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Soil erosion-related dynamics of soil bacterial communities and microbial respiration

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ABSTRACT

Soil erosion can dramatically change physicochemical soil properties, but little is known about the responses of bacterial communities and microbial respiration to soil erosion. In this study, three sites (upslope, mid-slope and downslope) with different erosional and depositional characteristics were selected along three transects of abandoned land in the Qiaozi watershed of the Chinese Loess Plateau to evaluate the impacts of soil erosion on bacterial communities and microbial respiration. Samples of the topsoil (0–10 cm) and subsoil (10–20 cm), classified as Calcic Cambisols, were collected from these sites. The results showed that lower bacterial abundance was observed in the topsoil of the downslope site (7.58×10^8 copies g^{-1} soil) relative to the upslope (9.32×10^8 copies g^{-1} soil) and mid-slope (8.70×10^8 copies g^{-1} soil) sites. However, no obvious change ($P > 0.05$) in the bacterial Shannon index and community composition was observed among the sites. Runoff-induced erosion and migration of sediment homogenized the bacterial communities along the eroded slopes. Soil microbial respiration in the topsoil of the downslope site (19.02 ± 0.25 mg CO_2-C kg^{-1} soil d^{-1}) was significantly ($P < 0.05$) higher than that of the upslope (15.12 ± 1.07 mg CO_2-C kg^{-1} soil d^{-1}) and mid-slope (17.75 ± 0.73 mg CO_2-C kg^{-1} soil d^{-1}) sites, indicating that the deposition of sediment and associated organic matter significantly increased the soil microbial respiration. Multiple stepwise regression analyses showed that available nitrogen was the main explanatory factor for the variation in soil microbial respiration in both the topsoil (60.2%, $P = 0.009$) and subsoil (80.3%, $P = 0.002$). Compared to the bacterial properties, the labile organic matter contributed more to the variation. Our work suggested that soil microbial respiration was primarily modulated by the quality of the organic matter.

1. Introduction

Soil erosion represents one of the main driving forces of soil carbon (C) dynamics (Li et al., 2016), and has elicited tremendous concern because it directly and indirectly contributes to the global C cycle (Park et al., 2014). The erosion process not only affects the spatial distribution of soil organic carbon (SOC) within a landscape but also influences the exchange of C between the soil and the atmosphere (Van Hemelryck et al., 2011). Over the past decade, the topic of the net impact of soil erosion on the global C cycle has been widely debated (Lal, 2005). On one hand, Lal and colleagues (Lal, 2005; Lal and Pimentel, 2008) declared that soil erosion is a source of atmospheric CO_2. On the other hand, Van Oost and other authors (Smith et al., 2005; Van Oost et al., 2008) argued that approximately 1 Gt C yr^{-1} might be sequestered through burial of SOC in the depositional environment.

To clarify the direction and magnitude of erosion-induced changes in the global C balance, the impact of soil erosion on the C dynamic has been widely investigated (Nie et al., 2014; Van Hemelryck et al., 2011). For example, Novara et al. (2016), through simulations, indicated that the transport of sediments along an eroded slope increases SOC mineralization by 43%. Based on indoor incubation experiment, Wei et al. (2016) reported that the CO_2 emission rate from the coarse aggregate fraction in a depositional site is significantly greater than that from the eroded site. Despite the fact that soil microorganisms represent a major

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component of the terrestrial biosphere, erosion-induced changes in soil microbial communities and the extent to which these changes are related to SOC dynamics have always been disregarded.

Soil microorganisms are sensitive to soil disturbances and play crucial roles in soil ecosystem functions by regulating the cycling of nutrient elements and the decomposition of organic matter (Hou et al., 2014). Most researchers consider the erosion process has a negative impact on microbial properties due to the reduction in soil nutrients, and indicate the mineralization of organic matter is mainly controlled by microbial community (Wei et al., 2016). In the study by Cleveland et al. (2014) and Xiao et al. (2017), the variation in soil microbial respiration was largely explained by the availability of labile organic matter. A systematic understanding of the relationships between microbial respiration and abiotic and biotic soil properties remains lacking due to the complicated interactions of physicochemical soil properties (e.g., pH, moisture and nutrient content), microbial community and respiration. Further understanding the responses of microorganisms to soil erosion and the links to SOC mineralization is very important for clarifying the mechanism governing soil C cycling. The goals of this study are to (i) investigate the response pattern of a bacterial community to soil erosion; (ii) explore the differences in soil microbial respiration between erosional and depositional sites; (iii) further evaluate the relationships between soil microbial respiration and abiotic and biotic soil properties.

Previous studies that focused on different land use types and vegetation patterns noted that an increase in soil nutrients was beneficial to the growth of soil microbes (Quideau et al., 2013; Six et al., 2006). Thus, in this study, our first hypothesis (H1) was that the bacterial abundance and diversity at the depositional site would be higher than the other sites due to the greater soil nutrient availability. In addition, our second hypothesis (H2) was that the deposition of sediments and associated organic matter resulted in an increase in the soil microbial respiration. To test our hypotheses, high-throughput sequencing was applied to intuitively discern the changes in the soil bacterial community. Furthermore, the radionuclide cesium-137 (^{137}Cs) was used to estimate the rates of soil erosion and deposition.

2. Materials and methods

2.1. Experimental sites

The study was located in the Qiaozi watershed (coordinates 34°36′-34°37′N, 105°42′-105°43′E) in the hilly-gully region of the Loess Plateau, situated in the vicinity of Tianshui, Gansu Province, China (Fig. 1). The climate is semi-arid, with a mean annual precipitation of 496–628 mm and a mean annual temperature of 10.7 °C. The main soil type is black cinnamonic soil (Calcic Cambisol, FAO), which is silty in texture (9% sand, 71% silt and 20% clay) and weakly resistant to erosion. Three transects were selected on a southern slope of the watershed. The transects were close to each other, with the distances between any two transects varying from 0.5 to 1 km. Along the slope, three sites (an upslope site, UP; mid-slope site, MP; and a downslope site, DP) were selected for each of the three transects at equal intervals of 20 m (Fig. 2). The slope gradient at the UP, MP and DP sites were 9.60 ± 1.21°, 11.53 ± 2.37 °, 5.65 ± 1.10 °, respectively. The land type of the three transects was abandoned land. The main crop grown on the land prior to abandonment was maize (*Zea mays L.*), and the dominated plants after 11 years of natural succession were *Heteropappus altaicus* and *Artemisia capillaries*.

2.2. Soil sampling and treatment

A 20 m × 20 m sampling plot was selected at each site. Three quadrats were randomly selected in each plot. Each quadrat had dimensions of 1 m × 1 m, and samples from each quadrat were collected using a 5-cm-diameter corer. Before collecting soil samples, the litter layer of the topsoil (approximately 1 cm) was removed. For the topsoil (0–10 cm) and subsoil (10–20 cm), nine soil core samples were collected within each quadrat and then mixed together. Additionally, to calculate soil erosion and deposition rates, soil samples at 0–30 cm depths were also collected at each quadrat. Thus, a total of 54 soil samples (3 transects × 3 sites × 2 depths × 3 quadrats) and 27 ^{137}Cs samples (3 transects × 3 sites × 3 quadrats) were collected in May-2016. Each soil sample was divided into two subsamples: one was sieved (2 mm) and stored immediately at −70 °C for the analysis of microbial properties; the other was air-dried for the determination of physicochemical soil properties. The ^{137}Cs samples were air-dried for the estimation of the ^{137}Cs inventory.

2.3. Laboratory analyses

2.3.1. Measurement of physicochemical soil properties

Air-dried soil samples were crushed with a wooden mallet and passed through a 2-mm sieve. Soil pH was determined with a digital pH meter (Woonsocket, RI, USA) using a soil-to-water ratio of 1:2.5 (w/v). Soil bulk density (BD) was analyzed using the cutting ring method, and the distribution of soil particle sizes was determined using the pipette method. Subsamples passed through a 1-mm sieve were used in the analysis of available nitrogen (N) via the alkali N-proliferation method (Duan et al., 2016). Subsamples passed through a 0.25-mm sieve were used in the analysis of SOC and total nitrogen (TN). The SOC was determined using the dichromate oxidation method (Walkley and Black, 1934); and TN was measured using the Kjeldahl (1883) method. Dissolved organic carbon (DOC) was measured as described by Li et al. (2015). The chloroform-fumigation extraction method was used to determine microbial biomass carbon (MBC) (Vance et al., 1987). The basic physicochemical soil properties at different sites and depths are presented in Table 1.

2.3.2. Measurement of ^{137}Cs inventory

Air-dried soil samples (0–30 cm) were passed through a 1-mm sieve. The fine fraction (under 1 mm) was used for the ^{137}Cs analysis. The ^{137}Cs content (Bq kg^{-1}) was determined using a hyperpure Li-drifted Ge detector coupled to a DSPec multichannel gamma-ray spectrophotometer (GMX50, PerkinElmer, USA). The detector had a 2.17 keV (^{60}Co) energy resolution and was calibrated using standard certified samples purchased from the China Institute of Atomic Energy. Gamma emissions from ^{137}Cs at 661.6 keV were counted for 28,800 s, yielding results with an analytical precision of ± 5%.

2.3.3. Determination of bacterial communities

The composite sample for each site and depth along the transects (a total of 18 composite samples, i.e., 3 transects × 3 sites × 2 depths) was used in the analysis of the bacterial community via Illumina MiSeq sequencing. Soil DNA was extracted with a Powersoil® DNA Isolation kit (Omega Bio-Tek, USA). The bacterial 16S ribosomal RNA gene was amplified by polymerase chain reaction (PCR) using the primers 338F (5′-barcode- ACTCCTACGGGAGGCAGCAG-3′) and 806R (5′-GGACTACHVGGGTWTCTAAT-3′). The PCR reaction was performed in a 20-μl reaction mixture containing 1 μl of template DNA (10 ng μl^{-1}), 2 μl of 2.5 mM dNTPs, 4 μl of 5 × FastPfu Buffer, 0.8 μl of each primer (5 μM) and 0.4 μl of FastPfu Polymerase (Sun et al., 2015). The PCR conditions were as follows: denaturation at 95 °C for 3 min, followed by 27 cycles at 95 °C for 30 s, 55 °C for 30 s, 72 °C for 45 s, and final extension at 72 °C for 10 min. The purified PCR amplicons were pooled at equimolar ratios and paired-end sequenced (2 × 250) on the Illumina MiSeq PE300 platform (Illumina Corporation, USA). Clustering of the screened sequences into operational taxonomic units (OTUs) was performed using UPARSE (version 7.1) at a 97% similarity threshold. Relative abundance (%) was defined as the number of OTUs affiliated with the same microbial taxa divided by the total OTUs number. Additionally, the Shannon index was calculated as the description of