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Research Article

Agricultural Practices Effects on Biogeographical Patterns of Bacterial Biodiversity in Soil Profiles along Precipitation Gradient in Northeast China Transect

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ABSTRACT

Although soil bacteria are ubiquitous and one is the more important community in the soil than the other and the bio-geographical pattern of soil microbial diversity driven by key global change that play a critical role in soil functioning of biologically diverse ecosystems. Previous studies discovered the biogeographical distribution pattern of soil bacteria communities in surface layer of black soil zone in northeast china. In this study, we selected global large scale to investigate the large scale distribution pattern of soil bacteria biodiversity and its driving effects on ecosystem of cropland in soil profile. In total, 897,776803 optimized sequencings were obtained from the 78 soil samples and soil bacteria community distribution was estimated from using the quantitative PCR and Illumina MiSeq and 16S rRNA sequencing methods. These sequencing belonged to East to West Northeast Transect NECT were across all soil samples of cropland, the dominant bacteria were classified into sub-groups and these groups across all the soil samples of cropland (>1% of all sequences) were *Proteobacteria*, *Acidobacteria*, *Actinbacteria*, Chloroflexi. The distribution and diversity of the soil bacteria were dominantly affected stronger by precipitation gradient. PCA analysis based on OTUs showed that the geographical distribution of community variables 38.12% similarity between them overall and the soil environmental factors explained approximately 20.71% of the variations. The relative abundance of community on phylum level, diversity of soil bacteria distribution increasing with the low precipitation gradient from east to west. Consequently, these findings may have important suggestions for understanding the effects of global change (e.g., precipitation) on the large scale of the biodiversity pattern had significant effect on ecosystem. Our understanding of how soil bacterial diversity patterns may respond to future global change effects in different regions to improve the biogeographic pattern in soil profile along a precipitation gradient.

Keywords: Soil microbial biodiversity; Agriculture; High-throughput sequencing; Land; Soil profile; Precipitation gradient

INTRODUCTION

Soil microbial biodiversity represents a significant challenge for better validity of soil resources and to implement more sustainable management of agricultural soil [1]. Knowledge of the biogeographical pattern of microbial diversity across the different types of the soil in different land uses and identification of potential biotic indicators of changes are critical to better understand the land-use effects on soil microbial biodiversity. These indicators will help to manage device strategies for examined microbial biodiversity [2]. Local to continental studies showed that have soil properties (e.g., Soil pH) are diverse of the diversity and structure of microbial community pattern, with land-use and plant diversity as a secondary confounded correlate [3,4]. Land-use has a primary diver of bacterial communities; biodiversity varies among soils as shown by bio-geographical study [5]. Furthermore, different types of soil found in land-use, it is essential for sustainable soil management to better understand the impacts of land-use on soil microbial biodiversity specific to soil type. Soil microbes are an essential component in biogeochemical cycling [6,7]. The structure

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and biodiversity of microbial diversity are predominantly is limited in soil horizons. As a result of microbial diversity that exists in the depth of the soil, while the biomass of microbes is often exhibited exponential decreases with increases the depth [8,9]. Its spatial distribution characteristics determined the environmental interaction between soil-vegetation, functional characteristics and biodiversity patterns of soil microbes have substantial effects on the growth of the above parts of the plants [10,11]. Although previous studies [12-14] across the different ecosystems have different bio-geographical patterns of microbial biodiversity, within different soil profiles their biodiversity and relationship between microbial-mediated nutrient cycling. Numerous studies, in next-generation developments high throughput sequencing, have made whole soil microbial diversity pattern affordable at various scales [15-18]. In a comparison of previous studies, comprehensive information on the bio-geographical pattern of soil bacterial communities in Chinese soil is limited, but recently some hard work in gathering some information was made mono ecosystems of the northeast parts of China [17,19]. In the previous years, modern biological techniques particularly high-throughput sequencing and supplied powerful technical support for studying spatial distribution patterns of bacterial communities [7]. The recent finding showed regular changings of bacterial community pattern, individual abundances, or biodiversity with environmental changes [20]. At the regional scale, critical environmental factors such as precipitation and temperature become more critical for the pattern of bacterial communities along precipitation gradients of both soil profile and habitat location [3,21,22]. The regional scale effect of soil pH and precipitation in shaping and pattern of microbial community composition have been well documented in a wide variety of habitats [23-26].

However, spatial scale effect for distribution of microbial assemblage in distinctive soil profiles remains poorly understood, as most studies focus only on those communities that are found near the surface horizons. Expanding our knowledge of bacterial diversity and distribution from the soil profile to habitant ingredients will improve our understanding of biodiversity and the functioning of environmental variables.

Research questions of the study

1. What 's the soil bacteria biodiversity pattern respond to the precipitation gradient across wide variety of taxonomic group?

2. How's the soil bacteria pattern change from high precipitation gradient to low precipitation gradient comparing with natural habitats?

3. What is the determining soil microbial pattern regularly distributed in soil depth?

4. How microbial communities respond to different environmental factors?

MATERIALS AND METHODS

Research design

MIn this experiment, seven study sites corresponding to three land-use type (cropland, grassland and forest) were selected in all experimental areas. A relatively flat area within each study site with homogenous soil conditions was enclosed to create three plots. At each site, three replicates plots with soil conditions.

Theoretical framework

This study was carried out on the east and west in northern China (Figures 1 and 2). Transect has a temperate continental and monsoon climate. There, spring is warm and windy; summer is short and hot with many rainy days; autumn usually sees early frost and plummeting temperature; winter is long, bitter cold with frequent polar outbreaks.

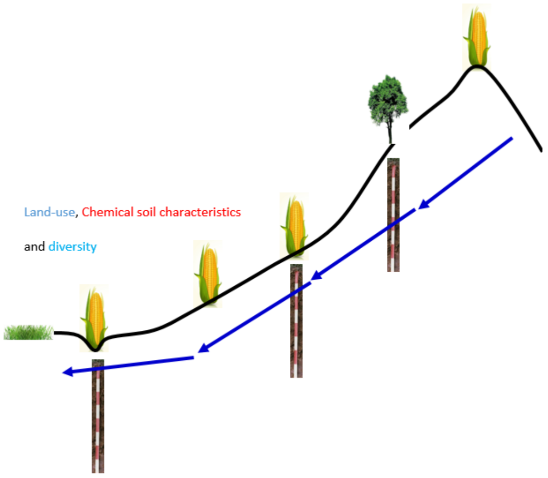

Figure 1: Design of cropland sites along with preciptation gradiens from east to west in Jilin.

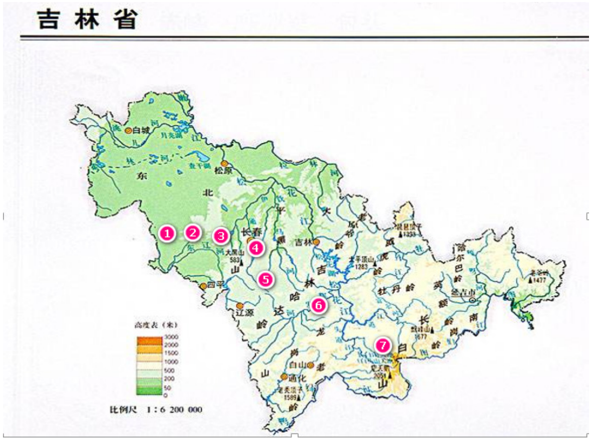

Figure 2: Soil sampling areas based on west to east in farmland along with Northeast China.

Sampling areas and its description

For the present study following seven different sampling sites were selected for sampling. Their names are listed below.

1. Changling

2. Sjian fang

3. Nongan

4. Changchun

5. Longwan

6. Dongliao

7. Beihe

In the main study sites, the size range of precipitation is 400 mm to 1000 mm in the elevation of 140 meters from (West) to 800 meters

(East) above sea surface; and have covered the Grassland in the west part and Forest in the east part, the total length of transect more than 500 KM. We choose four typical soil types, such as Alkali-saline soil, Black soil (chernozem), Black soil (Mollisol), and Dark-brown soil. In every site, we choose cropland to take samples.

Croplands were translated from local natural habitats, and corn has planted for more than 50 years in every site. We also took samples from secondary forest in Baihe and from secondary grassland in Changling. In each habitat, three soil profiles of 50 cm depth were collected, and the profile was divided into five sub-samples of 10 cm each. The fresh samples were taken in the lab and store -80 for DNA extraction.

These sampling sites situated in Changling (44° 35' 40" N, 123° 30' 44" E) , Sijianfang (44° 18′ 36”, 124° 07′ 34”), Nongan (44° 11′ 33”, 124° 37′ 54”), Changchun (43° 49'1.46" 125° 19'24.76") , Dongliao (42° 54′ 14”, 125° 25′ 37”) Baihe (42° 23′ 4”, 128° 5′ 38”) , see the details in Table 1.

Changling (Simplifies in Chinese): Changling is southwest part of (Singyuan city) in the northwest Jilin province between 44° 16′ 34 N, 123° 58′ 01 E with an altitude of 191 m (627 feet) elevated from sea level. Total residing area covered 5,787 km2 (2,234 sq. mi) with a population of 640,000. Changling bordering connected with Inner Mongolia to the west and connected with Nonagan county to the east, while Shuangliao and Gongzhuling to the south and at north Tongyu, Qianan and qian Gorlos county is situated. The weather of Changling affect by monsoon i.e. winter is long, dry and very cold due to Siberian anticyclone. Average monthly temperature and precipitation is (6.15°C-380.91 mm) and usually rainfall occurs in July and August.

Sijian fang (Simplifies in Chinese): It is located in the border between Nongan and Changling with latitude and longitude 44° 18’ N, 124° 70’ E with an altitude 190 m and its average temperature and precipitation is 6.15°C and 416.22 mm.

Nongan (Simplifies in Chinese): Nongan is a city of Jilin province, northeast (China) and administered of Changchun prefecture level. It lies at west side of Changchun city, also connected with Dehui at the east, while it is bordering with Kuancheng and Luyuan districts at the southeast and Siping to the southwest and Songyuan to the northwest. Nongan located at map of 44° 11’ N, 124° 37’ N with an altitude of 250 m high from sea level. Total population of Nongan is 960,759 according to 2010 census. Nongan average monthly temperature and precipitation is 5.45°C and 493.39 mm.

Changchun (Simplifies in Chinese): Changchun is a big city and capital of Jilin province (China) situated in the center of Songliao plain which is administered by the sub-provisional city. Total population of Changchun was 7,674,439 under its jurisdiction (2010 census). The total area of Changchun municipality is 20,571 km2. Changchun is a metropolitan area which comprising 5 districts and 4 development areas. Changchun is locally known as China’s “City of automobiles” and is industrial base with a specific focus on the automotive sector. The ministry of construction of P. R China awarded Changchun is one of the four cities “National garden cities” (2001) due to its high green urban-landscape. Changchun is located at 43° 60’ N, 125° 23’ E with an altitude of 200 m from sea level. The average monthly temperature is 6.29°C and its monthly average precipitation is 585.80 mm.

Dongliao (Simplifies in Chinese): Dongliao is located on the west side of Jilin province, northeast China. Dongliao controlled and administered by Liaoyuan city. Dongliao named because there is an origin of Dongliao River. It is located on global map location with an altitude of 42° 54’ N and longitude of 125° 25’ E. Dongliao is 310 m (892 ft) elevated from sea level with average monthly temperature 5.87°C and monthly average precipitation is 687.53 mm.

Lonwan (Simplifies in Chinese): Longwan district belongs to Huinan city in Jilin province, China. It is located at 42° 22’ N, 126° 26’ E on global map with an altitude of 670 m high from sea level. The average monthly temperature is 5.91°C and average monthly precipitation is 756.17 mm.

Baihe (Simplifies in Chinese): Baihe district is close to Tianchi, Changbai Mountains. Baihe 780 m high from sea level with the average monthly temperature and precipitation is 4.10°C, 840.37 mm.

DNA extraction test

The total genomic DNA was extracted from triplicate soil samples, each consisting of 0.5 g soil (wet weight) using soil DNA isolation Kit (MO BIO Laboratories) Shanghai Majorbio Bio-pharm Technology Co., Ltd, each soil sample was extracted according to the manufacturer’s instructions. The extracted soil DNA samples were stored at -20°C for further subsequent metagenomic analysis.

Data analysing

We used different methods to analyzing sequencing data of soil microbes. Firstly we sent samples to the company and they sent back us the raw data and we analyzed through SPSS softwere to pick out the original sequencing data from data and made graphs and tables which given below.

16S rRNA gene amplification, processing and data sequencing

DNA was extracted from the soil samples (0.5 g wet weight) using the Power Soil DNA Isolation Kit (MO BIO Shanghai LTD). Each sample three times amplified and then they combined in one sample for high throughput sequencing [17]. The V3-V4 hypervariable region of bacterial 16S rRNA was amplified using the primers 338 F: ACTCCTACGGGAGGCAGCA, 806R: GGACTACHVGGGTWTCTAAT. Functions of PCR were performed in 20 uL system, containing 4 uL × 5 FastPfu Buffer, 2 uL dNTPs (2.5 mmol/L), 0.8 uL Forward/Reverse primer (5 umol/L), 0.4 uL FastPfu Polymerase, and 10 ng Soil DNA as a template; some H_2O was added to the system reaching 20 uL. Thermal cycling conditions; 95°C for 3 min, followed by 27 cycles of 95° for 30 sec; 55°C for 30 sec; 72°C for 45 sec, then an extension at 72°C for 10 minutes.

We identified raw total sequences reads 48,874738, Quality-filtered raw reads were clustered into Operational Taxonomic Unit (OTU) at 97% sequencing similarity using the QIIME pipeline. The species diversity indices like Shannon and Chao diversity index (richness) and ACE diversity index (evenness) were estimated at 97% similarity sequencing using Mothur [27,28].

Statistical analysis

Principal Components Analysis (PCA) was used to compare the differences in soil bacterial diversity patterns on different habitats and PCoA was used to analyze the community differences between two layers of different soil profiles. In this study, the similarity of soil bacterial biodiversity was defined as the OTUs shared in all the soil samples relative abundance <0.1% shared in all the soil samples.

RESULTS

Soil bacteria community composition and trophic structure of farmland

The overall result of soil bacteria biodiversity pattern in farmland along with precipitation gradient were dominated by proteobacteria (26.6%), acidobacteria and actinobacteria (13.4% and 1.5%) characterized in this study. A total of 897,776803 sequences were extracted from 54 soil samples, the length of sequencing varied from 256.482 to 255.466 Base Pair (bp) given Table 1. To compare the soil bacteria community diversity among the soil samples in farmland from east site across the precipitation gradient of 400 mm shown in Table 2. The soil bacteria diversity decreased with increasing the precipitation in different samples.

Soil bacteria α and β biodiversity patterns upper and lower layer of farmland

α Alpha Biodiversity: The alpha-diversities of soil bacteria pattern between two layers are shown in Table 1. Soil bacteria the Shannon, Chao and simpson's indicate differed significantly ($P<0.001$) between two layers. Alpha biodiversity based on samples containing minimum number of sequencing data i-e bacterial community structure in farmland between two layers. A sequencing data showing in phylum level distribution of bacterial communities.

Beta biodiversity: In the analysis of beta biodiversity, cropland suggesting the clear destination of the soil bacteria in different seven sampling sites between two layers in soil profile shown in Figure 3. This finding was supported by Principle Coordinate Analysis (PCoA). In general, the PCoA analysis indicated 90% variations between two layers in soil bacteria biodiversity pattern.

Soil bacteria α and β biodiversity pattern from east to west

Biodiversity patterns across geographical precipitation gradient could result from community assembly mechanism at seven sampling sites in farmland. However the little has been done to separate effects pf both diversities on soil bacteria pattern. We compared all the samples from cropland and the results shows ▯ diversity varies from east to west along with precipitation gradient. The variation of environmental conditions and agricultural practices along gradient accounts for β diversity through mediating heterogeneous selection. The variation occurrence are given in Table 2 and Figure 1.

Relative abundance of soil bacteria pattern in soil profile

Relative abundance of soil bacterial diversity on phylum level 97% similarity presented inconsistent changing patterns along the precipitation they showed 75% similarity and the similarity as well as differences between bacterial community patterns in soil depth with PCA (Principal component analysis) level between 10 cm-20 cm and 40 cm-50 cm in all the samples and differences between in farmland sites but the effect of the human activity only on natural habitats given in Figure 4 and we can see the highest value in cropland in (10 cm-20 cm) as comparing to due to land-use effects but in (40 cm-50 cm) they have the lowest value due to high precipitation in depth of soil. The total result of bacterial community patterns in soil profiles from West to East that is 75% are similarity and the pattern of biodiversity is low in the depth of cropland. There as grassland and forest and we represent all data where the individual values contained in the matrix are represented in colours.

Table 1: Sequencing data of soil samples from east to west.

Habitats	Differences in depth	Shannon	Chao	Ace
East Cropland	10 cm-20 cm,	55 ± 13	55 ± 13	55 ± 13
40 cm-50 cm	6.813-2.170	5234-1711	5382-1768	55 ± 13
West Cropland	10 cm-20 cm,	55 ± 13	55 ± 13	55 ± 13
40 cm-50 cm	6.923-5.001	5180-3564	5129-4430	55 ± 13

Table 2: Mean annual temperature MAT, Mean annual precipitation along with sampling sites, soil type and altitude.

Sites	Areas	Latitude	Longitude	Altitude	Soil type	MAT	MAP
1	Changling	44° 35′ 40”	120°33’44”	140 m	Saline alkali soil	4.9°C	400 mm
2	Sijianfang	44° 18′ 35”	124°07′34”	190 m	Chernozem	4.9°C	430 mm
3	Nongan	44° 11′ 33”	124°37′54”	250 m	Chernozem	4.8°C	480 mm
4	Changchun	43° 59’ 59″	125°23′46″	200 m	Black soil	4.9°C	520 mm
5	Dongliao	42° 54′ 14”	125° 25′ 37”	310 m	Dark brown soil	5.0°C	600 mm
6	Longwan	42° 22′ 42″	126°26′49″	670 m	Dark brown soil	5.1°C	650 mm
7	Baihe	42° 23′ 04”	128° 5′ 38”	780 m	Dark brown soil	5.1°C	710 mm

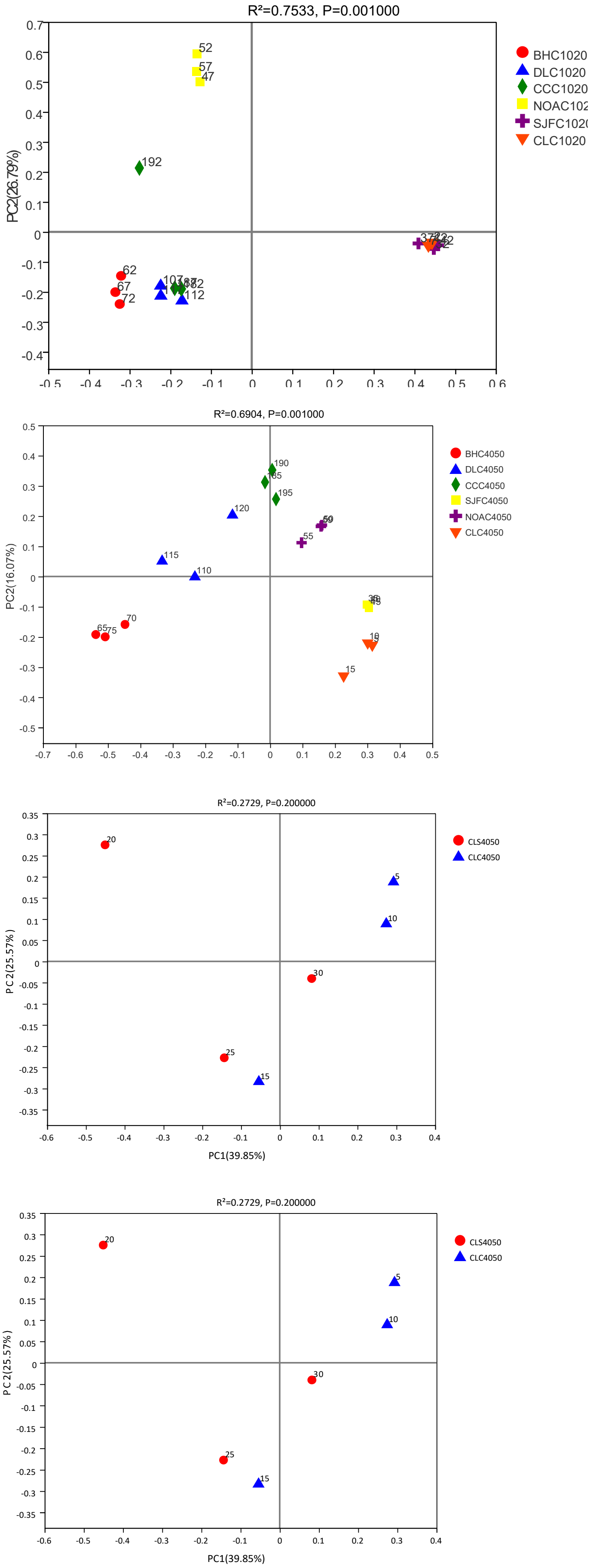

Figure 3: Beta diversity pattern along with soil profile. (A) The principle coordinate analysis PCoA ; (B) The soil bacteria along with bottom layer ; (C) In depth shows the difference between them; (D) The soil bacterial pattern shows in CLC between two layers.

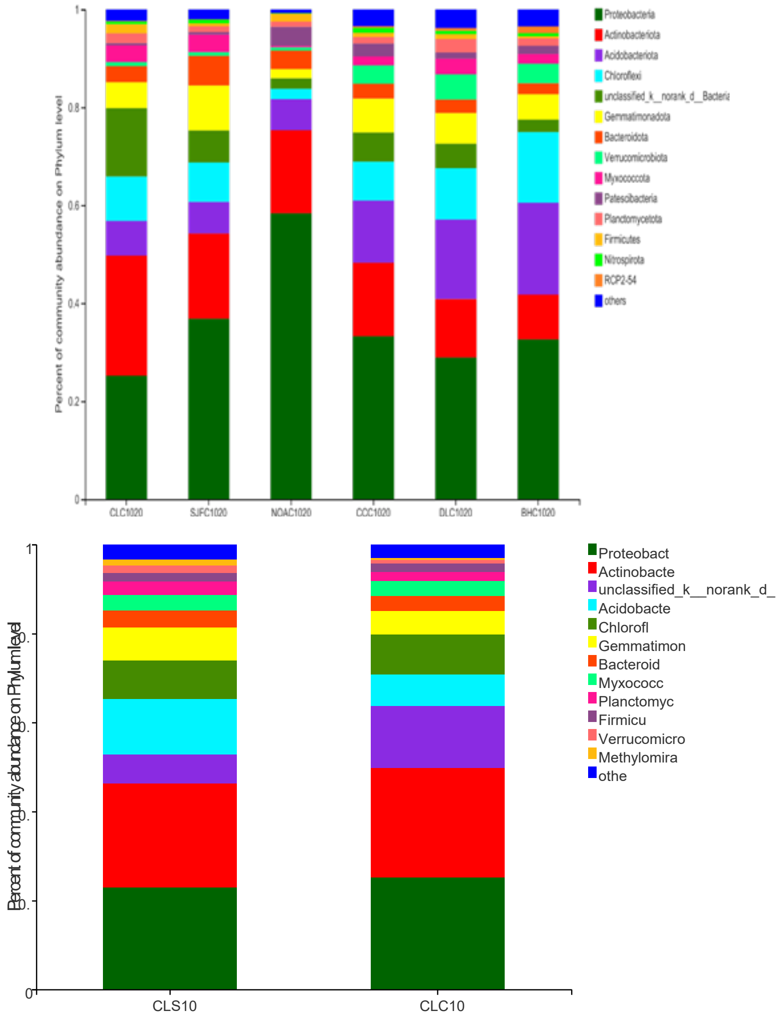

Figure 4: PCoA Community percent based on phylum. (A) Relative abundances of dominant soil bacteria subgroups; (B) for all of the soils separated according to the values. Relative abundances are based on the proportional frequencies of the DNA sequences that could be classified. The letter n in sub plan B below the column represents the number of samples for each soil sample in farmland.

Comparison of microbial patterns of farmland in the east (mainly work in white river)

The overall result of abundance of soil bacteria biodiversity pattern in farmland along with precipitation gradient characterized in this study are given in Table 1. A total of 897,776803 sequences were extracted from 78 soil samples, the length of sequencing varied from 256.482 to 255.466 Base Pair (bp). To compare the soil bacteria community diversity among the soil samples in farmland from east site across the precipitation gradient of 400 mm. The soil bacteria diversity decreased with increasing the precipitation in different samples in east site (mainly work in white river), the Principle Component Analysis (PCA) showed they are not related to the axis and the points between PCA1 and PCA2 are close to each other and indicated that the species composition of the samples corresponding to the two points is not similar.

Environmental factors that can be affect to soil a lot of chemical and physical properties also effects on the soil bacteria in soil profile. The results revealed that the phylotype richness, which is equivalent to the number of OTUs determined at the 97% similarity level from east to west and phylogenetic diversity ranged were (>1%) bacteria phyla Proteobacteria (38.60%) Acidobacteria (26.10%) Actinobacteria (7.40%) Chloroflexi (7.60%) from the 78 soils samples, other groups appeared to be in Figure 5. Based on the number of unique OTUs observed in between two layers in soil, indicating that the sequencing depth in this study is adequate to meet the purposes of the study.

Furthermore, Canonical Correspondence Analysis (CCA) which shows the main environmental factors are present in each location and we examined the bacterial diversity index correlation with factors showed in overall CCA1 20.71% and CC2 4.71% 10 cm-20 cm >40 cm-50 cm of cropland and to compared in all location and was also used to identify the major environmental variables in soil bacteria diversity abundance and structures. All soils were roughly separated into four groups according to the soil precipitation value, and the successions of communities with an increase of soil precipitation were clearly displayed (Figure 5). Of all the environmental variables, the total precipitation TP had the longest arrow along the RDA1 axis 44.79% and 29.60%, RDA has a similar effect in soil and when compared farmland samples as compared with the results showed cropland RDA1 axis 42.54% and 28.10%, like in samples of CLC is likely to be more affected by pH. The overall results of environmental factor in east site was the most important soil parameter in shifting the soil bacteria community along with depth and the bottom layer of the soil depth in cropland the precipitation is low contrast in soil pH as well as in depth of soil which shows in Figure 5 and in forest total precipitation gradient and soil PH in upper and lower layer seems to be same.

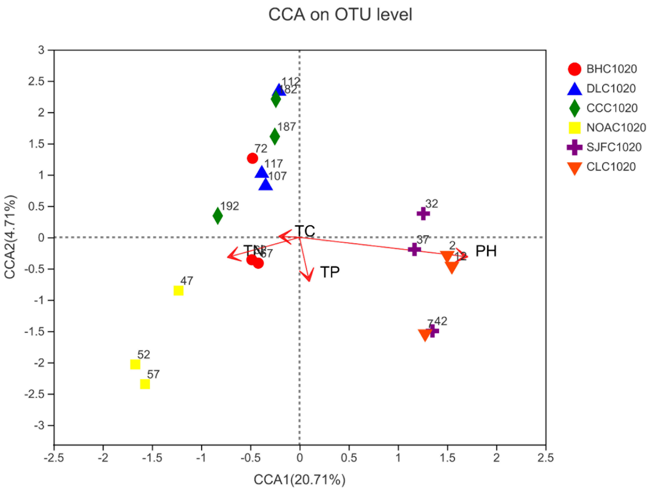

Figure 5: Canonical Correspondence Analysis (CCA) along with environmental factors. Canonical Correspondence Analysis (CCA) of soil bacteria community structure and environmental variables. The soil samples were marked with four different symbols according to their pH values. Grey arrows show the trajectory of biodiversity pattern changed with increasing of soil pH.

Comparison of micro-organisms pattern in farmland (mainly work in changling sampling site)

Farmland, is the kind of habitat and will have a major crop cultivated in this area, it shows that the soil bacteria diversity in that particular area will be least as comparing with other. Furthermore, farmland has negative effects on our environment such as soil, there as few research findings about Chinese farmlands functions but this paper gives how the soil bacteria diversity changes of farmland along with precipitation gradient in soil profile between two layers. Here we show near the surface layer of soil. In this layer, the Principle Component Analysis based on PCA on OTUs level, the distribution of bacteria phylogenetic similarity found in soil samples and other samples in different location in west site which shows variation of the bacterial community, in which BHC and DLC samples are close to each other. In addition, in which NOAC and CCC samples are furthest from others, indicating that there was greater diversity in the bacterial community the abundance of the total bacteria significantly decreased with increasing soil depth (R2 0.7533, P=0.001000) and (R2 0.6904, P=0.001000) respectively, and there are differences in the categories and proportions of dominant microorganisms (>1%) in different land-use methods soil bacterial diversity pattern (Shannon index) evenness (ACE index) and richness (Chao Index) 97% species similarity presented. Shannon diversity index was increased along with the depth with the highest value (6.81) at (10 cm-20 cm surface soil) in cropland and the lowest value (2.17) at (40-50). Besides, the evenness index declined with depth, with the highest values (5382) at 10 cm-20 cm respectively shows in Table 2.

DISCUSSION

Abundance of soil bacteria biodiversity pattern in farmland changed with precipitation

In previous reports and studies worked on the upper layer of the soil and showed soil properties only but the knowledge of soil bacteria pattern changes in depth with gradient is limited. The study objectives were to assess the effects of precipitation in soil profile of farmland from the east to west side. It investigated, how the pattern of soil bacterial community change in soil profile between two layers and biogeographical pattern affected on farmland. Thus, the difference between land-uses (east cropland and west cropland) declined with the increase in soil depths (40 cm -50 cm) because there are less and less human activity effects at this zone so there is no changes occurs inside the soil. It was found that the land uses had the strongest effects on soil bacterial diversity patterns in upper soil horizons then the deeper soil horizon (40 cm -50 cm).

In previous study, and other reports have showed that soil precipitation gradient increased from east to west in the soil profile of northeast China transect. Although we observed that the distribution of soil microbe regulations follows the same trend as soil layers in same soil type, we had not previously determined the distribution of the abundance of soil bacteria for these profiles between two layers. In this study, the soil bacteria community pattern was estimated by quantitative PCR. Quantitative PCR has its inherent limitations, such as biases in the soil DNA extraction, PCR amplification, or core genes targeted [29]. However, these limitations do not hamper its use as a highly sensitive and reproducible method for estimating the abundances of soil microbes across large scales [25,30]. In this study, although not all of the sequences generated and were identified as bacteria sequences, a high proportion (approximately 75%) of sequences were classified as soil bacteria (Table 1), which suggests that the results of this study at least partially represent the changes in bacteria abundance across the precipitation gradient in soil profile. The abundance of soil bacteria had a positive correlation with soil precipitation but no relationship with soil, suggesting that the abundance of soil bacteria biodiversity pattern in soil profiles is predominantly determined by soil health, which is consistent with the saprophytic status of the majority of bacteria [31].

This conclusion was also supported by the Canonical Correspondence Analysis CCA in cropland and forest (Figure 5), which showed that soil pH had the highest correlation value with soil microbes. Other environmental variables, such as the C/N ratio and the latitude, also showed a correlation with the changes of soil bacteria biodiversity pattern in soil profile, but the correlation values were less than that of soil pH [32].

The change law and its driving factors of soil microbial pattern from changbai mountain to songnen cropland under precipitation gradient in farmland

Global environmental change is a multifactorial phenomenon, and the concurrent action of different factors gives rise to large uncertainty in predicting effects. Precipitation gradient effects on soil microbial pattern from changbai mountain to Songnen cropland. Understanding soils is important, because they provide a range of ecosystem functions, including carbon storage, and are central to agriculture and sustainable management [33-36]. To address the impact of multiple drivers of global change, ecologists have used many tools, including observational approaches such as studying complex environmental gradients, long-term time series, and modeling. However, here we discussing how the precipitation gradient effects on the soil microbial pattern in soil profile.

Effects of agricultural practices on soil biogeographical patterns of soil microbes in soil profile

Principal component analysis was used to reflect the source of agricultural practices on soil biogeographic patterns of soil. In this study, a significantly positive correlation (at P<0.01 and P<0.05) was found between seven sampling sites, CLC indicating the source of these microbial community was possibly same [37].

In this study, some contents in a combination were strongly correlated which is represented in relative abundance of community percent showing significantly homology indicating that the source of these microbial community not only affect by the soil intrinsic properties but also anthropogenic activities such as heavy metals. Recently some studies reported that the level of soil is caused by agriculture practices i.e. water irrigation, mulching and chemical fertilizers [38]. The source of microbial communities in soil profile may be caused by the emission of vehicle exhaust and agriculture production [39]. The application of phosphate fertilizers (chemical) and organic fertilizer in soil.

CONCLUSION

This is the comprehensive study on soil bacteria diversity and composition of farmland in soil profile along with precipitation gradient in northeast china transect. Precipitation the main driving factor for the change of bacterial community composition and diversity in farmland and agricultural production activities had an effect on changes in the deep bacterial composition and diversity of farmland. The effect of agricultural production activities on the bacterial composition and diversity of the surface layer of farmland make the bacterial composition and diversity between different precipitation gradient sites are more similar and the effect of agricultural production activities on the deep bacterial composition and diversity of farmland soil make the bacterial composition and diversity more similar between different precipitation gradient sites. They are the 75% similarities in soil bacterial composition and diversity between the surfaces between different sampling points greater than between the deeper ones. The effect of agricultural production activities on the bacterial composition and diversity of the surface layer of farmland make the bacterial composition and diversity between different precipitation gradient sites more similar. Which suggested that precipitation the main driving factor for the change of bacterial community composition and diversity in farmland?

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