiration values were found for *C. korshinskii*, *A. adsurgens*, *P. virgatum*, and *H. altaicus* which were significantly higher than those for *Hippophae rhamnoides* and *A. capillaries* (Fig. 1-B). The maximum metabolic quotient was found in the rhizosphere soil of *P. virgatum*, followed by *C. korshinskii* and

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