

# Effects of plant cultivars on the structure of bacterial and fungal communities associated with ginseng

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## Research article

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## Abstract

## Background

There is a growing awareness of the importance of root-associated bacteria and fungi to plant growth. At present, little is known about whether different ginseng cultivars affect the soil rhizosphere microbial community.

## Results

Here, we examined the changes in the microorganismal diversity and composition of the rhizospheres of different ginseng cultivars. We found that fungal communities were more influenced by the cultivars than bacterial communities and revealed differences in the microbial community composition and diversity among the different ginseng cultivars. We found that fungal diversity was negatively correlated with bacterial diversity in CBGL, JYSH and SZSZ; however, TSBT had the lowest bacterial and fungal diversity. We also discovered certain rhizosphere microorganisms that may be associated with pathogenicity and the lifespan of ginseng cultivars, including *Bacillus*, *Alternaria alternata* and *Cladosporium* spp.

## Conclusions

Our results showed that the microbial diversity and community structures under different ginseng cultivars are significantly different and are related to the host cultivar. This result is helpful in providing information that could be used for the breeding of *Panax ginseng*.

## Background

Increasing evidence indicates that rhizosphere microorganisms have a significant influence on plant growth, root structure and nutrient uptake [1],[2] and the diversity and composition of rhizosphere microbial communities are essential for maintaining soil quality and plant health. Plant roots can promote or prevent the recruitment of rhizosphere microorganisms by secreting root exudates and volatile compounds [2]. [3]Some root exudates, such as various organic acids and amino acids as well as other compounds, are released into the rhizosphere and thus become nutrients for rhizosphere microbes [4], affecting the composition and diversity of rhizosphere microbial communities [5]. Moreover, the release of root exudates is affected by plant species, plant cultivars and environmental factors, which creates a unique environment for microorganisms [6]. Different plant cultivars may develop unique microbial communities through the interactions between plant roots and microorganisms, which may also lead to changes in the functions of microorganisms in the rhizosphere soil[7]. In particular, understanding the effect of plant cultivars (different plant genotypes) on soil microbial communities is very helpful for the cultivation of crops.

Rhizosphere microorganisms not only affect the growth of annual crops but also seriously affect the growth of perennial crops [8, 9], particularly ginseng. Ginseng root, a traditional Chinese medicine, has long been used in clinic for the treatment of various diseases, such as diabetes, hypertension[10] and Alzheimer's disease[11]. As people have begun to pay more attention to their health, ginseng has become an important edible medicinal edible plant [12]. In recent years, wild ginseng germplasm resources have been made scarce due to excessive exploitation. Thus, wild ginseng has been gradually displaced by cultivated ginseng on the market [13]. In general, the growth period of cultivated ginseng is only 4–5 years, and studies have suggested yield losses of up to 30%-60% in cultivated ginseng because of soil-borne diseases[14]. However, subsequent replanting usually fails due to obstacles to continuous

cropping[15]. Dong et al. (2018) suggested that the bacterial diversity decreased and fungal diversity increased in the rhizosphere soils of cultivated ginseng under continuous cropping[16]. Long-term ginseng cultivation leads to the prevalence of pathogenic microbes in rhizosphere soil, such as *Fusarium*, thus upsetting the balance of rhizosphere microorganisms, leading to the failure of ginseng continuous cropping [17]. These problems with continuous cropping hinder the development of the ginseng industry [18].

Cultivated ginseng is mainly divided into four cultivars according to their cultivation regions and root morphology, namely, COMMON, BIANLIAO, SHIZHU and GAOLI ginseng. Different ginseng cultivars show different levels of stress resistance. GAOLI ginseng, COMMON ginseng, BIANLIAO ginseng and SHIZHU ginseng are mainly cultivated in Korea (also cultivated in China and Japan), Fusong County in Jilin Province, Kuandian Manchu Autonomous County in Liaoning Province and Ji'an city, Tonghua city, Jilin Province, respectively. In addition, all ginseng seedlings are planted directly in the fields except Biantiao ginseng seedlings. In general, ginseng plantations typically grow young BIANLIAO ginseng seedlings for three years, then transplant them to the field where they continue to grow. Among the four ginseng cultivars, SHIZHU ginseng has high stress resistance, and BIANLIAO ginseng has a long survival time[19]. These characteristics may be related to rhizosphere microorganisms. However, to our knowledge, no study has investigated the contributions of different ginseng cultivars to shaping the rhizosphere microbial community.

Most research on rhizosphere communities has focused on bacterial communities. However, rhizosphere fungal communities are also important in soil microbial communities and may be associated with the spread of soil-borne disease. Therefore, the combination of fungal and bacterial microbial communities is more conducive to studying the changes in the rhizosphere microorganisms of the four ginseng cultivars. Therefore, in our study, the 16S rDNA and ITS regions from the total ginseng rhizosphere microorganism community were analyzed (1) to investigate the diversity and structure of the bacterial and fungal communities of the different ginseng cultivar rhizospheres and (2) to identify the dominant bacterial and fungal communities in the rhizosphere soil of different ginseng cultivars. The results of this study provide insight into the variations in the rhizosphere soil microbial community of different ginseng cultivars, which can provide a theoretical basis for the cultivation of ginseng and promote the development of ginseng as well as medicinal plants in the ginseng genus.

## Result

### Diversity of the rhizosphere microbial community of different cultivars

In total, we obtained 727476 and 1452196 high-quality reads from all samples, and 4242 and 4830 OTUs were identified for bacteria and fungi with 97% sequence similarity, respectively (Table S2). The number of OTUs of bacterial and fungal communities detected for CBGL, JYSH, SZSZ and TSBT were 3093, 3288, 2937, 2541 and 2261, 1652, 2372, 1113, respectively (Fig 1). Intriguingly, the proportion of shared OTUs for the fungal community was relatively smaller than that for the bacterial community between every two soil groups.

There were no significant differences in bacterial diversity in the rhizosphere soil between CBGL and SZSZ according to the alpha diversity indices (i.e., observed species, Chao 1, Ace and Shannon indexes) (ANOVA,  $p > 0.05$ , Table 1). Among these groups, the highest bacterial richness was detected in JYSH (2212.1429 of observed species). Moreover, the fungal diversity varied considerably across the rhizosphere soil of the different ginseng cultivars (ANOVA,  $p < 0.05$ , Table 1), and SZSZ had a significantly higher species richness than the other samples (1116.5000 of observed species) (Table 1). Furthermore, JYSH had a lower level of fungal richness (673.4286 of observed species) than the other groups (Table 1). TSBT had the lowest microbial richness for both fungi and bacteria (the observed species was

548.6667 for fungi and 1661.0000 for bacteria). In addition, we also found that fungal diversity was negatively correlated with bacterial diversity in CBGL, JYSH and SZSZ.

### Composition of the bacterial community

We assessed the taxonomic distributions of bacterial OTUs at different levels. Whether at the phylum level or at the order level, no significant differences in the composition of bacterial communities were detected among the rhizosphere soils of the different ginseng cultivars. At the phylum level, 10 dominant bacterial phyla were assigned, which made up 95% of the entire bacterial community. Proteobacteria, Acidobacteria and Verrucomicrobia were the most abundant phyla across all samples, accounting for 22.41% ~ 26.99%, 18.14% ~ 34.07% and 5.99% ~ 17.64% of the total valid reads in all samples, respectively (Fig 2a). Among them, Acidobacteria was the most abundant phylum in CBGL, and its relative abundance was significantly higher than that in the other groups (ANOVA,  $p < 0.05$ , Fig S1a), while Proteobacteria was the most abundant phylum across the other groups. The relative abundance of Proteobacteria was not different across the rhizospheres of the four ginseng cultivars (ANOVA,  $p > 0.05$ , Fig S1a). Moreover, there were significant differences among the four samples in their other main bacterial phyla, such as AD3, Nitrospirae, and TM7 (ANOVA,  $p < 0.05$ , Fig S1a).

At the class level, the abundant classes were Alphaproteobacteria (13.5682%), Spartobacteria (averaging 11.8407%), Acidobacteriia (averaging 8.4706%), Solibacteres (averaging 4.7707%) and Actinobacteria (averaging 4.5109%) (Fig 2c). At the genus level, the relative abundance of *Bacillus* was significantly higher in SZSZ and TSBT than in CBGL and JYSH (ANOVA,  $p < 0.05$ , Fig 3a; 4a).

### Composition of the fungal community

We also explored the fungal community by ITS sequencing with the same analysis method used for the 16S above. There were three dominant fungal phyla in the rhizosphere soil of all four ginseng cultivars. The relative abundances of Basidiomycota (range 19.2685% ~ 29.2577%), Ascomycota (range 26.0865% ~ 62.2524%), and Zygomycota (range 13.6333% ~ 45.7716%) accounted for more than 90% of the relative abundance across JYSH, CBGL, SZSZ, and TSBT (Fig 2b). However, the relative abundances of these dominant fungal phyla showed some differences across the four ginseng cultivars. The relative abundance of Ascomycota in SZSZ was significantly higher than that in the other samples (ANOVA,  $p < 0.05$ , Fig S1b). In addition, the relative abundance of Zygomycota in SZSZ was significantly lower than that in other ginseng cultivar rhizosphere soils (ANOVA,  $p < 0.05$ , Fig S1b).

At the class level, based on the average relative abundance, the main classes were Sordariomycetes (16.83%), Agaricomycetes (10.57%), Eurotiomycetes (9.29%), Dothideomycetes (8.81%) and Tremellomycetes (6.40%). Among them, Sordariomycetes was the dominant class in all groups except for TSBT, in which the main class was Agaricomycetes (15.54%) (Fig 2d). At the genus level, *Mortierella* was the most abundant genus among the four ginseng cultivars (Fig 3b). However, the distribution of dominant fungal genera showed differences across the four cultivars. *Mortierella* was more abundant in TSBT than in other samples (ANOVA,  $p < 0.05$ , Fig 4b), while *Alternaria\_alternata* and *Cladosporium\_sp\_agrAR069* were significantly more abundant in CBGL, JYSH and SZSZ than in TSBT (ANOVA,  $p < 0.05$ , Fig 5).

We performed beta diversity analysis for the rhizosphere bacterial and fungal communities to reflect the similarities among the different ginseng cultivars. The clustering results of the beta diversity analysis performed using the weighted UniFrac distance matrix and the Bray-Curtis distance matrix revealed a similar microbial community structure for the replicates in each group. We found that the bacterial and fungal compositions were obviously different among the four ginseng cultivars (Fig 6).

## Linear Discriminant Analysis Effect Size (LEfSe) of the bacterial and fungal communities in the rhizosphere of the four ginseng cultivars

To provide more information on the rhizosphere bacterial and fungal communities of the different cultivars, we used LEfSe to identify differentially abundant taxa among CBGL, JYSH, SZSZ and TSBT with an LDA score higher than 2.0 (Fig S2a). The LEfSe analysis of the rhizosphere bacterial community showed that there were 47 distinctly abundant taxa among the four ginseng cultivars. Of the 47 taxa, 11 were differentially abundant in CBGL, notably, Solibacteres, Acidobacteriia, DA052 and Gemmatimonadetes. The enriched taxa in JYSH were the phylum Nitrospirae and the classes Chloracidobacteria, Acidobacteria\_6 and Thermoleophilia. The distinctly abundant taxa in the rhizosphere soils of SZSZ were the classes Actinobacteria, Spartobacteria and Deltaproteobacteria and the Rhizobiales order. The Bacteroidetes, Ktedonobacteria, AD3, Verrucomicrobia and TM7 phyla and the Gammaproteobacteria class were enriched in TSBT (Fig 6a).

A total of 79 abundant fungal taxa were significantly different across CBGL, JYSH, SZSZ and TSBT (Fig S2b). Among the 79 fungal taxa, 20 taxa were enriched in CBGL, principally the Nectriaceae and Pleosporaceae families and the Tremellomycetes class. The abundant fungal taxa in the rhizosphere of JYSH were the Sordariales order and the Leotiomycetes and Capnodiales classes. The most distinctly abundant fungal taxa were Eurotiomycetes, Dothideomycetes and Agaricales in the SZSZ. The enriched fungal taxa in TSBT were the Zygomycota phylum and the Boletales order (Fig 6b).

## Discussion

### Fungi were more influenced by cultivars than bacteria

Studying the rhizosphere microbial community can shed new light on the growth and health of *P. ginseng*. In this study, we investigated the importance of cultivar factors in shaping the rhizosphere microbial communities of ginseng. The rhizosphere soil samples of four ginseng cultivars were collected from their respective main cultivation regions; different ginseng cultivars grow in unique ecological environments, so we could not collect the ginseng rhizosphere soil under identical conditions. In our study, we found that the proportion of shared fungal OTUs was much smaller than that of bacterial OTUs between any two pairs of samples, suggesting that the fungal communities were sensitive and more influenced by the cultivars than the bacterial communities. Previous studies reported that bacterial communities are more resistant and resilient to environmental disturbances in terms of structure and diversity than fungal communities [20]. One possible explanation for this phenomenon is that bacteria are able to metabolize a range of compounds; thus, bacterial communities are relatively stable. In a recent study of three *Agave* species, Devin Coleman-Derr et al. (2016) also found that there were shared a larger fraction of bacterial OTUs than fungal OTUs[21].

### Ginseng cultivars affected rhizosphere microbial diversity

We also found that the different ginseng cultivars had significantly different fungal diversity in the rhizosphere soil (Table 1, Table 2). The microbial diversity was probably affected by a wide variety of factors, such as geographic location as well as plant genotype and growth stage [22, 23]. In our study, all soil samples of the four ginseng cultivars were collected at the same growth stage, which was the fruiting period of ginseng cultivated for five years, so we can exclude the impact of different growth periods on the microbial community. Moreover, the rhizosphere microbial diversity of SZSZ and CBGL were similar, but the two sampling locations were not geographically close. In addition, the sampling locations of CBGL and JYSH were closer to each other than other location pairs, but their bacterial and fungal diversity were different, suggesting that geographic location is not the main factor causing changes in microbial diversity. Thus, we inferred that the cultivated varieties of ginseng affect the rhizosphere microbial diversity. Different

ginseng cultivars might have different compositions of root exudates, such as organic acids, which affect the diversity of rhizosphere microorganisms.

- Moreover, we also found that fungal diversity was negatively correlated with bacterial diversity in all groups except for TSBT. This could be explained by the fact that long-term cultivation depleted the soil of nutrients such as carbon. Ginseng grown continuously for six years might result in nutrient deficiency stress in the microbial community of rhizosphere soil, which would lead to an imbalance in microbial diversity. A similar phenomenon also occurred in *Rehmannia glutinosa* rhizosphere microbes under consecutive monoculture[24]. TSBT had the lowest bacterial diversity and fungal diversity of all the ginseng cultivar rhizosphere soils. This may have been caused by artificial factors, but the sampling methods for all rhizosphere soils were consistent, so we can rule out this possibility. However, this difference in diversity might be related to the cultivation method for BIANLIAO ginseng. Ginseng plantations typically grow young BIANLIAO ginseng seedlings for a period of time before transplanting them to the field [25]. The rhizosphere microbial community might be assembled early in plant development, and later transplantation may alter the natural microbial community diversity.

## Plant cultivars change the composition of the microbial community in the ginseng rhizosphere

Although no significant differences in the composition of bacterial and fungal communities were detected among ginseng cultivars or in the examination of different taxonomic levels, the taxonomic abundance of certain dominant bacterial groups showed significant differences among the cultivars. These findings demonstrate that ginseng cultivars affected the composition of the rhizospheric microbial community; however, the different cultivars might not result in different specific taxa in the community and could only lead to changes in the dominance of certain taxa in the microbial community. Some microorganisms had a special affinity for certain plant cultivars, which is in accordance with previous studies showing the effect of plant cultivars on rhizosphere communities. [26], [27], [28].

Significant differences in the abundances of dominant bacterial phyla were found. For example, Proteobacteria was significantly enriched in SZSZ, and Acidobacteria had a high abundance in JYSH. *Ying et al.* (2012) also showed that Proteobacteria and Acidobacteria were the dominant phyla in the ginseng rhizosphere [15]. Furthermore, Ascomycota was significantly abundant in SZSZ, and Agaricomycetes (belonging to the Basidiomycota phylum) was also more abundant in TSBT than in other samples. Ascomycota and Basidiomycota are known to promote resistance to pathogens and tolerance to abiotic stresses and are widely found in the rhizosphere soils of plants [29]. These biomarkers that were significantly present in the soils of the different ginseng cultivars indicate the specificity of the rhizosphere microorganisms of the different ginseng cultivars; these microorganisms may participate in the growth of different ginseng cultivars. It has also been shown that ginseng cultivars can affect the composition of the structure of rhizosphere microorganism communities. Moreover, the root morphologies of the four ginseng cultivars were different, and the different root morphologies might result in the colonization of unique microbial communities in the rhizosphere soil. *Laurent Philippot et al.* (2013) proposed that differences in root morphology could greatly affect the composition of rhizosphere microbes [30].

## Rhizosphere microorganisms associated with pathogenicity and the survival time of ginseng

In our research, we also found links with potentially pathogenic microorganisms. For bacteria at the genus level, *Bacillus* was significantly more abundant in SZSZ than in TSBT, CBGL and JYSH (ANOVA,  $p < 0.05$ , Fig. 4a). *Bacillus* species are gram-positive, sporulating aerobes or facultative anaerobes that are widely distributed in the soil environment; many isolates possess antifungal effects, promoting plant growth[31],[32]. The enrichment of the genus

*Bacillus* in the SZSZ could be related to SHIZHU ginseng having high stress resistance. *Bacillus* species can produce antimicrobial substances (AMS) to prevent the deleterious effects of phytopathogens [33],[34].

For fungi, *Mortierella* was the most abundant genus in the rhizosphere of all ginseng cultivars, accounting for 26.6722% of the total fungal sequences (Fig. 3b). Previous studies have suggested that some species of *Mortierella* can produce antibiotics, and several isolates have been proven as potential antagonistic agents against various plant pathogens [35]. This taxon might be regarded as an important indicator of *Fusarium* disease control in ginseng cultivation. In general, cultivated ginseng can only grow for 4–5 years [15]. This may be due to the long growth period of cultivated ginseng, which leads to an increase in pathogenic fungi, including *Fusarium*. However, BIAANTIAO ginseng can grow for more than ten years. *Mortierella* was obviously enriched in TSBT, accounting for 44.93%. The long survival time of BIAANTIAO ginseng may be related to the high abundance of *Mortierella*. Moreover, the relative abundances of *Alternaria alternata* and *Cladosporium sp agrAR069* were significantly higher in CBGL, JYSH and SZSZ than in TSBT in our study (Fig. 4b). Root rot is a common and severe disease caused by many pathogens, such as *Alternaria alternata* and *Cladosporium spp.*, and occurs under the continuous cropping of watermelon [36],[37]. In summary, BIAANTIAO ginseng was not easily infected compared with the other ginseng cultivars. Understanding the potential relationships between the different ginseng cultivars and rhizosphere microorganisms is conducive to the development of the ginseng industry.

## Conclusions

In here, the result reveals for the first time that there are differences in the rhizosphere of ginseng cultivars, confirming that rhizosphere plays a vital role in the growth of ginseng. Some microorganisms had a special affinity for certain ginseng cultivars. This result is helpful in providing information that could be used for the breeding of *Panax ginseng*.

## Methods

### Sample collection and DNA extraction

Rhizosphere soil samples were collected in August 2018 from four ginseng cultivars, and five to eight biological replications were obtained at the four locations. The JYSH, TSBT, CBGL and SZSZ samples are the rhizosphere soil from six-year-old COMMON, BIAANTIAO, SHIZHU and GAOLI ginseng plants, respectively (Table S1). All the ginseng plants were planted directly in the field for six years, but the BIAANTIAO ginseng was grown for three years in ginseng plantations, transplanted to the field, and allowed to grow for three years. The four different ginseng cultivars were planted in their respective main cultivation regions. Each rhizosphere soil sample was collected from at least three healthy, disease-free ginseng plants. The nonrhizosphere soil was removed, and the rhizosphere soil was passed through a 2 mm sieve. Finally, the soil samples were stored at  $-80^{\circ}\text{C}$  for subsequent bacterial and fungal DNA extraction. Total soil genomic DNA was extracted by the E.Z.N.A.® soil DNA kit in accordance with the manufacturer's instructions.

### PCR, amplicon quantification and sequencing

The primers pairs 341F (5'-ACTCCTACGGGAGGCAGCAG-3') / 806R (5'-GGACTACHVGGGTWTCTAAT-3') and ITS1-1 (5'-CTTGGTCATTTAGAGGAAGTAA-3') / ITS1-2 (5'-GCTGCGTTCTTCATCGATGC-3') were used to amplify V3-V4 regions of the bacterial 16S rRNA gene and the fungal ITS1 gene, respectively. All PCRs were performed using NEB Phusion High-Fidelity PCR Master Mix following the manufacturer's recommendations with 30ng DNA, 4μL PCR primer cocktail and 25μL PCR Master Mix. Moreover, negative controls (no templates) were included in this step to check for primer or

sample DNA contamination. Then, PCR products were verified by electrophoresis on 1% agarose gel and purified by AmpureXPbeads Kit (AGENCOURT) to remove the unspecific products. The library quality was checked by Agilent 2100 bioanalyzer instrument (Agilent DNA 1000 Reagents). Qualified libraries were sequenced by PE250 pair-end sequencing using the HiSeq (HiSeq SBS Kit V2, Illumina) platform.

## Data Analysis

Raw sequences with ambiguous bases, an average Phred score less than 20 and a length lower than 10 bp were filtered out using Trimmomatic software (v-0.36)[38]. Additionally, the chimeric sequences were identified and removed using UCHIME software (v4.2.40)[39]. The operational taxonomic units (OTUs) of bacteria and fungi were clustered at 97% sequence similarity using UPARSE (version 7.0.1090)[40]. OTUs identified as chloroplast, mitochondria or singleton OTUs were removed. Subsequently, the bacterial and fungal OTUs were determined using RDP Classifier v2.2 (Ribosomal Database Project) against the Greengenes (v201304) database and the UNITE (Version 7.2) database. In brief, a Venn plot was used to show the number of unique and common OTUs in different groups by the 'VennDiagram' R package (v 3.1.1). The alpha diversity of the bacterial and fungal communities was characterized by the observed species, Chao 1, Ace and Shannon indexes to analyze the phylogenetic diversity of each group using MOTHUR (v1.31.2). Then, the beta diversity of the microbial community was assessed using QIIME software (v 1.80) to assay the differences in community diversity among the different groups along with the Bray-Curtis distance and weighted UniFrac distance[41]. Moreover, a heatmap was generated using the 'aheatmap' function in the NMF package in R (v 3.1.1) to display the beta diversity.

One-way analysis of variance (ANOVA) was performed to analyze the impacts of the cultivars on the rhizosphere microbial community using SPSS. Principal coordinate analyses (PCA) were performed in the 'ade4' package in R (v 3.1.1)( $p < 0.05$ ). Furthermore, linear discriminant analysis (LDA) effect size (LEfSe) was also used to detect significantly different taxa (LDA scores greater than 2.0 at a p-value  $< 0.01$ ) with differential abundance in the Galaxy online analytics platform (<http://huttenhower.sph.harvard.edu/galaxy>).

## Declarations

## Availability of data and materials

The soil samples we collected came from the field and were allowed by the owner. The detailed 16S rRNA and ITS raw sequence data were available in the NCBI Sequence Read Archive (SRA) under accession number ———.

### Ethics approval and consent to participate

Not applicable.

### Consent for publication

Not applicable.

### Competing interests

Not applicable.

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# Authors' contributions

All authors contributed to the study conception and design. Material preparation, data collection and analysis were performed by Huaying Wang, Xiaoxue Fang, Hao Wu and Xinyu Cai. The first draft of the manuscript was written by Hongxing Xiao and all authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

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# Abbreviations

Not applicable

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## Tables

	Cultivars	Observed species	Chao 1	ace	Shannon index
bacteria	CBGL	1963.0000±17.7864b	2465.9696±28.3406b	2492.4715±24.5144b	6.0317±0.0469b
	JYSH	2212.1429±20.1109a	2689.7811±28.2172a	2706.1426±22.9505a	6.2483±0.0132a
	SZSZ	1925.0000±19.0770b	2388.5531±27.8456b	2416.7648±26.7192b	6.0215±0.0643b
	TSBT	1661.0000±3.7148c	2071.4741±24.1967c	2089.2090±19.9270c	5.8348±0.0098c
fungi	CBGL	1008.5000±10.5492b	1080.4754±14.4322b	1088.2817±15.7466b	4.7211±0.0531b
	JYSH	673.4286±28.0305c	698.8566±28.5005c	695.8340±29.5827c	4.1511±0.0257c
	SZSZ	1116.5000±17.4428a	1177.4825±21.1894a	1178.8988±21.1666a	5.0374±0.0489a
	TSBT	548.6667±8.4406d	599.2131±14.7052d	598.9407±15.8586d	3.2559±0.0491d

Table 1 The number of Observed species, Chao 1, ace, Shannon index from four cultivated strains of ginseng in bacteria and fungi, data are means ± standard error.

Note: different letters represent the statistical differences among dcultivated strains of ginseng soil samples at ( $p < 0.05$ )

## Figures

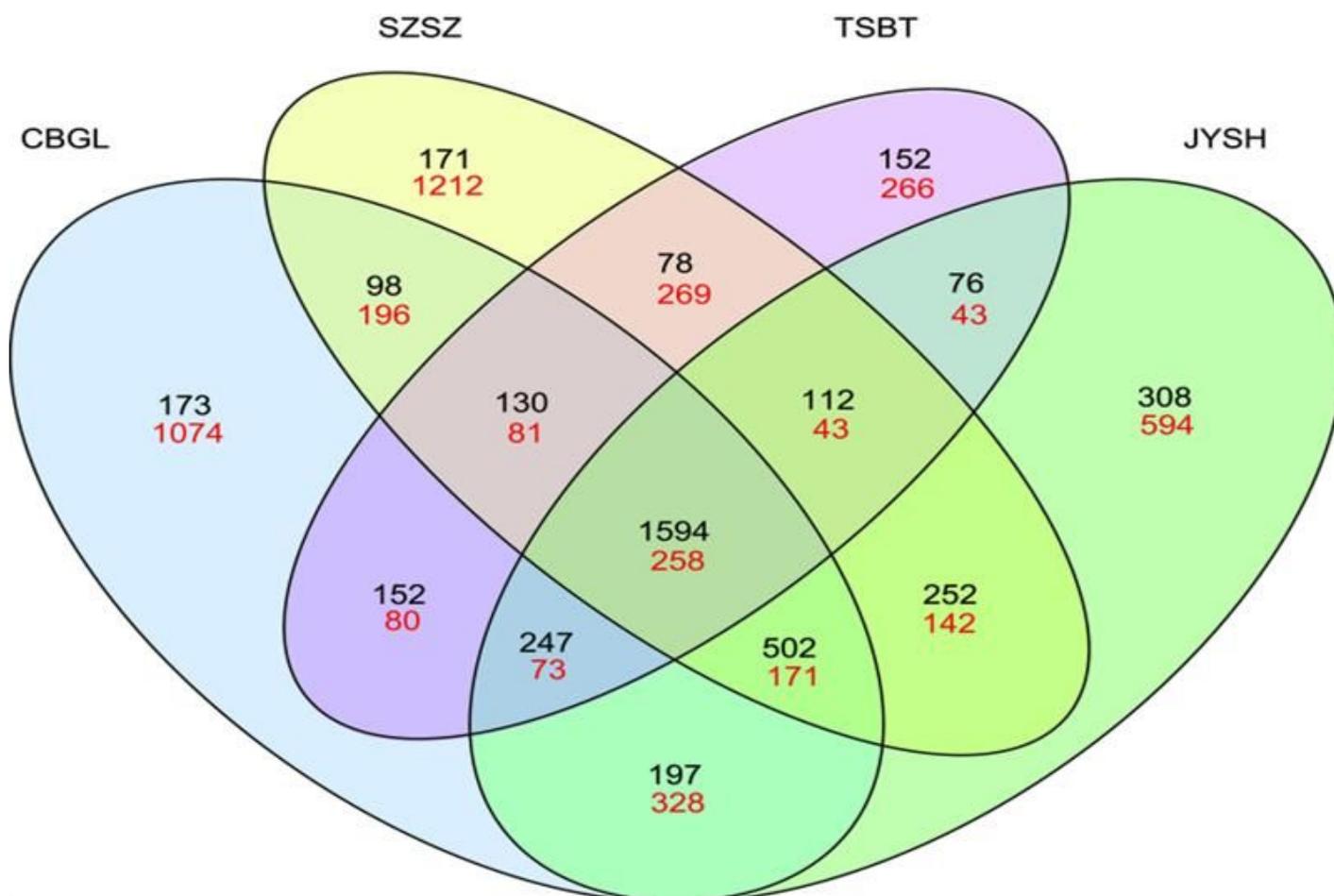
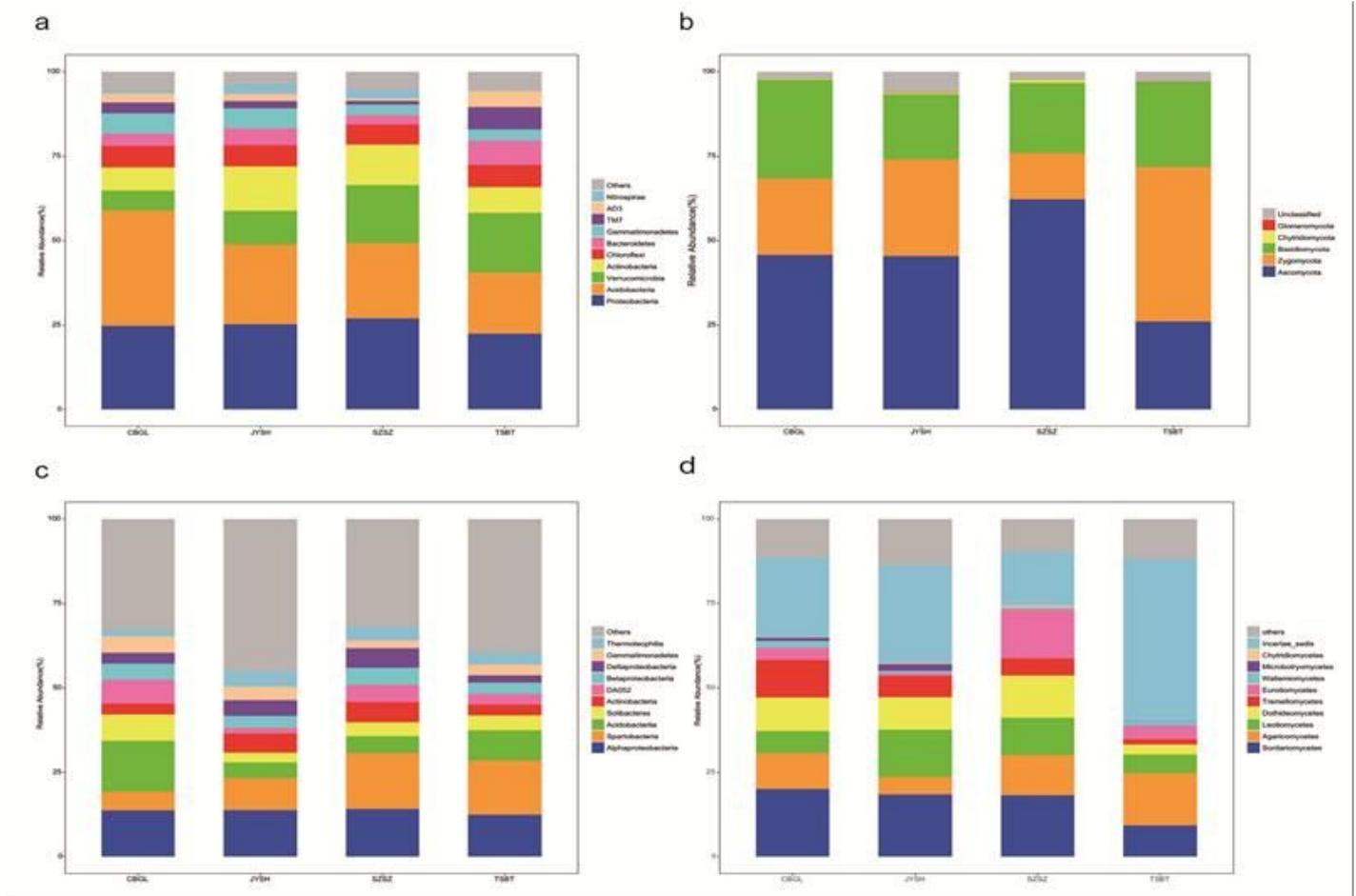


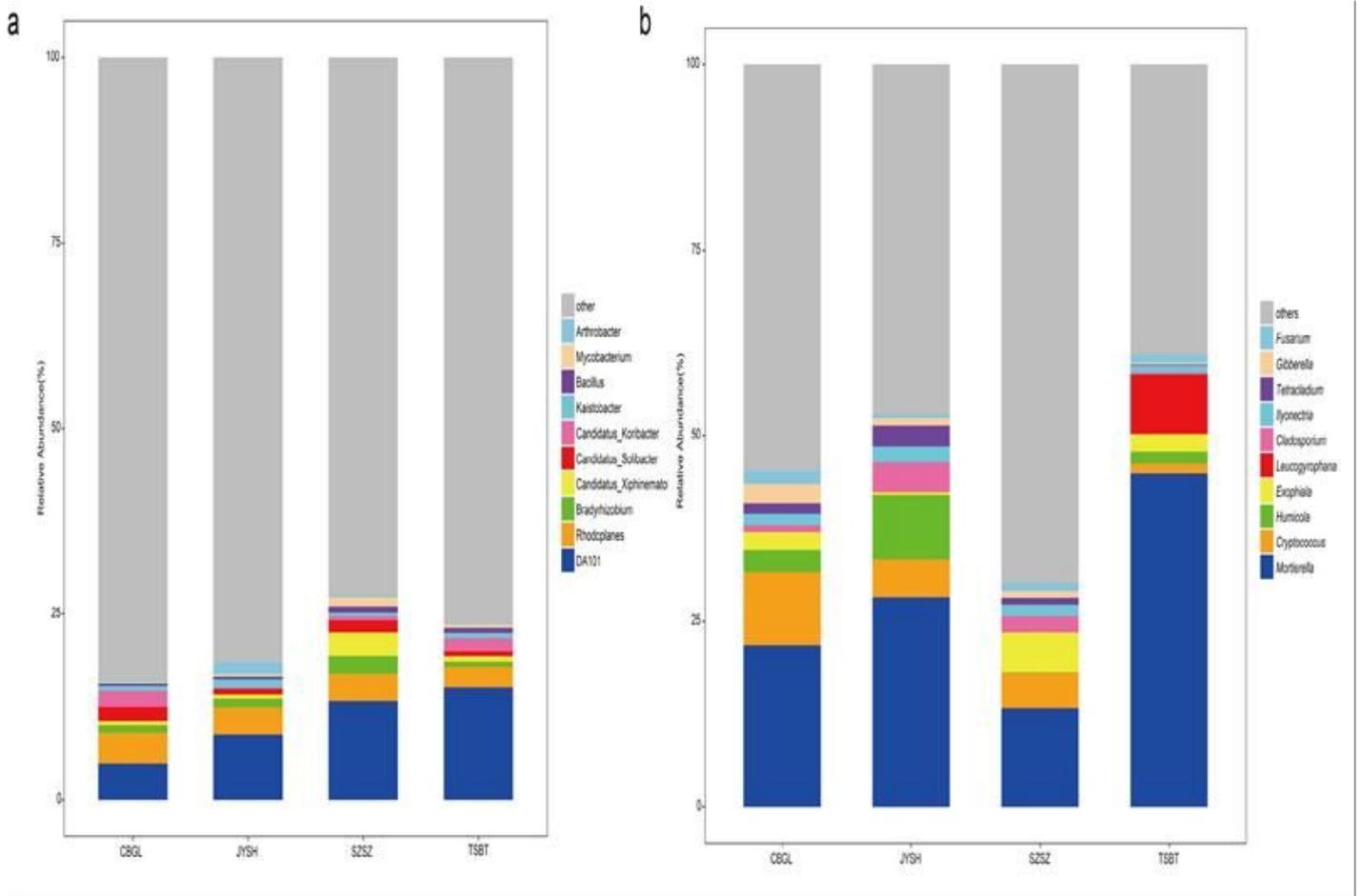
Figure 1

Venn diagrams of shared bacterial (black) and fungal (red) OTUs across groups from four ginseng cultivars



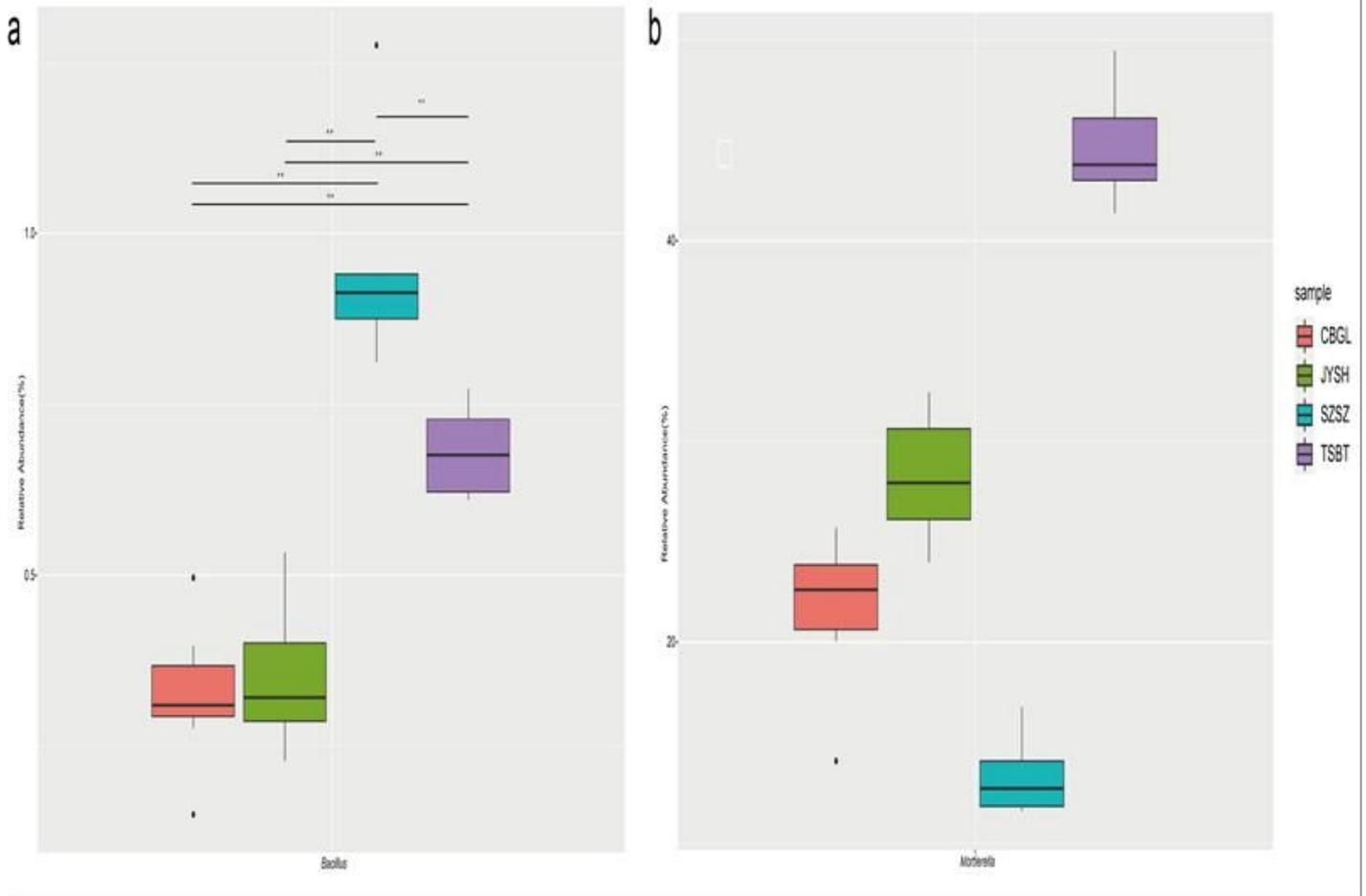
**Figure 2**

The composition and structure of bacterial and fungal community from the four ginseng cultivars. The phylum level of bacteria (a) and fungi (c), and the order level of bacteria (b) and fungi (d). The relative abundances in the top 10 were chosen to exhibit. Others represented of low relative abundance that ranks lower than top 10



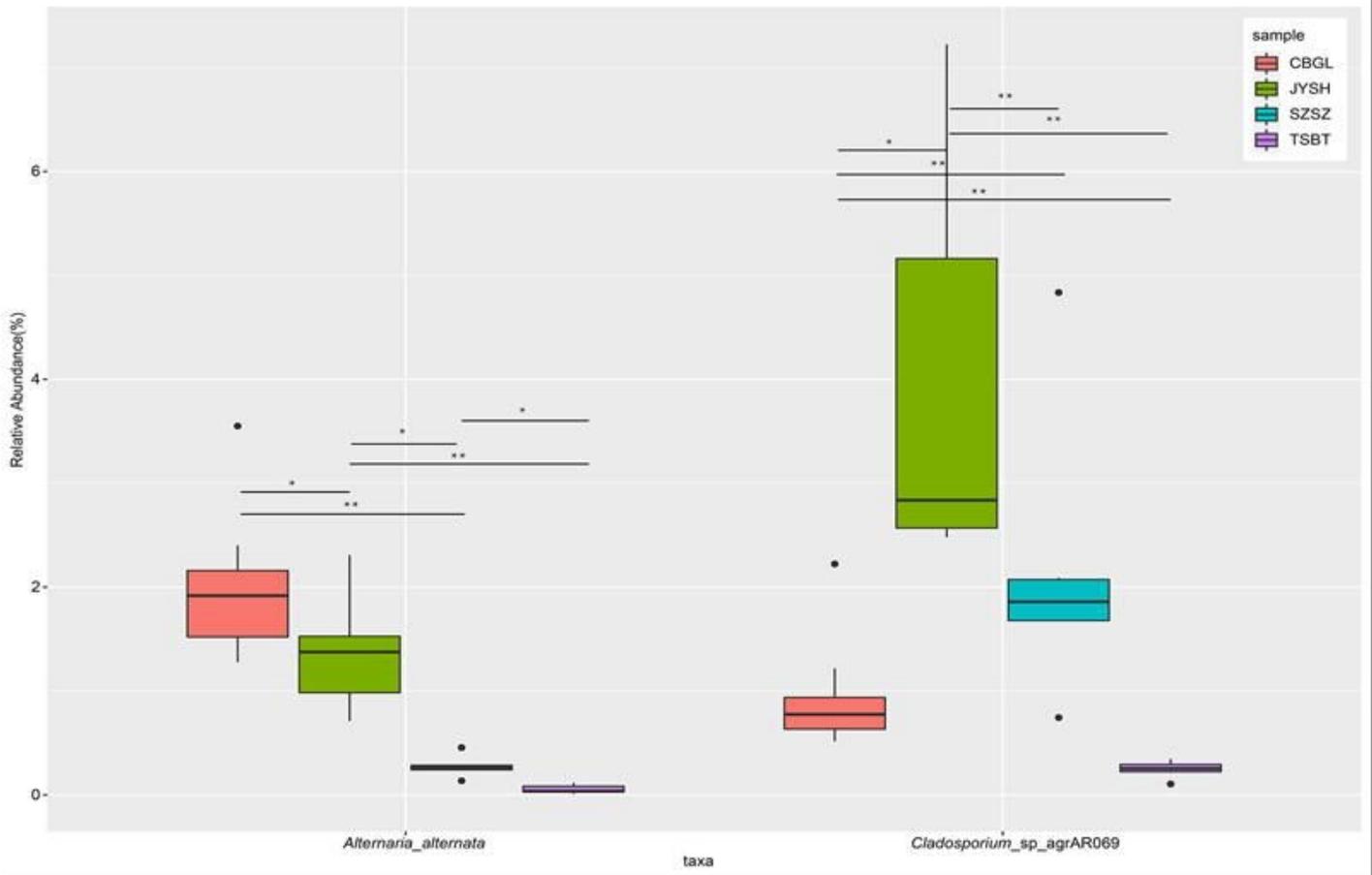
**Figure 3**

The composition and structure of bacterial (a) community and fungal community (b) from the four ginseng cultivars at the genus level



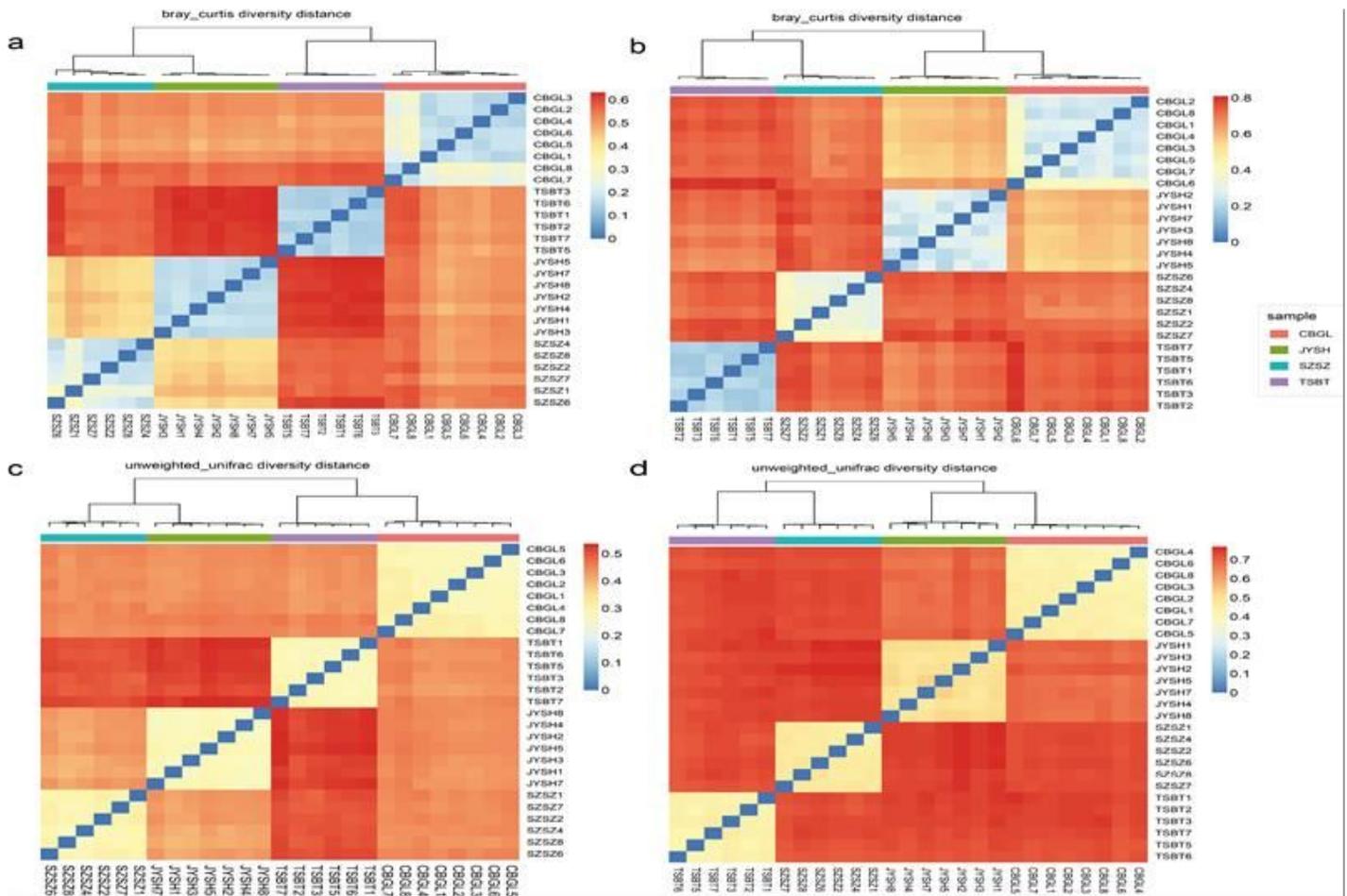
**Figure 4**

The relative abundances of Bacillus (a) and Mortierella (b) (mean  $\pm$  SE) in rhizosphere soils across different ginseng cultivars \*Significant at the 0.05 probability level. \*\*Significant at the 0.01 probability level.



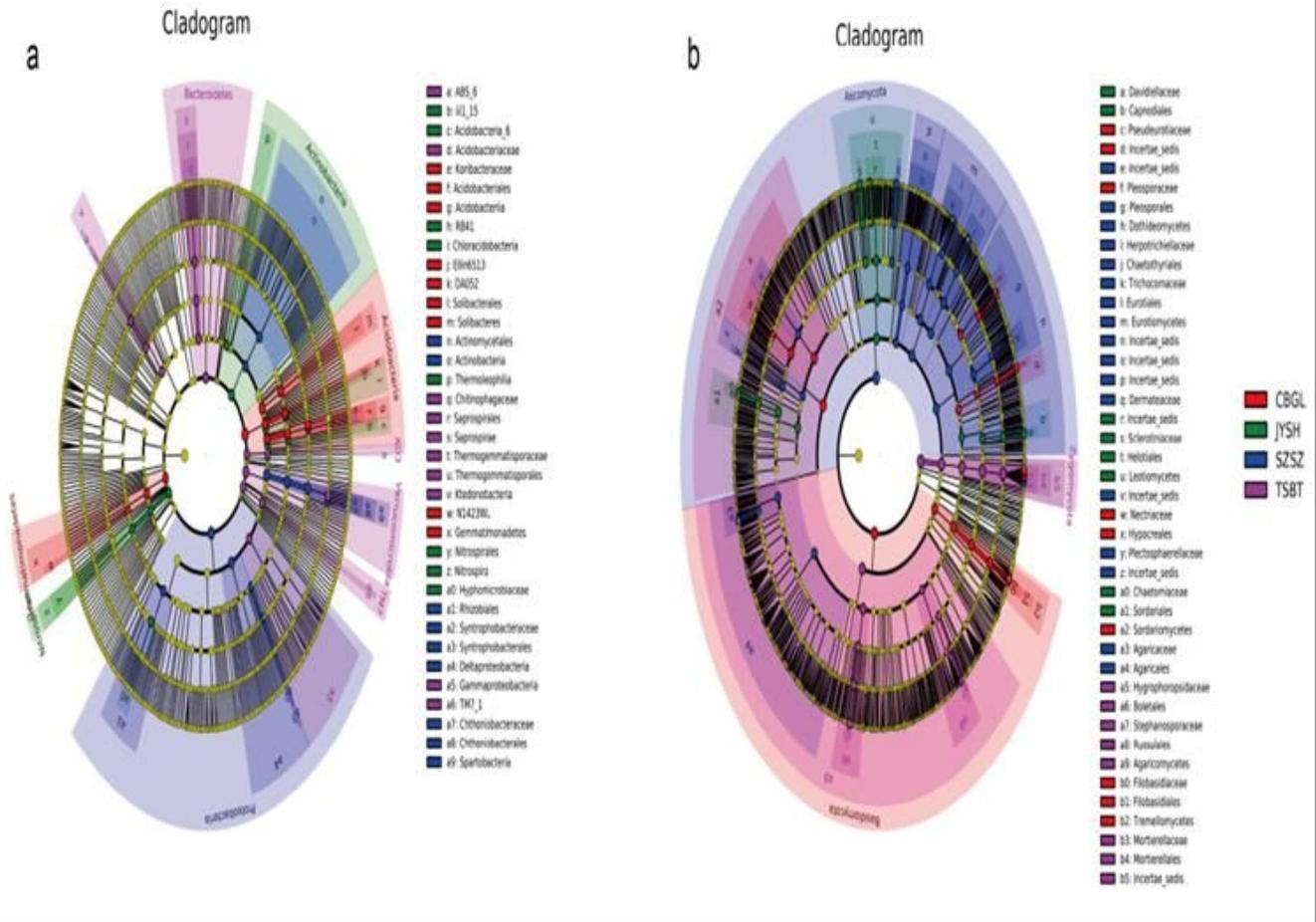
**Figure 5**

Relative abundances of *Alternaria\_alternata* and *Cladosporium\_sp\_agrAR069* (mean  $\pm$  SE) in rhizosphere soils across different ginseng cultivars \*Significant at the 0.05 probability level \*\*Significant at the 0.01 probability level



**Figure 6**

Beta diversity analysis based on bray\_curtis distance and unweighted\_unifrac distance from the different ginseng cultivars rhizosphere in bacteria (a), (c) and fungi (b), (d)



**Figure 7**

LefSe analysis showing the different biomarkers among different ginseng cultivars rhizosphere in bacteria (a) and fungi (b). Different colored regions represented different constituents (red for CBGL, green for JYSH, blue for SZSZ and purple for TSBT) and the diameter of each circle is proportional to the relative abundance of the taxon. The inner to outer circle corresponds to the level of the phylum to the genus

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