



Effects of soil depth and plant–soil interaction on microbial community in temperate grasslands of northern China



Xiaodong Yao ^{a,b}, Naili Zhang ^c, Hui Zeng ^{a,b}, Wei Wang ^{a,*}

^a Department of Ecology, College of Urban and Environmental Sciences and Key Laboratory for Earth Surface Processes of the Ministry of Education, Peking University, Beijing 100871, China

^b Peking University Shenzhen Graduate School, Shenzhen University Town, Shenzhen 518055, China

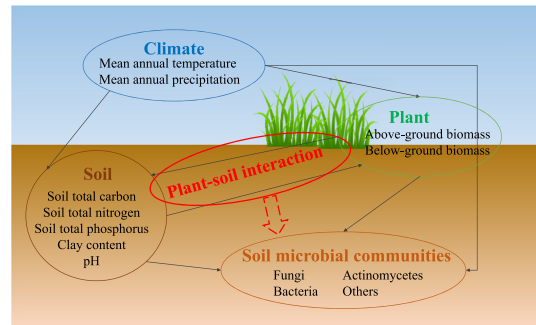
^c State Key Laboratory of Vegetation and Environmental Change, Institute of Botany, The Chinese Academy of Sciences, Beijing 100093, China

HIGHLIGHTS

- The dominance of fungi decreased with soil depth independent of steppe types.
- Plant–soil interaction on soil microbial distribution depends on soil depth.
- In- and external factors of the plant–soil system affects the interactive effect.

GRAPHICAL ABSTRACT

A significant plant–soil interaction effect only occurring at depths of 10–20 cm soil layer.



Variables (PC1)	10–20cm, R ² =0.90		
	Coef	SE	P > z
Soil			
Plant			
Climate	1.07	0.20	0.00
Soil × Plant	0.29	0.10	0.01
Soil × Climate	0.38	0.09	0.00
Σ _{main}	1.07		
Σ _{inter}	0.67		

➤ A significant plant–soil interaction effect only occurring at depths of 10–20 cm soil layer.

ARTICLE INFO

Article history:

Received 31 August 2017

Received in revised form 7 February 2018

Accepted 12 February 2018

Available online xxxx

Editor: Charlotte Poschenrieder

Keywords:

Plant and soil
Interactive effect
Soil depth
Regional scale
PLFA
Steppes

ABSTRACT

Although the patterns and drivers of soil microbial community composition are well studied, little is known about the effects of plant–soil interactions and soil depth on soil microbial distribution at a regional scale. We examined 195 soil samples from 13 sites along a climatic transect in the temperate grasslands of northern China to measure the composition and factors influencing soil microbial communities within a 1-m soil profile. Soil microbial community composition was measured using phospholipid fatty acids (PLFA) analysis. Fungi predominated in topsoil (0–10 cm) and bacteria and actinomycetes in deep soils (40–100 cm), independent of steppe types. This variation was explained by contemporary environmental factors (including above- and below-ground plant biomass, soil physicochemical and climatic factors) >58% in the 0–40 cm of soil depth, but <45% in deep soils. Interestingly, when we considered the interactive effects between plant traits (above ground biomass and root biomass) and soil factors (pH, clay content, and soil total carbon, nitrogen, phosphorous), we observed a significant interaction effect occurring at depths of 10–20 cm soil layer, due to different internal and external factors of the plant–soil system along the soil profile. These results improve understanding of the drivers of soil microbial community composition at regional scales.

© 2018 Elsevier B.V. All rights reserved.

* Corresponding author.

E-mail addresses: yaododo@pku.edu.cn (X. Yao), zhangnl@ibcas.ac.cn (N. Zhang), zengh@pkusz.edu.cn (H. Zeng), wangw@urban.pku.edu.cn (W. Wang).

1. Introduction

Understanding the complex patterns of biodiversity and community structure, and exploring their driving forces are important topics in community ecology (de Vries et al., 2012). Numerous studies have documented that soil microbial community performs important roles in regulating the carbon (C) and nitrogen (N) cycling (Schimel and Schaeffer, 2012; Waring et al., 2016; Zhou et al., 2012) and determining the responses of terrestrial ecosystems to environment changes (Bardgett et al., 2014; Singh et al., 2010). Thus, our knowledge of the patterns and drivers of soil microbial community composition is critical to better understand the important role and function of soil microorganisms in regulating ecosystem structure, process and functioning.

Soil microbes can modify the plant species diversity and productivity (van der Heijden et al., 2008) and greatly affect the maintenance of soil fertility (Leff et al., 2015). On the other hand, plant and soil properties also significantly affect soil microbial communities (de Vries et al., 2012; Fierer et al., 2009; Lange et al., 2014; Lloret et al., 2015). Previous studies have reported that plants can affect soil microbial community at regional scale (Chen et al., 2015; de Vries et al., 2012) by providing different quantity and quality of leaf litter and root inputs to soil microbial communities (De Deyn et al., 2008). However, abiotic factors (climate and soil variables) are considered as more important influential factors for predicting the soil microbial communities structure at regional scale (Chen et al., 2015; Hu et al., 2014; Fierer and Jackson, 2006; Lauber et al., 2009). There are some studies on the impact of integrated climate, soil and plant factors on the distribution of soil microbial communities (Chen et al., 2015; Hu et al., 2014). Surprisingly, few studies have considered the interactive effect of plant and abiotic factors on soil microbial community composition, and this will lead to our lack of comprehensive understanding of the role of microorganisms play in the ecosystem.

Plant and soil factors are closely interrelated (Ke et al., 2015; Van der Putten et al., 2013), and subsequently affect soil microbial communities. For instance, higher plant aboveground biomass (AB) is usually associated with higher soil organic carbon (SOC), which is caused by increased plant litter and C exudation into the rhizosphere (De Deyn et al., 2008). SOC significantly affects microbial communities, as it provides an integrated measure of the biotic and abiotic factors that control the microbial biomass pool size (Fierer et al., 2009). Chen et al., (2016) reported that while relatively little single effect was observed for the plant factors, a large overlap was observed with the soil factors, indicating that plant factors may indirectly affect microbial communities through soil factors. Although soil microbial communities may be strongly affected by the interactive effects of plants and soils, plant–soil interactions have seldom been considered in studying the drivers of soil microbial community distribution at a regional scale (Chen et al., 2015, 2016; Hu et al., 2014). Soil microbial communities may be rapidly able to respond to changes in plant–soil interactions (Herrera Paredes et al., 2016; Ke et al., 2015). However, the drivers of soil microbial community distributions are difficult to study because of the increased environmental complexity arising from the existence of the interactions between plants and soils (Ye and Sugihara, 2016). Therefore, there is a critical need to examine the role of the interactions between plant and soil factors in the composition of soil microbial communities.

Abiotic and biotic factors were observed to noticeably change with soil depth (Peng and Wang, 2016). The strong soil nutrient and environmental gradients observed within the soil profile might influence the abundance and composition of soil microbial communities (Chu et al., 2016; Delgado et al., 2012; Fierer et al., 2003; Šnajdr et al., 2008; Stone et al., 2014; Zhou et al., 2014). For instance, most of the soil nutrients in subsurface layer are lower than the surface (Jobbágy and Jackson, 2001). Lower soil nutrient availability may facilitate the growth of fungi over bacteria, as fungi possess a competitive advantage related to nitrogen and phosphorus absorption (van der Heijden et al., 2008). On the other hand, there are more plant materials input in the surface

soil, which leads to a higher proportion of recalcitrant organic matters in surface soil (Sanaullah et al., 2016). As fungi tend to decompose more complex organic matter, the fungal to bacteria (F/B) ratio decreases with depth (Struecker and Joergensen, 2015). These two different results considering the factors of soil nutrients and plant materials indicate that there are still some unclear mechanisms for the distribution of soil microbial community compositions at different soil depths. Thus, we should consider both soil and plant factors in order to gain a clear understanding of the patterns and drivers of soil microbial communities along the soil depth profile.

Here, our main aims were to assess the effects of soil–plant interactions and soil depth on soil microbial communities at a regional scale. The factors influencing the distribution of soil microbial community are quite different in different spatial scales (de Vries et al., 2012; Fierer et al., 2009; Griffiths et al., 2011; Lange et al., 2014; Lauber et al., 2009; Lloret et al., 2015). At the regional scale, both plant and soil factors were observed to significantly affect soil microbial communities (de Vries et al., 2012; Chen et al., 2015; Chen et al., 2016), which will help us to assess the impact of plant, soil and their interaction on soil microbial communities. We measured the phospholipid fatty acids (PLFAs) of soil microbial communities and the major influencing factors (plants, soils and climate) in a 1 m soil profile along a climate transect of temperate grassland in northern China. We hypothesized that (1) there are more plant materials input in the surface soil, which leads to a higher proportion of recalcitrant organic matters in surface soil (Sanaullah et al., 2016). Since fungi tend to decompose more complex organic matter, the dominance of fungi in the surface soil will be higher than the subsurface (Struecker and Joergensen, 2015). This pattern should be similar independent of steppe types, as all of the surface soil of meadow, typical and desert steppe contains more plant materials. (2) The plant and soil parameters would interact affecting the microbial communities (Herrera Paredes et al., 2016), but this interaction would depend on soil depth, since the internal and external factors in the plant–soil system differ between different soil layers (Nuccio et al., 2016; Wei et al., 2014; Zechmeister-Boltenstern et al., 2015; Zhong et al., 2016).

2. Materials and methods

2.1. Study area

Thirteen study sites with little human disturbance were selected in July 2013, covering three community types, including meadow steppe (4 sites), typical steppe (4 sites) and desert steppe (5 sites) along a climate transect in Inner Mongolia, China (38.98°–50.17°N, 107.97°–119.38°E, Supplementary Fig. S1). The meadow steppe is dominated by *Stipa baicalensis*, *S. grandis* and *Leymus chinensis*. The typical steppe is dominated by *S. krylovii*, *L. chinensis*, *S. grandis* and *Artemisia frigida*. The dominant plant species in desert steppe include *S. breviflora*, *Cleistogenes songorica* and *Neopallasia pectinate* (Peng and Wang, 2016). The mean annual temperature (MAT) ranges from −1.9 to 7.5 °C and mean annual precipitation (MAP) ranges from 198 to 433 mm along the desert, the typical and the meadow steppe. MAT and MAP data for our study sites were obtained from the closest meteorological stations. The soils were classified as chernozems in meadow steppe, castanozems in typical steppe and brown calcic soils in desert steppe based on the Chinese soil classification system. They were categorized respectively as chernozems, kastanozems and haplic calcisols according to the soil taxonomy system of the Food and Agriculture Organization (FAO) of the United Nation (Peng and Wang, 2016).

2.2. Sampling design

There were three soil pits (1 × 1 × 1 m) per site at a 10 m interval distance. Soil samples were collected from five soil depths (0–10 cm,

Download English Version:

<https://daneshyari.com/en/article/8860263>

Download Persian Version:

<https://daneshyari.com/article/8860263>

[Daneshyari.com](https://daneshyari.com)