



Full Length Article

The Divergence of Bacterial Communities among Continuous Cropping, Rotational Cropping and New Planting Potato Soils

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Abstract

In this study, the diversity, composition and structure of bacterial community were studied in continuous cropping, rotational cropping and new planting potato soils in Hunan Province of China by using high-throughput 16S rRNA gene Illumina sequencing. The results showed that continuous cropping soil had the lowest microbial diversity, while rotational cropping and new planting soils exhibited the similar levels of microbial diversity according to Shannon and Richness indices ($P < 0.05$). The principal coordinates analysis (PCoA) showed a perfect separation among bacterial community structures of continuous cropping, rotational cropping and new planting potato soils. Community composition analysis showed that continuous cropping potato soil had higher relative abundances of non-beneficial bacteria (*Rhodanobacter*, *Gaiella*, *Flavobacterium* and *Burkholderia*) that were unfavorable for soil quality and its development as well as agricultural production. In addition, soil property analysis revealed that pH value and total organic carbon (TOC) content in continuous cropping soil was significantly lower than those in rotational cropping and new planting potato soils. Relationship between soil properties and microbial communities indicated that total phosphorus, available phosphorus, available potassium and TOC contents as well as pH were important physicochemical factors that significantly affected bacterial diversity and community structure in continuous cropping, rotational cropping and new planting soils. Therefore, the pH value and TOC content were determined as the most important physicochemical factors to alter the microbial community in continuous cropping potato soils. Collectively, these results provided valuable insights into the mechanisms of continuous-cropping obstacle, which might contribute to improve soil microbial diversity and to enhance soil productivity of continuous cropping potato soil. © 2020 Friends Science Publishers

Key words: Bacterial abundance; Community structure; Microbial diversity; Potato; Relationship

Introduction

Potato has become the fourth major food crop after rice, maize and wheat in China. China is the largest potato producer, accounting for 1/4 of total planting area and 1/5 of total production in the world (Jin *et al.* 2018). However, due to limited cultivated lands, blind pursuit of economic interests and lack of scientific planting concept, a large amount of potato is generally planted by a continuous cropping pattern that results in continuous-cropping obstacle with poor growth as well as yield and quality reduction of potato (Qin *et al.* 2017a). Changes in soil physical properties, enrichment of soil-borne pathogens, and the autotoxicity of root exudates have been recognized as the key influencing factors to lead to the continuous-cropping

obstacle (Bennett *et al.* 2012; Huang *et al.* 2013). At present, rhizosphere microenvironment of plant is commonly considered as the most important influencing factor (Dias *et al.* 2015). Several studies have compared the soil microenvironment between rotational cropping and continuous cropping patterns of some crops (Govaerts *et al.* 2007; Xuan *et al.* 2012). Therefore, understanding how rhizosphere microenvironment of potato is influenced by continuous cropping pattern can contribute to soil health and potato production.

The composition of soil microbial community and relative abundance of soil microorganism play essential roles in enhancing soil quality, improving soil ecosystem functions, and maintaining plant health and growth (Helgason *et al.* 2009; Kong *et al.* 2011). Soil microbial

diversity, community composition and structure are influenced by multiple factors, including soil types, planting patterns and management practices (Garbeva *et al.* 2004; Berg and Smalla 2009; Jangid *et al.* 2011). Therefore, it is critically necessary to employ appropriate planting pattern to enhance soil ecosystem functions (Acosta-Martínez *et al.* 2010; Bender *et al.* 2016). Different planting patterns of crops change soil properties, leading to the changes of soil microbial communities (Helgason *et al.* 2009; Lienhard *et al.* 2013). Li *et al.* (2018) have showed that the bacterial community is altered in the sweet potato soils with continuous cropping pattern for 1, 2, 3, and 4 years by pyrosequencing approach. Liu *et al.* (2014) have found that soil bacterial communities exhibit differential responses to the potato with continuous cropping pattern using pyrosequencing approach. In addition, previous studies have mainly revealed that different crop planting patterns (mainly including continuous cropping and rotational cropping patterns) and different planting histories affect soil community composition, diversity and structure (Govaerts *et al.* 2007; Kong *et al.* 2011; Hurisso *et al.* 2013). However, the questions, such as how continuous cropping of potato affects soil microbial communities; which species in soil are changed; and what are the key factors of soil properties influencing corresponding alteration of microbial communities, remain largely unexplored.

In the present study, we aimed to (i) investigate the differences of soil microbial diversity, community composition and structure among continuous cropping, rotational cropping and new planting potato soils by utilizing high-throughput 16S rRNA gene Illumina sequencing; (ii) compare the differences of the soil physicochemical properties among continuous cropping, rotational cropping and new planting potato soils; (iii) and establish the correlation between soil properties and microbial community diversity and structure. Moreover, we attempt to more systematically reveal what changes would continuous cropping pattern bring to soil properties and microbial community. Our results provided data support and theoretical basis for promoting sustainable development of potato industry through appropriate planting pattern and improving soil microecological environment of continuous cropping potato soil.

Materials and Methods

Experimental Design and Soil Sampling

The experimental field was located in Experimental Base of Hunan Agricultural University, Hunan Province, China. Field experiments of continuous cropping and rotational cropping patterns began in 2012. The field was divided into nine plots, each of 18×13 m² in size. Three plots were selected for continuous cropping and rotational cropping patterns each year, respectively. The other three plots of newly cultivated soil were designed for a new planting

potato experiment in 2017. After 6 years of continuous cropping and rotational cropping patterns and 1 year of new planting potato experiment, nine plots were used up (three replicates). Soil samples were simultaneously collected from plots in the harvesting period of potato in May 2017. From each plot, 30 potato plants were randomly selected, one core for 0–20 cm layer soil was collected from each plant, and one soil sample consisted of 15 cores. All 18 soil samples (three plots × 2) were placed into sterile plastic bags. Each composite sample was passed through a 2 mm sieve and divided into two parts. One part was air-dried for soil property analysis, and the other part was stored at –80°C for DNA extraction.

Physicochemical Characteristics of Soils

The following physicochemical properties of collected soil samples were determined: pH, total organic carbon, nitrate nitrogen, ammonia nitrogen, total nitrogen, available phosphorus, available potassium, and total phosphorus. Analysis of soil properties was performed by the Department of Nanjing Institute of Geography, CAS, using the previously published methods (Tan *et al.* 2019).

DNA Extraction and Amplicon Sequencing

DNA extraction of soil samples and amplicon sequencing were performed following Tan *et al.* (2019). The V4 region of the 16S rRNA gene was amplified using the purified DNA as a template with following primers: 515F (5'-GTGCCAGCMGCCGCGGTAA-3')/806R (5'-GGACTACHVGGGTWTCTAAT-3'). PCR amplification was conducted on a SelectCycler II (Select BioProduct). The purified amplicons were quantified by using a Qubit fluorometer, and the library was constructed with VAHTSTM Nano DNA Library Prep Kit for Illumina® (Vazyme Biotech Co., Ltd., Nanjing, China). The samples were sequenced by Miseq-sequencing machine (Illumina).

Sequence Preprocessing

Sequence preprocessing was consistent with the methods of Gu *et al.* (2019). The barcodes were assigned to the raw reads. After removal of barcodes and primers. The pair-ended sequences were quality-filtered by using Flash program (Feng *et al.* 2017). UPARSE algorithm was applied to remove chimeras and generate OTU table (Magoc and Salzberg 2011). All the sequence preprocessings were performed in an in-house pipeline (<http://mem.rcees.ac.cn:8080>) with various bioinformatics tools (such as FLASH, Btrim and UPARSE program).

Ecological and Statistical Analysis

Shannon and Richness diversity indices were calculated

Table 1: Physicochemical properties of continuous cropping, rotational cropping and new planting potato soils. CC: continuous cropping, RC: rotational cropping, NP: new planting. TOC, total organic carbon; TN, total nitrogen; NO₃-N, nitrate nitrogen; NH₄-N, ammonia nitrogen; AP, available phosphorus; AK, available potassium; WC, water content; TP, total phosphorus.

Sample	TP (mg kg ⁻¹)	TN (mg kg ⁻¹)	NH ₄ -N (mg g ⁻¹)	NO ₃ -N (mg kg ⁻¹)	AP (mg kg ⁻¹)	TOC (%)	pH	AK (mg kg ⁻¹)
CC	759.56 ± 41.78b	873.96 ± 32.76b	15.30 ± 4.53a	121.51 ± 5.24a	91.75 ± 6.45b	0.91 ± 0.06c	4.86 ± 0.09c	80.66 ± 2.80b
RC	891.12 ± 89.45a	1107.68 ± 133.69a	19.46 ± 14.97a	124.62 ± 15.02a	127.4 ± 16.71a	1.41 ± 0.20a	6.22 ± 0.25a	106.57 ± 5.99a
NP	336 ± 26.48c	930.29 ± 57.24b	14.51 ± 3.18a	116.17 ± 6.78a	15.45 ± 8.46c	1.13 ± 0.14b	5.54 ± 0.08b	46.4c ± 3.28c

Different letters represent the significant difference among soils at $P = 0.05$

according to the methods of Gu *et al.* (2019). Unweighted principal coordinate analysis (PCoA) was performed to evaluate the alteration of microbial community structure (Gu *et al.* 2019). The Pearson correlation approaches were used to construct the relationship between microbial diversity and soil properties (PCC: Pearson correlation coefficient). Mantel test and canonical correspondence analysis (CCA) were used to analyze the contributions of soil properties to bacterial community.

Results

Physicochemical Properties of Continuous Cropping, Rotational Cropping and New Planting Potato Soils

ANOVA showed that there were significant differences in soil properties ($P = 0.05$) among continuous cropping, rotational cropping and new planting soils, except for NO₃-N and NH₄-N contents (Table 1). TP, AP, TOC and AK contents as well as pH value in rotational cropping soil were significantly higher than those in continuous cropping and new planting soils. However, the TOC content and pH value in continuous cropping soil were lower than those in other samples. The lowest TP, AP, TOC and AK contents were observed in new planting soil. In addition, TP, TN, AP, TOC and AK contents as well as pH value were significantly lower in continuous cropping soils when only compared with rotational cropping soil.

Bacterial Diversity and Community Structure of Continuous Cropping, Rotational Cropping and New Planting Potato Soils

After data processing, 716,221 valid reads were obtained from the 18 soil samples. All the reads were classified into 31,167 OTUs. The Shannon (Fig. 1a) and Richness (Fig. 1b) indices were used to analyze the alpha-diversity of bacterial communities in continuous cropping, rotational cropping and new planting soils. We found that continuous cropping soil had the lowest microbial diversity, while rotational cropping and new planting soils had the similar levels of bacterial diversity. Moreover, we further analyzed beta-diversity of microbial communities in continuous cropping, rotational cropping and new planting soils. The PCoA showed a perfect separation among bacterial community structures of continuous cropping, rotational cropping and new planting potato soils (Fig. 2). In addition, the dissimilarity tests of bacterial communities were carried out

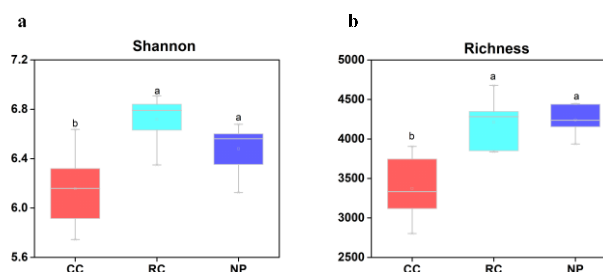


Fig. 1: Diversity indices based on 16S rRNA gene of bacterial community in continuous cropping, rotational cropping and new planting potato soils. (a) Shannon index; (b) Richness index. Different letters represent the significant difference among soils at $P = 0.05$. CC: continuous cropping, RC: rotational cropping, NP: new planting, similarly hereinafter

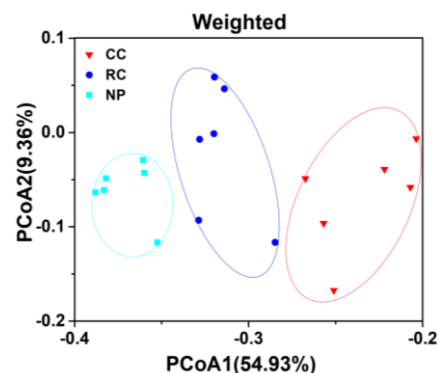


Fig. 2: Principal component analysis (PCA) of bacterial community structures in continuous cropping, rotational cropping and new planting potato soils

using ANOSIM and MRPP based on Bray-Curtis distance, and the results showed that the significant differences also existed in soil bacterial communities among continuous cropping, rotational cropping and new planting soils (Table 2). In summary, we concluded that there were significant differences for alpha- and beta-diversity among continuous cropping, rotational cropping and new planting soil bacterial communities.

Microbial Community Compositions of Continuous Cropping, Rotational Cropping and New Planting Potato Soils

All bacterial operational taxonomic units (OTUs) of 18 soil samples were identified into 949 genera and 36 phyla at a similarity level of 97%. The cladogram indicated the

Table 2: Dissimilarity test of bacterial community structure in continuous cropping, rotational cropping and new planting potato soils based on Bray-Curtis distance. CC: continuous cropping, RC: rotational cropping, NP: new planting

Comparison	MRPP			ANOSIM
	Delta	P	R	P
NP VS. CC	0.6017	0.002**	1	0.004**
NP VS. RC	0.6074	0.001***	1	0.002**
CC VS. RC	0.6094	0.004**	0.987	0.003**

Difference is significant at $P = 0.01$ level. *Difference is significant at $P = 0.001$ level.

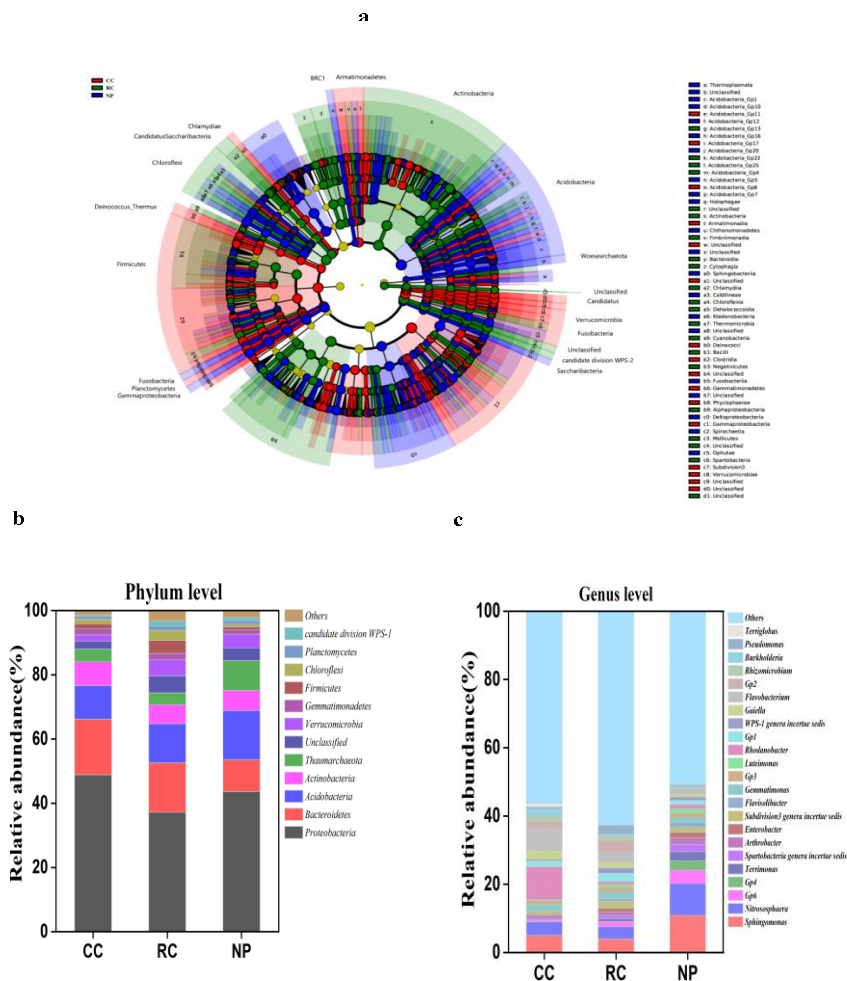


Table 3: Relative abundances of dominant phyla and genera in soil bacterial communities of continuous cropping, rotational cropping and new planting potato soils. CC: continuous cropping, RC: rotational cropping, NP: new planting

Dominant phyla (>1%)	Relative abundance in potato soil communities		
	CC	RC	NP
<i>Proteobacteria</i>	48.88a	37.199a	43.656a
<i>Acidobacteria</i>	10.447b	12.8ab	15.344a
<i>Bacteroidetes</i>	17.337a	15.403a	9.912b
<i>Actinobacteria</i>	7.435a	5.96a	6.242a
Unclassified	2.474b	5.319a	3.921ab
<i>Firmicutes</i>	1.583b	4.043a	0.861b
<i>Planctomycetes</i>	0.926b	1.374a	1.227a
<i>Verrucomicrobia</i>	1.948b	5.016a	4.267a
<i>Chloroflexi</i>	1.39b	3.144a	0.835b
<i>Gemmatimonadetes</i>	1.889a	1.946a	1.382a
Candidate division WPS-1	0.424b	1.544a	0.957b
<i>Thaumarchaeota</i>	3.928b	3.629b	9.324a
Dominant genera (>1%)			
<i>Sphingomonas</i>	5.006b	3.929b	10.884a
<i>Nitrososphaera</i>	3.926b	3.612b	9.32a
Gp6	0.472c	1.431b	3.916a
Gp4	0.049b	0.147b	2.738a
<i>Terrimonas</i>	0.081b	0.715b	2.658a
<i>Spartobacteria genera incertae sedis</i>	0.389c	1.045b	2.145a
<i>Arthrobacter</i>	0.971b	1.002b	1.953a
<i>Enterobacter</i>	0.291b	1.068ab	1.593a
Subdivision3 genera incertae sedis	0.936c	2.139a	1.53b
<i>Flavisolibacter</i>	0.184b	0.686ab	1.414a
<i>Gemmatimonas</i>	1.889a	1.946a	1.382a
Gp3	1.119a	1.428a	1.313a
<i>Luteimonas</i>	0.199b	0.779b	1.294a
<i>Rhodanobacter</i>	9.604a	0.835b	1.226b
Gp1	1.728ab	2.486a	1.198b
WPS-1 genera incertae sedis	0.424b	1.544a	0.957ab
<i>Gaiella</i>	2.443a	1.781ab	0.883b
<i>Flavobacterium</i>	6.817a	3.000b	0.728c
Gp2	1.904b	3.32a	0.565c
<i>Rhizomicrobium</i>	1.747a	1.241a	0.507b
<i>Burkholderia</i>	1.986a	0.54b	0.464b
<i>Pseudomonas</i>	0.444b	2.634a	0.381b
<i>Terriglobus</i>	1.126a	0.094b	0.123b
Others	55.797	61.488	50.485

Different letters represent the significant difference among soils at $P = 0.05$

(1.948%) and candidate division WPS-1 (0.424%) were observed in continuous cropping soil ($P < 0.05$; Fig. 3b).

The 23 dominant genera (relative abundance >1%) across all samples were *Spartobacteria genera incertae sedis*, *Arthrobacter*, *Enterobacter*, Subdivision 3 genera incertae sedis, *Flavisolibacter*, *Gemmatimonas*, Gp3, *Luteimonas*, *Rhodanobacter*, Gp1, WPS-1 genera incertae sedis, *Gaiella*, *Flavobacterium*, Gp2, *Rhizomicrobium*, *Burkholderia*, *Pseudomonas* and *Terriglobus* (Fig. 3c). The relative abundances (Table 3) of genera Subdivision3 genera incertae sedis (2.139%), Gp1 (2.486%), WPS-1 genera incertae sedis (1.544%), Gp2 (3.32%) and *Pseudomonas* (6.817%) in rotational cropping soil were significantly higher than those of continuous cropping and new planting soils ($P = 0.05$) and the highest relative abundances of genera *Rhodanobacter* (9.604%), *Gaiella* (2.443%), *Flavobacterium* (2.443%), *Burkholderia* (1.986%) and *Terriglobus* (1.126%) and the lowest relative abundances of genera *Flavisolibacter* (0.184%), Gp6 (0.472%), *Spartobacteria genera incertae sedis* (0.389%), *Enterobacter* (0.291%), Subdivision3 genera

incertae sedis (0.936%) and WPS-1 genera incertae sedis (0.424%) were observed in continuous cropping soil. Overall, the microbial composition and relative abundance of bacterial phyla and genera were significantly different among continuous cropping, rotational cropping and new planting soils.

The Relationship Between Soil Properties and Bacterial Community

Table 4 shows the relationship analysis between soil properties and five alpha-diversity indices of bacterial communities by Pearson correlation approach. The results showed that TP content was significantly positively correlated with Shannon (PCC = 0.519, $P = 0.027$) and Pelou_evenness (PCC = 0.593, $P = 0.010$). AP content was significantly positively correlated with Simpson (PCC = 0.592, $P = 0.010$) and Chao1 (PCC = 0.471, $P = 0.048$). TOC content was significantly positively correlated with Shannon (PCC = 0.687, $P = 0.002$) and Richness (PCC = 0.701, $P = 0.001$) as well as Pelou_evenness (PCC = -0.630,

Table 4: Relationship between soil properties and alpha-diversity of continuous cropping, rotational cropping and new planting potato soils

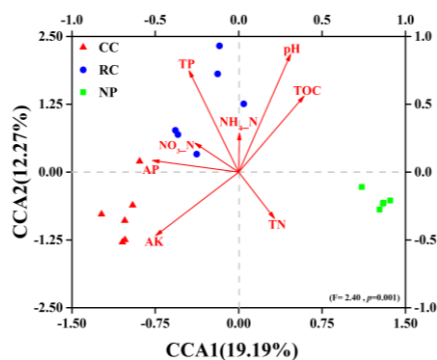
Soil properties	Shannon		Simpson		Richness		Pelou_evenness		Chao1	
	PCC	P	PCC	P	PCC	P	PCC	P	PCC	P
TP	0.519	0.027*	0.681	0.002**	0.269	0.280	0.593	0.010**	0.002	0.994
TN	-0.010	0.970	-0.302	0.223	0.156	0.536	-0.074	0.771	0.295	0.234
NH ₄ -N	0.195	0.437	0.099	0.697	0.197	0.432	0.188	0.455	0.163	0.519
NO ₃ -N	0.225	0.368	0.383	0.117	0.001	0.998	0.309	0.213	-0.126	0.619
AP	0.135	0.593	0.592	0.010**	0.186	0.459	0.263	0.292	0.471	0.048*
TOC	0.687	0.002**	0.220	0.380	0.701	0.001***	0.630	0.005**	0.436	0.071
pH	0.628	0.005**	0.343	0.163	0.633	0.005**	0.583	0.011*	0.462	0.054
AK	0.372	0.128	0.739	0.001***	0.059	0.816	0.479	0.044*	-0.260	0.297

PCC= Pearson correlation coefficient. *Difference is significant at $P = 0.05$ level. **Difference is significant at $P = 0.01$ level. ***Difference is significant at $P = 0.001$ level

Table 5: Correlation analysis between soil properties and bacterial community structures based on Mantel test

Soil properties	r.BC	p.BC	r.JC	p.JC
TP	0.1962	0.016*	0.1930	0.029*
TN	-0.0099	0.479	0.0566	0.192
NH ₄ _N	0.0012	0.395	-0.0313	0.698
NO ₃ _N	-0.0085	0.478	-0.0981	0.919
AP	0.6436	0.001***	0.7175	0.001***
TOC	0.2978	0.005**	0.2636	0.007**
pH	0.5054	0.001***	0.4534	0.001***
AK	0.635	0.001***	0.7138	0.001***

*Difference is significant at $P = 0.05$ level. **Difference is significant at $P = 0.01$ level. ***Difference is significant at $P = 0.001$ level

**Fig. 4:** CCA plots of bacterial community structures correlated with soil physicochemical properties

$P = 0.005$). Moreover, pH was significantly positively correlated with Shannon (PCC = 0.628, $P = 0.005$) and Richness (PCC = 0.633, $P = 0.005$) as well as Pelou_evenness (PCC = 0.583, $P = 0.011$). AK was significantly positively correlated with Simpson (PCC = 0.739, $P = 0.001$) and Pelou_evenness (PCC = 0.479, $P = 0.044$). Therefore, the TP, AP, TOC and AK contents as well as pH value were important physicochemical factors to affect alpha-diversity of bacterial communities in continuous cropping, rotational cropping and new planting soil. To investigate the contribution of above-mentioned soil factors to microbial community of continuous cropping, rotational cropping and new planting potato soils, a CCA was conducted to study the relationship between soil properties and microbial community structures (Fig. 4). The CCA plots also clearly showed that pH, TP, AP, AK and TOC contents were the five long vectors, and pH was the

longest vector. To identify the most important factors influencing the soil bacterial community, the Mantel test based on both Bray-Curtis and Jaccard distances was adopted. The results further confirmed that pH, TP, AP, AK and TOC contents were significantly positively correlated with microbial community (Table 5). Overall, it was concluded that pH, TP, AP, AK and TOC contents were the important soil factors to powerfully drive the bacterial community assembly in continuous cropping, rotational cropping and new planting potato soils.

Discussion

Continuous-cropping problem, also called the continuous-cropping obstacle, is common phenomenon in the cultivation of potato in China. It has been reported that long-term continuous cropping pattern brings negative effects to soil micro-ecosystem, leading to the deterioration of soil physicochemical properties, occurrence of various soil-borne diseases and decline of the crop yield (Huang *et al.* 2013; Zhang *et al.* 2018). Recently, the comparative studies on soil properties of crop under continuous cropping and rotational cropping pattern have been reported (Liu *et al.* 2017; Li *et al.* 2018). TOC content and pH value were significantly lower in continuous cropping soils than those in rotational cropping and new planting soils which were consistent with the previous studies that continuous cropping of sweet potato causes soil acidification and a significant decline in soil organic carbon (Li *et al.* 2018). In addition, when only compared with rotational cropping soil, TP, TN, AP, TOC and AK contents as well as pH value were significantly lower in continuous cropping soils, which was consistent with the previous studies that long-term continuous cropping pattern leads to the decreased soil available nutrients in potato (Liu *et al.* 2015; Zhou *et al.* 2018). Moreover, several studies have revealed that the accumulation of allelochemicals in plant exudates may contribute to continuous-cropping obstacle (Song *et al.* 2018), while it is a far more controversial idea (Wu *et al.* 2016). Thus, more studies tend to focus on the response of soil microbial communities and their correlations with the changes of soil properties to continuous-cropping obstacle (Xiong *et al.* 2015).

Soil microbial diversity and community structure are closely associated with soil quality, ecosystem functions,

and sustainable development (Govaerts *et al.* 2007; Kong *et al.* 2011), thereby impairing the plant growth, development, health and productivity. Our results showed that continuous cropping soil had the lowest level of alpha-diversity compared with rotational cropping and new planting potato soils according to Shannon and Chao1 indices. This finding was consistent with some previous reports that long-term continuous cropping pattern decreases microbial diversity and alters community structure compared with the crop rotation system of tobacco (Chen *et al.* 2018), soybean (Liu *et al.* 2017), cotton (Zhang *et al.* 2013), rice (Xuan *et al.* 2012) and sweet potato (Li *et al.* 2018). The soil of higher microbial diversity was more likely to maintain the function of soil ecosystems, enhance the resistance of abiotic and biotic environmental stresses and give defense against soil-borne diseases (Garbeva *et al.* 2004; Li *et al.* 2010). However, rotational cropping and new planting soils had similar level of alpha-diversity, indicating that crop rotation was an effective planting pattern for maintaining the function of soil ecosystems. It has been reported that long-term continuous cropping pattern leads to soil-borne diseases in potato (Qin *et al.* 2017b), indicating that lower level of soil microbial diversity may be associated with the occurrence of soil-borne diseases (Shi *et al.* 2019). In addition, beta-diversity analysis based on PCoA and dissimilarity tests showed that the microbial community structure of continuous cropping, rotational cropping and new planting potato soils was significantly different. Microbial community structure is also regarded as an indicator of soil health (Valadares-Pereira *et al.* 2017). Overall, continuous cropping pattern of potato decreased soil microbial diversity and altered community structure that affected directly or indirectly the soil quality and ecosystems, consequently resulting in negatively influenced potato production.

The cladogram analysis showed that the microbial community components of continuous cropping, rotational cropping and new planting soils had significant differences from phylum to genus levels ($P < 0.05$). This finding was consistent with that the microbial community composition is significantly different among continuous cropping, rotational cropping and new planting soils of other plants according to Sun *et al.* (2014) and Liu *et al.* (2017). In addition, the relative abundance of some bacterial phyla and genera was significantly altered among continuous cropping, rotational cropping and new planting potato soils. The relative abundances of phyla *Firmicutes* (4.043%), *Chloroflexi* (3.19%) and candidate division WPS-1 (2.92%) in rotational cropping soil were significantly higher than those of continuous cropping and new planting soils, while the lowest abundances of *Acidobacteria* (10.447%), *Planctomycetes* (0.926%), *Verrucomicrobia* (1.948%) and candidate division WPS-1 (0.424%) were observed in continuous cropping soil ($P = 0.05$). Previous reports have indicated that phylum *Firmicutes* may be involved in the defense against vanilla *Fusarium* wilt disease in soils of

sugar beet (Li *et al.* 2018). The phyla *Verrucomicrobia* and *Acidobacteriaca*n play important roles in soil biogeochemical cycling processes (Shen *et al.* 2017) and nutrient cycling (Yang *et al.* 2019a), respectively. The phylum *Planctomycetes* is involved in the absorption of plant nutrients, especially in the utilization of carbon and nitrogen sources (Bhattacharyya *et al.* 2017). The phylum candidate division WPS-1 shows a significantly positive relationship with soil nutrient cycling (Ji *et al.* 2018). Phylum *Chloroflexi* can also play an important role in the biogeochemical chlorine cycle (Krzmarzick *et al.* 2012), which may explain why the pH value was increased in rotational cropping soil. In addition, the highest relative abundances of genera *Rhodanobacter* (9.604%), *Gaiella* (2.443%), *Flavobacterium* (2.443%), *Burkholderia* (1.986%) and *Terriglobus* (1.126%) were observed in continuous cropping soil. Some of these genera are regarded as non-beneficial bacteria in soils according to previous studies. For example, *Rhodanobacter* and *Flavobacterium* have the denitrification ability that is defined as the reduction of nitrate or nitrite to gaseous nitrogen (Prakash *et al.* 2012; Hatayama *et al.* 2016), thus leading to the decreased content of nitrogen nutrition in soil (Green *et al.* 2012; Liu *et al.* 2019), which is unfavorable to agricultural production. *Gaiella* is negatively correlated with microbial activity and biomass in soils that plays the important role in nutrient cycling and ecosystem sustainability (Yao *et al.* 2003; Yang *et al.* 2019b). Some species of *Burkholderia* are recognized as pathogens of plants and animals (Bergmark and Poulsen 2012). Overall, rotational cropping pattern significantly increased the relative abundances of beneficial bacteria that could significantly promote the absorption of nutrients, improve the utilization efficiency of organic matter and enhance the resistance against diseases. However, continuous cropping pattern increased the relative abundances of non-beneficial bacteria that were unfavorable for soil quality development and agricultural production.

Furthermore, evaluation of the relationship between the soil physicochemical properties and bacterial community in continuous cropping, rotational cropping and new planting soils provides direct insights into the mechanisms of continuous-cropping obstacle (Li *et al.* 2018), which can contribute to improvement of soil productivity and health for continuous cropping potato soil. In this study, pH value as well as TP, AP, AK and TOC contents were the important soil factors to powerfully drive the bacterial community assembly in continuous cropping, rotational cropping and new planting potato soils, and the CCA plots also showed that pH was the longest vector. Previous studies have indicated that the microbial community and diversity of the bacterial communities in continuous cropping and rotational cropping soybean soils are affected by pH, TN, TP, AK, AN and AP contents (Liu *et al.* 2017), and soil pH has also been proved to be the most important influential factor (Fierer and Jackson 2006). In addition, the alterations of bacterial community in the

sweet potato soils with continuous cropping pattern are mainly driven by soil pH and soil organic matter (Li et al. 2018). Our results showed that TOC content and pH value were significantly lower in continuous cropping soils than those in rotational cropping and new planting soils. Overall analyses of relationship between the soil physicochemical properties and bacterial community revealed that the pH value and TOC content are the most important physicochemical factors to alter the microbial community in continuous cropping potato soils.

Conclusion

This study investigated the divergence of bacterial communities among continuous cropping, rotational cropping and new planting potato soils. In general, the continuous cropping pattern of potato decreased the microbial diversity, increased the abundances of non-beneficial bacteria, and altered the community structure compared with rotational cropping and new planting potato soils. In addition, the pH value and TOC content were determined as the most important physicochemical factors to alter the microbial community in continuous cropping potato soils. This study provided valuable insights into the occurrence mechanisms of potato continuous-cropping obstacle, which might contribute to improving soil microbial diversity and enhancing soil productivity of continuous cropping potato soil.

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