Effects of vegetational type and soil depth on soil microbial communities on the Loess Plateau of China

Lie Xiao, Guo-Bin Liu & Sha Xue

To cite this article: Lie Xiao, Guo-Bin Liu & Sha Xue (2016) Effects of vegetational type and soil depth on soil microbial communities on the Loess Plateau of China, Archives of Agronomy and Soil Science, 62:12, 1665-1677, DOI: 10.1080/03650340.2016.1170811

To link to this article: http://dx.doi.org/10.1080/03650340.2016.1170811

Accepted author version posted online: 28 Mar 2016. Published online: 11 Apr 2016.

Submit your article to this journal

Article views: 14

View related articles

View Crossmark data
Effects of vegetational type and soil depth on soil microbial communities on the Loess Plateau of China

Lie Xiao\textsuperscript{a,b}, Guo-Bin Liu\textsuperscript{a} and Sha Xue\textsuperscript{a}

\textsuperscript{a}State Key Laboratory of Soil Erosion and Dryland Farming on the Loess Plateau, Institute of Soil and Water Conservation, Northwest Agriculture and Forestry University, Yangling, China; \textsuperscript{b}State Key Laboratory Base of Eco-hydraulic Engineering in Arid Area, Xi’an University of Technology, Xi’an, China

ABSTRACT

Soil microbial communities are very sensitive to changes in land use and are often used as indicators of soil fertility. We evaluated the microbial communities in the soils of four types of vegetation (cropland (CP), natural grassland (NG), broadleaf forest (BF) and coniferous forest (CF)) at depths of 0–10 and 10–20 cm on the Loess Plateau in China using phospholipid fatty acid (PLFA) profiling and denaturing gradient gel electrophoresis (DGGE) of DNA amplicons from polymerase chain reactions. The soil microbial communities were affected more by vegetation type than by soil depth. Total organic carbon, total nitrogen, soil-water content, pH, bulk density (BD) and C:N ratio were all significantly associated with the composition of the communities. Total PLFA, bacterial PLFA and fungal PLFA were significantly higher in the BF than the CP. The DGGE analyses showed that NG had the most diverse bacterial and fungal communities. These results confirmed the significant effect of vegetation type on soil microbial communities. BFs and natural grass were better than the CFs for the restoration of vegetation on the Loess Plateau.

ARTICLE HISTORY

Received 6 November 2015
Accepted 17 March 2016

KEYWORDS

Vegetation types; soil depths; PLFA; PCR-DGGE; Loess Plateau

Introduction

Soil microorganisms play an important role in the decomposition of organic matter and in nutrient cycling and energy transfer in terrestrial ecosystems (Li et al. 2012). The characteristics of soil microbial communities have been increasingly used as important indicators of soil fertility (Pereira et al. 2008). Exploring the response and dynamic shifts of these communities in various types of restoration programs can contribute to a more complete assessment of the effectiveness of ecological reconstruction and can provide guidance for the revegetation of fragile ecosystems.

Soil microbial communities and their diversity can be affected by the type of vegetation cover (Yoshitake et al. 2013; Yang & Zhang 2014). Phospholipid fatty acid (PLFA) analysis characterizes the structure of a living microbial community at the time of sampling and is suitable for detecting rapid changes in the community (Frostegård et al. 2011). Denaturing gradient gel electrophoresis (DGGE) analysis reflects the genetic diversity of a microbial community and allows the screening of multiple samples with the advantages of being reliable, reproducible and rapid (Nakatsu et al. 2000). Many studies have used PLFA and PCR-DGGE fingerprinting to spatially and temporally compare microbial communities within and between locations or among treatments (Stagnari et al. 2014; Qin et al. 2015). Yoshitake et al. (2013) reported that shifts in the structure of a microbial community reflect the differences in the quality of the soil organic matter during vegetation...
succession. Xue et al. (2008) and Yang and Zhang (2014), using PLFA biomarkers and DGGE analyses, found that land-use conversion had a greater effect than tea-garden and orchard age on the structure of the microbial communities. These studies demonstrated that PLFA analysis and PCR-DGGE are powerful tools for assessing the microbial communities in various environments.

The Loess Plateau in China has suffered from serious soil erosion. The Chinese government thus implemented the Grain for Green project in which a large amount of cropland (CP) was planted with grasses and forests and was abandoned for natural recovery. Various methods of revegetation have been evaluated by studying the plant communities (Wang et al. 2009b; Zhang & Dong 2010) and the physical (Jian et al. 2015), chemical (Fu et al. 2010; Cheng & An 2015) and biological (Li et al. 2013; Xue et al. 2014) properties of the soil. The diversity of the microbial communities under different types of vegetation on the Loess Plateau, however, has been inadequately studied. Different soil layers may contain fundamentally distinct microbial communities that are specialized for their microenvironment (Huang et al. 2011) and play important roles in soil formation and the biogeochemistry of terrestrial ecosystems. The objective of the present study was therefore to evaluate the structure and composition of the soil microbial communities under different vegetation types and soil depths by PLFA analysis and DGGE and to determine the best vegetation type for the restoration of vegetation on the Loess Plateau.

Materials and methods

Study site

The study was conducted in the Yanhe watershed in Yan’an, Shaanxi province, China (108°38’–110°29’E, 36°21’–37°19’N). The watershed has an area of 7725 km² and a semiarid climate with a mean annual temperature of 9.2°C and an average of 142 frost-free days. The area receives a mean annual precipitation of 500 mm, most of which falls between July and September. The soil type is primarily loessial soil (Calcaric Cambisol, FAO) that is particularly susceptible to erosion. The soil texture is 64% sand, 24% silt and 12% clay.

The study area suffers the most serious loss of soil and water on the Loess Plateau. To remedy the severe erosion, much of the sloped CP was reconverted to forest, mainly with black locust (Robina pseudoacacia) and Chinese pine (Pinus tabuliformis), and grassland. Abandoning the sloped CP for natural recovery was also an effective way to repair the ecological environment. We selected four types of vegetation to study the effects of different patterns of vegetation restoration on soil microbial communities: a broadleaf forest (R. pseudoacacia, BF), a coniferous forest (P. tabuliformis, CF) and a natural grassland (NG) (dominant species: Artemisia sacrorum) that has been recovering for 30 years represented the common types of vegetation restoration, and a CP site that has been cultivated with millet (Setaria italica) for 40 years was used as a reference site.

Soil sampling

Soil samples were collected from 20 × 30 m plots in July 2011. Four replicate plots for NG and three replicate plots for the other three vegetation types were established, totaling 13 plots. These plots were considered to be true replicates because the distance between them exceeded 100 m. Ten soil cores were collected in each plot with stainless steel cylinders with diameters and heights of 5 cm from depths of 0–10 and 10–20 cm after removal of the vegetation and litter. The 10 soil cores from each layer were thoroughly mixed to produce a composite sample. A total of 26 soil samples were thus collected. Another set of samples was collected adjacent to the above samples for determining the bulk densities (BDs) in the two soil layers. All samples were double-bagged to prevent moisture loss and were transported immediately to the laboratory for analysis.

Plant roots, debris and macrofauna were removed from the bulked samples, which were then divided into two subsamples. One subsample was air-dried, crushed and sieved through a 0.25-mm
mesh for the analysis of total organic carbon (TOC) and total nitrogen (TN). The other subsample was sieved through a 2-mm mesh and stored at −80°C until the PLFA analysis and DNA extraction.

**Soil physicochemical properties**

Soil-water content (SWC) was determined as the percentage of the dry weight after drying the samples at 105°C overnight. BD was calculated as the dry weight divided by the volume. TOC and TN were determined using the Walkley–Black and Kjeldahl methods (Bremner 1996; Nelson & Sommers 1996), respectively. pH was measured with an automatic acid-base titrator (Metrohm 702) for 1:2.5 soil:water suspensions.

**PLFA analysis**

The extraction of PLFAs was performed based on Bligh and Dyer method as described by Frostegård et al. (1993). Briefly, 3 g of frozen dried soil samples were extracted with a 1:2:0.8 chloroform:methanol:citrate buffer, and the lipids were separated into neutral lipids, glycolipids and phospholipids on a silicic acid column. The phospholipids were subjected to a mild alkaline methanlysis, and the fatty acid methyl esters were detected using an Agilent 7890 gas chromatograph (Agilent Technologies, Santa Clara, CA, USA) coupled with a flame ionization detector. The system was controlled with Agilent Chemestation and MIDI Sherlock software (Version 4.5; Microbial ID, Inc., Newark, NJ, USA). An Agilent Ultra 2 column, 25 m long × 200 μm I.D. × 0.33 μm film thickness, was used with hydrogen as the carrier gas. An external standard of 19:0 methyl ester was used for quantification.

The fatty acid nomenclature followed Ratledge and Wilkinson (1988). Some lipids can serve as indicators of specific microbial groups. In particular, branched saturated (iso- and anteiso-) lipids, including i15:0, a15:0, i16:0 and i17:0, are indicators of Gram-positive bacteria (G⁺PLFA). We used 16:1ω9, cy17:0, 18:1ω9c, 18:1ω9t and cy19:0 as indicators of Gram-negative bacteria (G⁻PLFA). The bacterial PLFAs (BactPLFAs) were assumed to be represented by the sum of the marker PLFAs for G⁺PLFA, G⁻PLFA and normal saturated fatty acids: 14:0, 15:0, 16:0, 17:0 and 18:0. The lipid 18:2ω6 indicated fungal PLFA (FungPLFA) (Zelles 1997). The FungPLFA/BactPLFA ratio was used as an index of the ratio of fungal/bacterial biomass in the soil (Strickland & Rousk 2010).

**DNA extraction, PCR and DGGE**

Total DNA was extracted from 5.0 g of each sample as described by Zhou et al. (1996). The DNA was then purified using the Rapid DNA Gel Extraction Kit (DP1702, BioTeke, Beijing, China) as recommended by the manufacturer.

The variable V3 region of bacterial 16S rDNA was amplified using nested PCR. The DNA extracted from the samples was subjected to a first round of PCR with primers 63F (Fantroussi et al. 1999) and 1378R (Heuer et al. 1997). The first-round PCR products were diluted 10-fold and used as templates in a second round of PCR with primers 338F-GC and 518R (Ovreås et al. 1997) to produce DNA fragments approximately 236 bp in length. The PCRs were performed in a final volume of 25 μl containing 2.5 μl of 10× PCR buffer, 2 μl of deoxynucleotide triphosphates (2.5 mmol L⁻¹), 1.25 units of Taq DNA polymerase (2.5 U μl⁻¹, Tiangen Biotech Co., Ltd., Beijing, China), 0.5 μl of the primers (10 pmol μl⁻¹ each) and 1.0 μl of template DNA. The products were amplified on a Bio-Rad C1000 Touch™ thermal cycler under the following conditions: for the first round, 94°C for 5 min; 30 cycles of 94°C for 30 s, 56°C for 30 s and 72°C for 1 min; and a final extension at 72°C for 7 min; for the second round, 94°C for 5 min; 30 cycles of 94°C for 30 s, 65°C for 30 s and 72°C for 30 s, and a final extension at 72°C for 7 min.

The fungal DNA extracted from the samples was amplified with primers NS1 and Fungi-GC (Hoshino & Morimoto 2008) targeting 18S rDNA to produce fragments approximately 400 bp in
length. Except for the primers, the contents of the PCRs were the same as for the bacterial amplifications. The DNA was amplified under the following conditions: 94°C for 5 min; 30 cycles of 94°C for 30 s, 60°C for 1 min and 72°C for 1 min and a final extension at 72°C for 7 min.

The PCR products were electrophoresed on a 2% agarose gel (w/v; 120 V for 20 min) and stained with ethidium bromide to confirm amplification. The PCR products were stored at −20°C until subsequent DGGE analysis.

Twenty microliters of the PCR products were electrophoresed on 8% (w/v) polyacrylamide (37.5:1 acrylamide:bis-acrylamide) gels in 1× Tris acetate-EDTA (TAE) buffer. The linear gradients were 40–70% denaturant for bacteria and 20–35% denaturant for fungi, where 100% denaturant contained 7 M urea and 40% (v/v) formamide. All DGGE analyses used the DCode™ Universal Mutation Detection System (Bio-Rad Laboratories, Hercules, CA, USA). The products were electrophoresed for 12 h at 60 V and a constant temperature of 60°C. After electrophoresis, the gels were stained with 5 mg L$^{-1}$ ethidium bromide for 30 min in TAE buffer, rinsed for 5 min with deionized water and photographed (Gel Doc 2000, BioRad Laboratories).

**Statistical analysis**

The physicochemical properties and the PLFA biomarkers of the soils from the vegetation types and soil depths were compared using one-way analyses of variance. If a significant difference at $P < 0.05$ was observed, a comparison among the means was performed using Duncan’s multiple-range test. The photographs of the gels were analyzed with BioRad Quantity One software (version 4.5, Bio-Rad Laboratories) to obtain relative band intensities and positions. Principal component analysis (PCA) was used to determine the effect of vegetation type and soil depth on the structural and functional diversities of the microbial communities. All statistical analyses were conducted using SPSS (version 16.0). A redundancy analysis (RDA) was conducted using Canoco 4.5 to identify the relationships among the microbial communities and the physicochemical parameters of the soil.

**Results**

**Soil physicochemical analysis**

Some physicochemical properties differed among the vegetation types and soil depths (Table 1). TOC, TN and the C:N ratio varied considerably between different vegetation types, with a ranking of BF > CF > NG > CP. TOC, TN and the C:N ratio decreased with soil depth, which was not significant for CP and NG. In contrast, BD, SWC and pH increased with soil depth, except for SWC in BF and CF. BD varied with a ranking of BF < CF < CP < NG, which had no significant difference between the two soil depths. pH varied with a ranking of BF < CF < NG < CP, which significantly increased with soil depth, except CP.

Table 1. Physicochemical properties of the soils under four vegetation types on the Loess Plateau.

<table>
<thead>
<tr>
<th>Vegetation type</th>
<th>Soil depth (cm)</th>
<th>BD (g cm$^{-3}$)</th>
<th>SWC (%)</th>
<th>TOC (g kg$^{-1}$)</th>
<th>TN (g kg$^{-1}$)</th>
<th>pH</th>
<th>C:N</th>
</tr>
</thead>
<tbody>
<tr>
<td>CP</td>
<td>0–10</td>
<td>1.21bc</td>
<td>9.9b</td>
<td>3.67a</td>
<td>0.47a</td>
<td>8.50de</td>
<td>7.8a</td>
</tr>
<tr>
<td></td>
<td>10–20</td>
<td>1.26c</td>
<td>12.3b</td>
<td>3.26a</td>
<td>0.43a</td>
<td>8.54e</td>
<td>7.6a</td>
</tr>
<tr>
<td>NG</td>
<td>0–10</td>
<td>1.07ab</td>
<td>5.0a</td>
<td>13.06bc</td>
<td>1.32bc</td>
<td>8.35c</td>
<td>9.9bc</td>
</tr>
<tr>
<td></td>
<td>10–20</td>
<td>1.12abc</td>
<td>6.1a</td>
<td>8.79ab</td>
<td>0.92abc</td>
<td>8.45d</td>
<td>9.6b</td>
</tr>
<tr>
<td>BF</td>
<td>0–10</td>
<td>0.96a</td>
<td>18.0d</td>
<td>29.82d</td>
<td>2.40d</td>
<td>8.00a</td>
<td>12.2e</td>
</tr>
<tr>
<td></td>
<td>10–20</td>
<td>1.05ab</td>
<td>17.8d</td>
<td>15.19bc</td>
<td>1.38bc</td>
<td>8.12b</td>
<td>10.9 cd</td>
</tr>
<tr>
<td>CF</td>
<td>0–10</td>
<td>1.01a</td>
<td>19.2d</td>
<td>18.43c</td>
<td>1.53c</td>
<td>8.11b</td>
<td>11.8de</td>
</tr>
<tr>
<td></td>
<td>10–20</td>
<td>1.03a</td>
<td>15.0c</td>
<td>8.39ab</td>
<td>0.78ab</td>
<td>8.27c</td>
<td>10.8 cd</td>
</tr>
</tbody>
</table>

Data are the means of 3–4 replicates. Different letters within a column indicate significant differences identified by Duncan’s test ($P < 0.05$). CP, cropland; NG, natural grassland; BF, broadleaf forest; CF, coniferous forest; BD, bulk density; SWC, soil-water content; TOC, total organic carbon; TN, total nitrogen.
**PLFA composition**

The total PLFA content ranged from 5.97 to 8.55 nmol g\(^{-1}\) in the 0–10-cm layer and from 5.25 to 7.78 nmol g\(^{-1}\) in the 10–20-cm layer. Total PLFA content differed significantly between the two layers only in NG (\(P < 0.05\)) (Figure 1a). FungPLFA, BactPLFA, G\(^{+}\)PLFA and G\(^{-}\)PLFA contents had similar trends as total PLFA. Specifically, BactPLFA, G\(^{+}\)PLFA and G\(^{-}\)PLFA contents in NG and G\(^{+}\)PLFA contents in BF differed significantly between the two layers (\(P < 0.05\)). The Fung/BactPLFA content did not differ significantly between the vegetation types and soil layers, but the Fung/Bact PLFA ratio was slightly higher in CF in both layers. The G\(^{+}/G^{-}\) PLFA ratio was significantly higher in NG and BF than in CF and CP and significantly higher in the 0–10-cm than the 10–20-cm layer (\(P < 0.05\)).

The first principal component (PC1) of the PCA of the mol% of the individual PLFAs explained 48.9% of the variation in the data, and PC2 explained 11.9% (Figure 2a). The PLFA patterns differed significantly among the four vegetation types along the first component (\(P < 0.001\)). The PLFA patterns were similar in the two soil layers under the same vegetation type, especially in NG. The loadings of the individual PLFAs (Figure 2b) indicated that CP and CF had relatively high abundances of 14:0, 16:0 and 18:1\(\omega 9\)c; NG had relatively high abundances of a15:0, i17:0, 17:0, 18:2\(\omega 6\) and cy19:0 and BF had relatively high abundances of 15:0, i16:0, 16:1\(\omega 9\), 18:1\(\omega 9t\) and cy17:0. The RDA indicated that TOC, TN, C:N, SWC, BD and pH all had large impacts on the composition of the microbial communities, and soil depth had the lowest impact on the PLFA patterns (Figure 5a).

**Bacterial community analysis**

The PCR-DGGE banding patterns of the bacterial communities were similar among the four vegetation types in both soil layers. Fifty-four distinct bands were detected. NG had the most and BF the fewest bands at both depths (Table 2). The 0–10-cm layers had fewer bands than the 10–20-cm layers among the four vegetation types. The PCA indicated that the first, second and third components explained 22.3, 20.6 and 20.5% of the variance, respectively (Figure 3). The positions of the samples in the PCA plots indicated that the structures of the bacterial communities were affected by both vegetation type and soil depth. The PCA distance between the two soil layers varied with a ranking of CP < NG < BF < CF, which demonstrated the relative impact of soil depth on the bacterial communities among the vegetation types. The RDA showed that the diversity of the bacterial communities was strongly affected by SWC and pH (Figure 5b).

**Fungal community analysis**

The DGGE banding patterns of the fungal communities showed that NG had the most bands with high intensities and the highest number of bands in both soil layers. BF had the fewest bands of the four vegetation types (Table 2). The PCA loadings of the first, second and third components were 27.8, 22.9 and 16.6%, respectively (Figure 4). The location of the samples on the PCA plots indicated that the fungal communities of CP, NG and BF were most affected by vegetation type, and soil depth had a larger impact on the CF communities. The RDA suggested that BD, pH, SWC and the C:N ratio had large influences on the fungal communities (Figure 5c).

**Discussion**

**PLFA profiles of the vegetation types**

Vegetation type has a large impact on soil physical and chemical characteristics, which contribute to the structure of soil microbial communities (Menon et al. 2013; Yang & Zhang 2014). The PCA of individual PLFA data indicated that the PLFA profiles of the vegetation types were each
Figure 1. The content of PLFA (a), FungPLFA (b), BactPLFA (c), G⁺PLFA (d), G⁻PLFA (e) (nmol·g⁻¹) and Fung/Bact PLFA (f), G⁺/G⁻ PLFA (g) in the four vegetation types at two soil depths. (CP, cropland; NG, natural grassland; BF, broadleaf forest; CF, coniferous forest. Different letters indicate significant differences at P < 0.05. Error bars show standard deviations).
Figure 2. PC1 vs. PC2 of the principal component analysis of PLFA profiles in the four vegetation types at two soil depths. (a) Score plot of the different vegetation types at two soil depths. (b) Loading values of the individual PLFA (for abbreviations, see Figure 1).

Table 2. Total bands on the DGGE gels.

<table>
<thead>
<tr>
<th>Vegetation type</th>
<th>Soil depth (cm)</th>
<th>Bacteria</th>
<th>Fungi</th>
</tr>
</thead>
<tbody>
<tr>
<td>CP</td>
<td>0–10</td>
<td>29</td>
<td>20</td>
</tr>
<tr>
<td></td>
<td>10–20</td>
<td>32</td>
<td>22</td>
</tr>
<tr>
<td>NG</td>
<td>0–10</td>
<td>36</td>
<td>25</td>
</tr>
<tr>
<td></td>
<td>10–20</td>
<td>36</td>
<td>22</td>
</tr>
<tr>
<td>BF</td>
<td>0–10</td>
<td>24</td>
<td>19</td>
</tr>
<tr>
<td></td>
<td>10–20</td>
<td>27</td>
<td>19</td>
</tr>
<tr>
<td>CF</td>
<td>0–10</td>
<td>30</td>
<td>19</td>
</tr>
<tr>
<td></td>
<td>10–20</td>
<td>33</td>
<td>24</td>
</tr>
</tbody>
</table>

CP, cropland; NG, natural grassland; BF, broadleaf forest; CF, coniferous forest.
compositionally distinct. Han et al. (2007) also reported different microbial community composition among CP, shrubland and grassland in northern China. This differentiation may be attributed to the different quantity and quality of litter input and root exudates among different types of vegetation (Marschner et al. 2001), which significantly influence the composition of soil microbial communities (Chen et al. 2007). In the present study, TOC and TN were significantly higher after CP was restored with NG and BF, so these two vegetation types had higher levels of PLFAs. Rousk et al. (2010) reported that pH had large effects on microbial PLFA composition; monounsaturated PLFAs 16:1ω5, 16:1ω7c and 18:1ω7 increased significantly with pH. The lower pH in CF may have contributed to the lower amount of total PLFA than in CP. SWC can also significantly influence microbial communities, with higher levels increasing the bacterial communities (Williams 2007). The biomass of fungi compared to bacteria indicates the activity of the two decomposition pathways of soil food webs (de Vries et al. 2006). The present research found that BactPLFA was higher than FungPLFA by almost one order, which was consistent with the results of many other researches (Yoshitake et al. 2013; Zhang et al. 2015). The Fung/BactPLFA content did not differ

![Figure 3](image-url). PC1 vs. PC2 (a) and PC1 vs. PC3 (b) of the principal component analysis of DGGE banding patterns of bacterial communities in the four vegetation types at two soil depths (for abbreviations, see Figure 1).
significantly between the vegetation types and soil layers, which indicated that vegetation types had no significant impact on the activity of the two pathways of soil food webs.

The availability of C has a large impact on microbial communities (Yoshitake et al. 2013) and may be the main factor determining their structure. Microbial biomass and organic-C contents decrease as soil depth increases (Stone et al. 2014). An analysis of PLFAs also indicated that microbial communities decrease with soil depth. Studies of grassland (Huang et al. 2011) and forest (Fritze et al. 2000) also found similar results. The PCA of the PLFA analysis indicated that the microbial communities in the different vegetation types had similar structures in the 0–10-cm and 10–20-cm layers. Steenwerth et al. (2002) also found similar structures of the microbial communities in 0–6-cm and 6–12-cm soil layers in a grassland ecosystem, and Allison et al. (2007) reported that deeper, low-C soils were more similar to high-C remnant prairie soils than to low-C agricultural soils and suggested that C was not the primary factor controlling the composition of the microbial communities in these soils.

Figure 4. PC1 vs. PC2 (a) and PC1 vs. PC3 (b) of the principal component analysis of DGGE banding patterns of fungal communities in the four vegetation types at two soil depths (for abbreviations, see Figure 1).
DGGE profiles of the vegetation types

Variations in the physiochemical conditions (e.g. TOC, TN, CEC, pH and SWC) in soil profiles may contribute to the genetic diversity of soil microbial communities (Qin et al. 2015). In the present study, the DGGE banding patterns of the bacterial and fungal communities varied among the four vegetation types, consistent with the findings by Wallis et al. (2010) and Hossain and Sugiyama (2011). Bacteria and fungi are both decomposers in soils, but they have different decomposition pathways. Fungi assimilate a higher proportion of soil C and are composed of more recalcitrant C compounds relative to bacteria (Hackl et al. 2005). In our study, the surface litter in CF had more recalcitrant C compounds than BF, which may have contributed to the significantly different microbial communities between the two vegetation types. N addition inhibits bacterial growth but stimulates fungal growth (Rousk & Bååth 2007). The significantly different C:N ratios in the four vegetation types may also have contributed to the variations of the microbial communities (Agnelli et al. 2004).

Analysis of the 16S and 18S rDNA gene fragments suggested that the number of bacterial and fungal DGGE bands tended to increase with soil depth. Each DGGE band usually represents at least one bacterial or fungal species; the present study thus showed that the number of bacterial and fungal species increased with soil depth. Changes in microbial biomass, though, are not always accompanied by changes in the diversity or activity of microbial communities (Xue et al. 2008). Our results suggested that the microbial populations were large, but the microbial community structure...
was simpler in the upper soil layer (Wang et al. 2009a). DGGE profiles of soil samples collected along vertical soil cores in a fallow CP were relatively stable (Gelsomino et al. 1999), but those of microbial communities in a forest soil profile differed significantly (Agnelli et al. 2004). This inconsistency may be due to differences in soil characteristics. The much higher pH and the much lower increase in the C:N ratio in the soil profile in the present study relative to those in the forest sampled by Agnelli et al. (2004) may account for the similar or slightly higher microbial diversities in the deeper soil layers compared to the shallower soils. These indicated that the variation in soil properties along the soil profile caused by the changes in land use thus appears to have shaped the microbial communities in the different soil layers.

Conclusions

Revegetation is often used as a useful method to restore degraded land. Our study showed that the structure and composition of soil microbial communities were more affected by vegetation type than soil depth. The soil physicochemical properties were significantly associated with the characteristics of the soil microbial communities. Total PLFA, bactPLFA and fungPLFA were significantly higher in the black locust forest, and the DGGE analyses showed that NG had the most diverse bacterial and fungal communities. These results suggest that vegetation restoration has a significant effect on soil microbial communities. BF and NG were better than CF for vegetation restoration on the Loess Plateau. The combination of PLFA analysis and DGGE can provide a more precise assessment of the composition of soil microbial communities.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by the National Natural Science Foundation of China [41371510]; Science and Technology Research and Development Program of Shaanxi Province, China [2011KJXX36] and Program for West Younger Scholar, Chinese Academy of Sciences [XAB2015A05].

References


