

CHARACTERISTICS OF BACTERIAL COMMUNITIES IN THE RHIZOSPHERE SOIL OF *ARALIA CONTINENTALIS* KITAG. BASED ON HIGH THROUGHPUT SEQUENCING

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(Received 10th Sep 2021; accepted 6th Dec 2021)

Abstract. By analyzing the structure of communities and distribution law of soil bacterial communities in different years, this paper provides a reference for cultivation management aiming to improve growth, development, and yield. The changes of soil bacterial community structure were analyzed by Illumina Miseq high-throughput sequencing techniques using growing period soils that were unplanted (A1), planted for 1 year (A2), 4 years (A3), or 10 years (A4). The V3-V4 hypervariable regions of 16 S rRNA genes were PCR amplified by genomic extraction, after sequencing Illumina HiSeq 2500 a high-throughput sequencing platform, bioinformatics were used to analyze the abundance, diversity index and community structure of soil bacteria in different planting years. The soil bacteria belonged to 25 Phylums, 76 Classes, 175 Orders, 255 Families, 395 Genuses, 423 Species. Among them, the dominant bacteria are Proteus, Acinetobacter, Actinomycetes, etc. There are significant differences in soil bacterial communities in different places. The diversity of bacterial communities increased with planting years the community structure, the abundance of beneficial microorganisms such as Proteus, Acinetobacter, Actinomycetes, Bacteroides and Chlorophyta decreased, which suggests that planting years are the main factors affecting soil microbial activity. The results have deepened the understanding of the microbial community structure and diversity in the rhizosphere of *Aralia continentalis* Kitag.

Keywords: *continuous cropping obstacles, Aralia continentalis Kitag., bacterial community, high throughput sequencing*

Introduction

Aralia continentalis Kitag. is a species of the *Aralia* genus distributed in the northeastern region (Wang, 2017). *Aralia* is similar to ginseng. The root and root bark of *Aralia continentalis* Kitag. have a wide range of medicinal properties. The total saponin content of *Aralia continentalis* Kitag. root bark is three times that of ginseng, and the curative effect of some diseases is similar to that of ginseng (Fan et al., 2010). Its buds that grow in early spring are rich in protein, carbohydrates, fat, cellulose, calcium and amino acids, and have high nutritional value (Duan et al., 2019). Its potential medicinal and edible values have gradually attracted people's attention.

In recent years, artificially domesticated *Aralia continentalis* Kitag. has been widely planted, and some achievements have been made in the introduction and domestication of *Aralia continentalis* Kitag. at home and abroad (Han et al., 2003; Fan et al., 2013). There are few reports on the research on the soil bacterial community of *Aralia continentalis* Kitag. Soil bacteria play a key role in the ecosystem, participating in energy conversion and material circulation (Jiang et al., 2018). The diversity of soil bacteria composition has a key impact on crop growth and production (Han et al., 2020). Existing studies have shown that soil bacteria and plants have formed a mutually beneficial relationship. On one hand, plants affect the changes

in soil physical and chemical properties through rhizosphere exudates or litter, thereby affecting the growth of bacteria, thereby affecting the composition of the community, species richness and diversity, etc. (Yin et al., 2020); on the other hand, some plants show more vigorous growth in the presence of the entire bacterial community, and some bacteria can also inhibit plant diseases or related pathogenic bacteria and promote improved disease resistance and stress resistance (Qiu et al., 2019). This study uses high-throughput sequencing to analyze the status of soil bacterial communities in *Aralia continentalis* Kitag. at different ages, which can provide some references for exploring the diversity of soil bacteria in *Aralia continentalis* Kitag., and can also be used to study more effective soil management methods and changes in *Aralia continentalis* Kitag.

Materials and methods

Sample collection and analysis

This study was carried out with *Aralia continentalis* Kitag. experimental base of Changchun University in China, and 4 experiment fields with consistent field management were set up (Fig. 1). The row of *Aralia continentalis* Kitag. is 15-20 cm soft and 7-8 cm wide, covering 0.5-0.8 cm of soil. No other plants were planted in the experimental base during this period. Soil sampling was carried out in July 2019, and the soil in the nursery area without *Aralia continentalis* Kitag. (A1) and the soil with *Aralia continentalis* Kitag. was planted for 1 year (A2), 4 years (A3), and 10 years (A4) were taken. Six plots of 2 m × 2 m were set up on each plot, each plot was distributed, and rhizosphere soil was sampled by “shaking root method”, collected soil samples were numbered and loaded into sterile polyethylene sealing bags for DNA extraction and high-throughput sequencing.

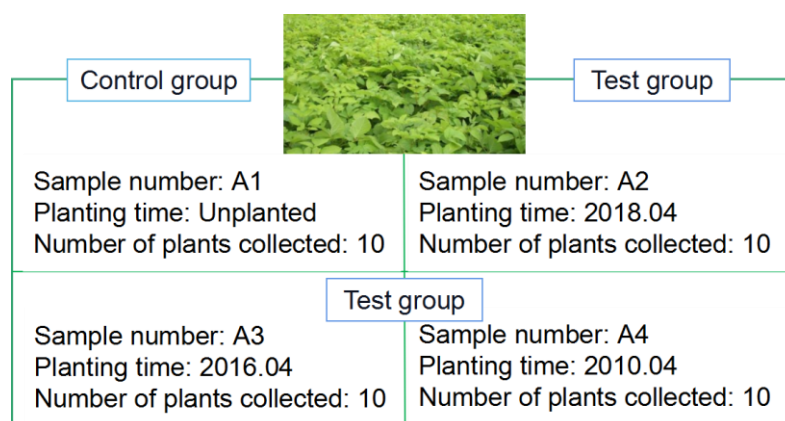


Figure 1. Test plot information

Test process

After extracting the total DNA of the sample, primers are designed according to the conserved regions, and sequencing adapters are added to the ends of the primers, PCR amplification is performed, and the products are purified, quantified and homogenized to form a sequencing library. The built library is first subjected to

library quality inspection. The qualified library was sequenced with Illumina HiSeq 2500 (*Table 1*).

Table 1. Primer list

Name	Sequenced region	Primer name	Primer sequence
Bacteria	16s: V3 + V4	338F 806R	5'ACTCCTACGGGAGGCAGCA-3' 5'-GGACTACHVGGGTWTCTAAT-3'

Data analysis

The original sequencing data were filtered and merged to obtain the optimized sequences. The optimized sequences were clustered to get OTU, then the species classification was obtained according to the sequence composition of OTU; Based on OTU analysis results, taxonomic analysis was performed on samples at various taxonomic levels to obtain the community structure map, species cluster heat map, genus level phylogenetic tree and taxonomic tree of each sample at the taxonomic level of phylum, class, order, family, genus, and species. Alpha diversity analysis was used to study the species diversity within a single sample. Ace, Chao1, Shannon and Simpson indices of each sample were statistically calculated at 97% similarity level to draw sample dilution curve and rank abundance curve; Beta diversity analysis was used to compare the differences of species diversity between different samples.

According to overlap relation between PE reads, the paired-ends sequence data obtained from Hiseq sequencing were merged into tags of one sequence, then quality control and filtering was performed for reads quality and Merge effect. (1) PE reads merge: FLASH v1.2.7 software was used to merge reads through overlap, the obtained merged sequences were Raw Tags; (2) Tags filtering: Trimmomatic v0.33 software was used to filter merged Raw Tags to get high quality Clean Tags; (3) Chimera removal: UCHIME v4.2 software was used to identify and remove chimera sequences to get Effective Tags.

Results and analysis

OTU analysis and species classification of soil bacteria in Aralia continentalis Kitag. with different planting years

It can be seen from *Table 2* that there is a big difference in the number of soil samples from different planting years. A total of 689980 pairs of reads were obtained by sequencing. After splicing and quality control filtering, 654659 optimized sequences were obtained. Among them, the number of reads of A1 (65367 pairs) is the least, and that of A4 (292452 pairs) is the most, which is more than four times of A1. There was no significant difference in avglen (BP), GC (%), Q20 (%), q30 (%) and effective tags (%) among A1, A2, A3 and A4 samples. It can be seen from *Figure 2* that, at the 97% similarity level, the number of OTUs in A4 is the most, while the number of OTUs in A1 is the least (1526 in A1, 1673 in A2, 1694 in A3 and 1703 in A4). The total number of OTUs is 1493, accounting for 86.90% of the total OTUs of soil bacteria in *Aralia continentalis* Kitag. The number of OTUs unique to A3 and A4 is 6, It accounted for 0.35% of the total OTU of soil bacteria in *Aralia continentalis* Kitag., and the number of OTU unique to A1 and A2 was 0.

Table 2. Statistics of sequencing data processing

Sample ID	PE reads	Raw tags	Clean tags	Effective tags	AvgLen (bp)	GC (%)	Q20 (%)	Q30 (%)	Effective (%)
A1	65367	62245	62157	61008	419	56.43	97.08	91.93	93.33
A2	108213	102223	102062	98315	420	56.06	96.81	91.3	90.85
A3	223948	213012	212724	207687	420	55.87	96.96	91.65	92.74
A4	292452	278087	277716	270767	420	56.5	96.99	91.81	92.59

PE Reads is the paired-ends reads count obtained from sequencing; Raw Tags is the count of original sequences merged from paired-ends reads; Clean Tags is the count of optimized sequences after filtering of raw tags; Effective Tags is the count of effective sequences after filtering chimera from Clean Tags; AvgLen (bp) is the average sequence length of sample; GC(%) is the GC content of sample, i.e. the percentage of G and C bases in all bases; Q20(%) is the percentage of bases which quality value is no less than 20 in all bases; Q30(%) is the percentage of bases which quality value is no less than 30 in all bases; Effective (%) is the percentage of Effective Tags in PE Reads



Figure 2. OTU Venn. The number of overlapping parts between multiple color patterns is the total number of OTUs among multiple samples, and the number of non-overlapping parts is the unique number of OTUs of each sample

Analysis of bacterial community structure and abundance in soil of *Aralia continentalis* Kitag. with different planting years

The OTU representative sequences of each sample were annotated at each level to obtain the statistical information of species at each level of each sample (Table 3). The average number of species of A1, A2, A3 and A4 at the phylum, class and order level were 23, 74 and 170 respectively, and the relevant values of each sample were very close to the average value. There were significant differences in the number of species at the family, genus, and species level, and A1 was in the family, genus, and order level. The number of species was the least at the level of 240, 371 and 394, respectively, and A4 was the most at the level of 253, 391 and 419, respectively.

It can be seen from Figure 3A that *Aralia continentalis* Kitag. growing for 10 years has the largest number of soil bacteria (25 phyla), and A1 has the least number of soil bacteria (22 phyla). The species abundance information of each sample is shown in Figure 3A (in order to make the histogram more intuitive and clearer in reflecting the species composition, only the top 10 species with higher abundance are shown, and other species are classified as others, unclassified represents the species without taxonomic annotation on the pair.) The relative abundances of *Proteobacteria*, *acidobacteria*, *Actinobacteria*, *Bacteroidetes* and *Chloroflex I* were 35.6%, 18.3%, 9.6%, 8.7% and 8.3%, respectively. In the four soil samples, the sum of the relative

abundances of the five phyla accounted for 80.5% of the total number of soil bacteria. However, the content of *Proteus* in A2, A3 and A4 was higher than that in A1, *acidobacteria* and *Curvularia* in A1, A3 and A4. The content of actinomycetes in A3 and A4 was lower than that in A1 and A2, which indicated that different planting years had different effects on the growth of different bacteria. According to the similarity of species or richness, the samples were clustered, and the species richness clustering heat maps of different classification levels were obtained (Fig. 3B). The bacteria in the four samples were roughly divided into four clusters.

Table 3. Statistics of species of samples by grade

Sample	Kingdom	Phylum	Class	Order	Family	Genus	Species
A1	1	22	72	168	240	371	394
A2	1	23	73	170	246	384	411
A3	1	23	74	171	249	388	416
A4	1	25	75	174	253	391	419
Total	1	25	76	175	255	395	423

Analysis results of bacterial community abundance at phylum level

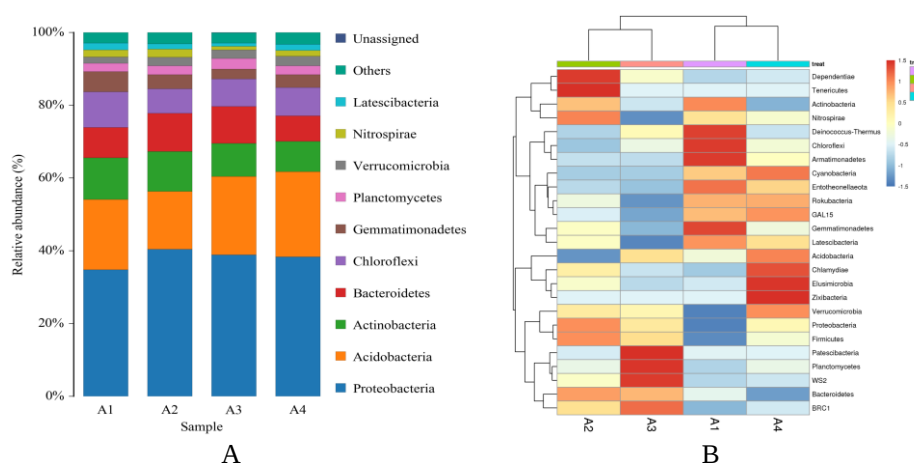


Figure 3. The relative abundance histogram (A) and the relative abundance cluster diagram (B) of bacteria community on the phylum level

Analysis results of bacterial community abundance at class level

According to Figure 4A, the main groups of soil bacterial community of *Aralia continentalis* Kitag. are gamma *Proteobacteria*, Alpha *Proteobacteria*, subgroup_6, *Bacteroidia*, *Blastocatellia* _Subgroup_, and their relative species abundance averaged were 4%, 12.3%, 5.6%, 4.9% and 3.7% respectively. *Gammaproteobacteria* in the rhizosphere soil of *Aralia continentalis* Kitag. is the dominant class. It can be seen from Figure 4B that among the four samples, bacteria are roughly divided into four clusters, 15 classes such as *Dehalococcoidia* and *Chlamydiae* are closely related to each other, 17 classes such as *Deltaproteobacteria* and *Actinobacteria* are the second cluster, 22 classes such as *Gemmatimonadetes* and *Anaerolineae* are the third cluster, and 22 classes such as *Parcubacteria* and *Rubrobacteria* are the fourth cluster.

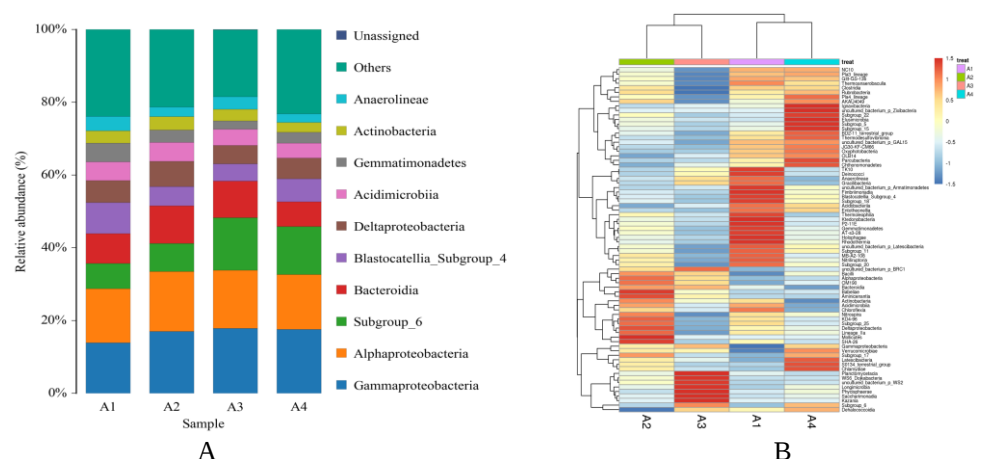


Figure 4. The relative abundance histogram (A) and the relative abundance cluster diagram (B) of bacteria community on the class level

Analysis results of bacterial community abundance at order level

It can be seen from Figure 5A that the main bacterial communities in the four samples are betaproteobacteriales, uncultured _ bacterium _ Subgroup _ 6, Rhizobiales, Chitinophagales, Pyromonadales, Sphingomonadales, Gemmatimonadales, Myxococcales, Microtrichales, Cytophagales, and their relative species abundance averaged were 5.5%, 10.2%, 5.1%, 4.8%, 3.9%, 3.2%, 2.9%, 3.1%, 2.8% and 2.3%, respectively. The dominant strains were Betaproteobacteriales and Uncultured _ bacterium _ Subgroup _ 6. It can be seen from Figure 5B that in the four samples, bacteria are roughly divided into four clusters, 26 orders such as Caulobacteriales and Anolineales are the first cluster, 13 orders such as Mbnt15, Bacteroidales and Pseudomonas are the second cluster, 28 orders such as S085, Enterobacteria and Chthoniobacteria are the third cluster, and 33 orders such as Babeliales, Micromonosporales and Babeliales are the fourth clusters. At order level, the bacterial composition of the four samples was significantly different. The main bacteria in sample A2 are the second cluster, the main bacteria in sample A3 are the fourth cluster, the main bacteria in sample A1 are the first cluster, and the main bacteria in sample A4 are the third cluster.

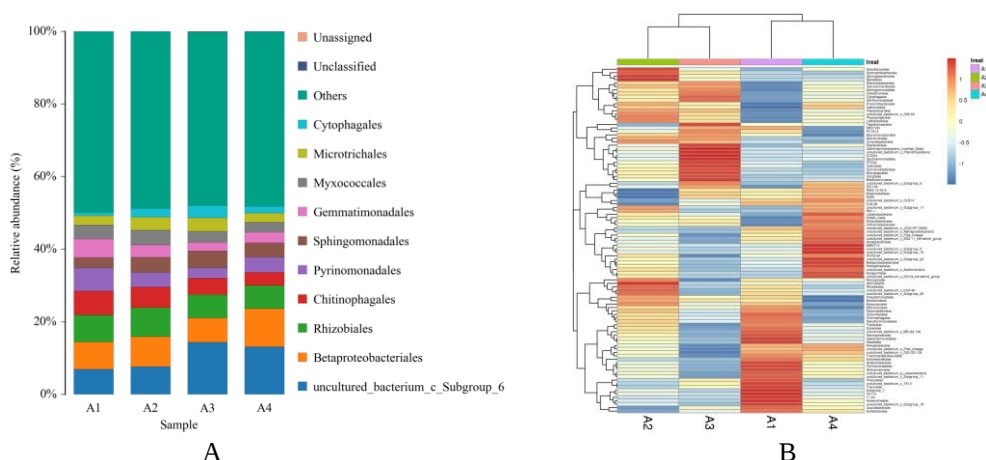


Figure 5. The relative abundance histogram (A) and the relative abundance cluster diagram (B) of bacteria community on the order level

Analysis results of bacterial community abundance at family level

The main bacterial communities in the four samples were uncultured _ bacterium _ c_Subgroup_6, Pyrinomonadaceae, Chitinophagaceae, Nitrosomonadaceae, Sphingomonadaceae, Gemmatimonadaceae, Xanthobacteraceae, Microscillaceae, Burkholderiaceae, and their relative species abundance averages were 8.9%, 3.9%, 3.7%, 3.5%, 3.2%, 2.8%, 2.5%, 2.0%, 1.8%, respectively. It can be seen from *Figure 6B* that the composition of soil bacterial community of *Aralia continentalis* Kitag. planted for one year, four years and ten years is similar, while the composition of soil bacterial community of *Aralia continentalis* Kitag. planted for less than one year is larger than that of the three. In the four samples, soil bacteria are roughly divided into three clusters, and 33 families, such as Anaerolineaceae, Scolimonadaceae and Micrococcaceae, are closely related to each other, 28 families, such as Methylophilaceae and Pedosphaeraceae, are clustered in the second cluster, while 39 families, such as Devosiaceae and Polyangiaceae, are clustered in the third cluster (*Fig. 6*).

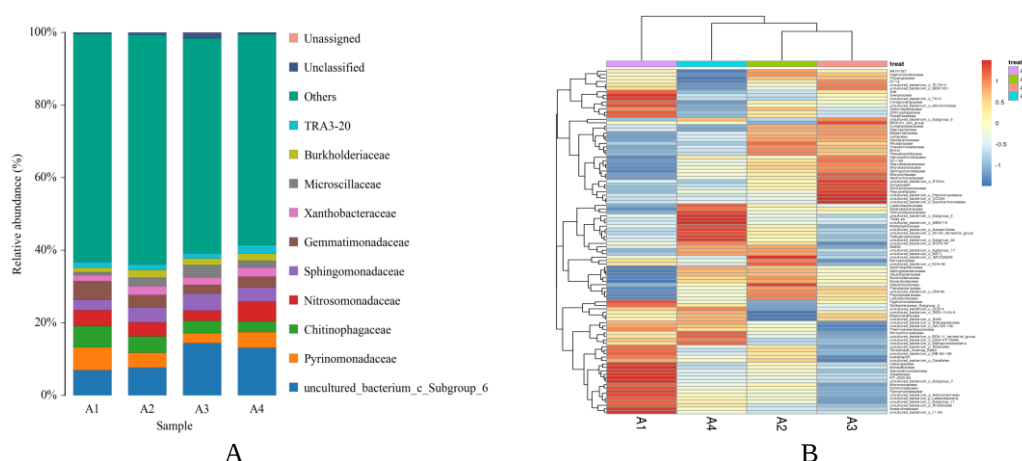


Figure 6. The relative abundance histogram (A) and the relative abundance cluster diagram (B) of bacteria community on the family level

Analysis results of bacterial community abundance at genus level

Figure 7A shows that the main bacteria in the soil of the four samples were uncultured _ bacterium _ c _ Subgroup _ 6, RB41, uncultured _ bacterium _ f _ Gemmatimonadaceae, Sphingomonas (sphingosine monomonas), uncultured _ bacterium _ f _ Chitinophagaceae, MND1, uncultured _ bacterium _ f _ Microscillaceae, uncultured _ bacterium _ f _ TRA3-20, Nitrospira, uncultured _ bacterium _ o _ PLTA13 relative species abundance averages were 6.5%, 7.5%, 4.9%, 3.5%, 3.5%, 3.5%, 2.6%, 2.3%, 1.8%, respectively. *Figure 7B* shows that the bacterial composition of the soil with less than one year of cultivation is similar to that of the long white log with 1 year and 10 years. The difference is large after four years of cultivation compared to other years.

Phylogenetic analysis of dominant bacteria in soil of *Aralia continentalis* Kitag. with different planting years

The representative sequence data of genera with relatively high abundance were selected, by QIIME software, and multiple sequence alignment was carried out. Then the

phylogenetic tree was built, and the graph was drawn (Fig. 8). Data on the occurrence of representative sequence systems correspond to the first 13 genera and bacteria with high abundance in the soil samples. The results showed that there were 13 main genera in the rhizosphere soil samples of *Acidobacteria*, *Patescibacteria*, *Proteobacteria*, *Nitrospirae*, *Rokubacteria*, *Actinobacteria*, *Planctomycetes*, *Chloroflexi*, *Bacteroides*, *Firmicutes*, *Latescibacteria*, *Verrucomicrobia*, *Gemmatimonadetes*. Among them, *Proteobacteria* accounted for the largest proportion.

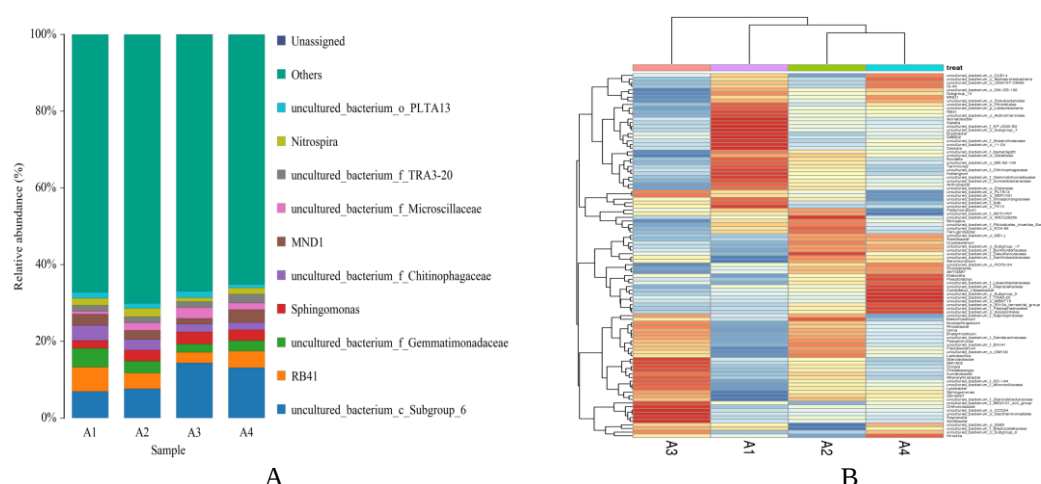


Figure 7. The relative abundance histogram (A) and the relative abundance cluster diagram (B) of bacteria community on the genus level

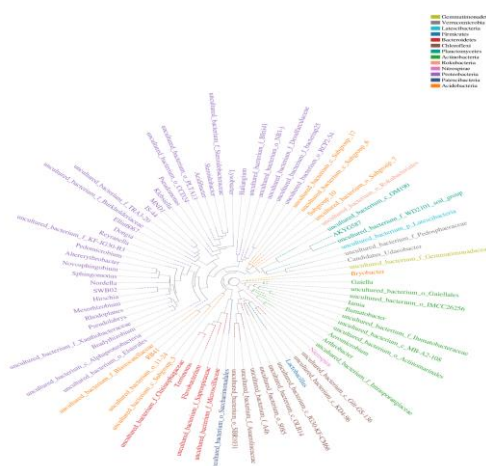


Figure 8. Species phylogenetic tree

Analysis of soil bacterial diversity index of *Aralia continentalis* Kitag. in different planting years

The diversity index of soil alpha in different planting years is shown in Table 4. The OTU coverage rates of A1, A2, A3 and A4 were all above 99%, indicating that the sequencing results reflected the real situation of soil bacteria in the samples. The difference between ACE index and Chao1 index of each sample was obvious, which indicated that the species abundance of each sample was significant. The ace and Chao1

indices of sample A4 were the highest, 1705.1625 and 1, respectively. The results showed that the abundance of bacteria in the soil of *Aralia continentalis* Kitag. planted for 10 years was the highest, while the ace and Chao1 indices in sample A1 were the lowest, indicating that the abundance of bacteria in the soil of *Aralia continentalis* Kitag. planted for less than 1 year was the lowest; the Shannon index and Simpson index of sample A4 and A2 were the highest, indicating that the bacterial diversity in the soil of *Aralia continentalis* Kitag. planted for 4 and 10 years was the highest. According to the alpha diversity index of each sample, the abundance and diversity of soil bacteria of newly planted *Aralia continentalis* Kitag. are relatively low, and with the increase of planting years, the abundance and diversity of soil bacteria are also increasing, among which, the increase range is larger in the two years after planting, and the increase range is smaller and smaller with the increase of planting years. The results showed that *Aralia continentalis* Kitag. interacted with soil bacteria in the process of growth, and soil bacteria would adapt to the environment with the change of environment.

Table 4. Alpha diversity index statistics

Sample ID	OTU	ACE	Chao1	Simpson	Shannon	Coverage
A1	1,526	1,572.04	1,580.79	0.0057	6.1821	0.9972
A2	1,673	1,683.11	1,686.89	0.0041	6.3762	0.9993
A3	1,694	1,699.83	1,701.67	0.0042	6.3267	0.9998
A4	1,703	1,705.16	1,706.46	0.0041	6.376	0.9999

OTU presents the number of OTU; Chao1, Ace, Shannon and Simpson represent each index respectively. Coverage represents the Coverage of the sample library

With the continuous random sampling of effective sequences, the number of OTU is increasing, but after the OTU reaches a certain value, the curve tends to balance and no longer changes with the increase of sequence number. It shows that the sequencing data can reflect species diversity and species richness in the sample. *Figure 9* shows that at the level of 97% sequence similarity, the OTU number shows the following trend: $A1 < A2 < A4 < A3$, sparse curve of soil bacteria in different planting years tend to be flat, and the OTU coverage of the samples has reached saturation. It can reflect the composition of bacterial community in the soil of L. The curve of A3 and A4 is flatter than that of A1 and A2, which indicates that the uniformity of soil bacteria planted with long years is higher than that of short years (*Fig. 10*).

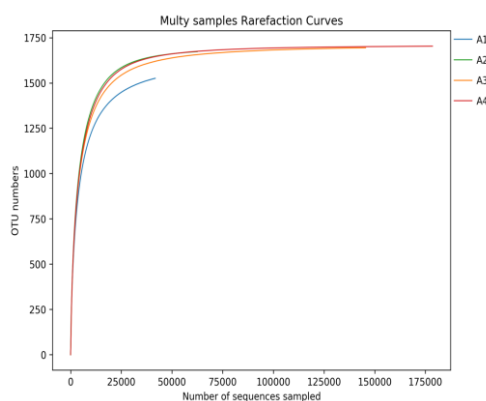


Figure 9. Dilution curve of soil samples at 97% level

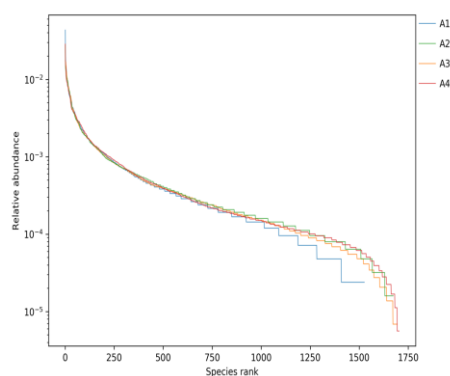


Figure 10. Rank-abundance curve of soil samples

Based on the distance Matrix between samples obtained by the distance algorithms (binary, Bray, weighted, unweighted) , the heat map of soil bacterial community diversity is drawn by the R language tool. In *Figure 11A* and *B*, the cross between sample A1 and A3 is the deepest red. The results showed that the greatest difference was measured between the bacteria in the soil of the unplanted and cultivated land. The cross between sample A3 and A4 is deepest blue. It shows that the similarity of soil bacteria between the newly planted 4 years and the cultivated 10 years is the greatest.

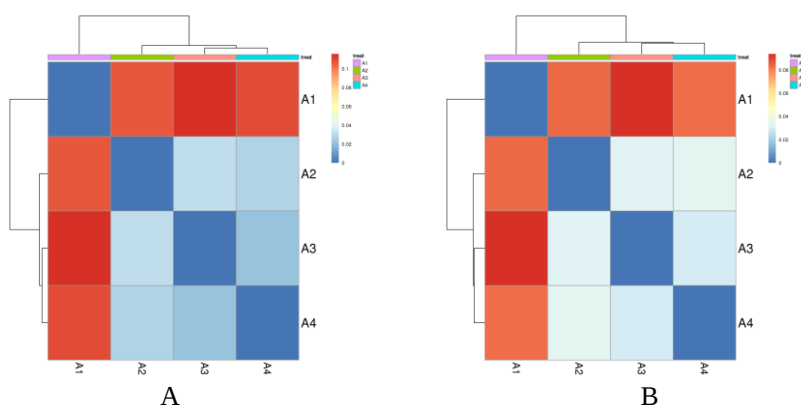


Figure 11. Heat map of soil bacterial community diversity in different samples

Correlation analysis of soil bacterial species of *Aralia continentalis* Kitag. in different planting years

According to the abundance and change information of species in various varieties, Spearman rank correlation analysis and screening data were used to construct the genus level correlation network (*Fig. 12*). The average abundance of RB41 (acidobacteria) was the highest, followed by iamia, but they had little correlation with other species, Novosphingobium and subgroup_ The average abundances of Novosphingobium and Devosia are small, but they are highly correlated with many other species_10 was negatively correlated with Devosia. The results showed that the species composition and diversity of bacterial community were influenced not only by the interaction between different bacterial species, but also by other factors such as environmental factors.

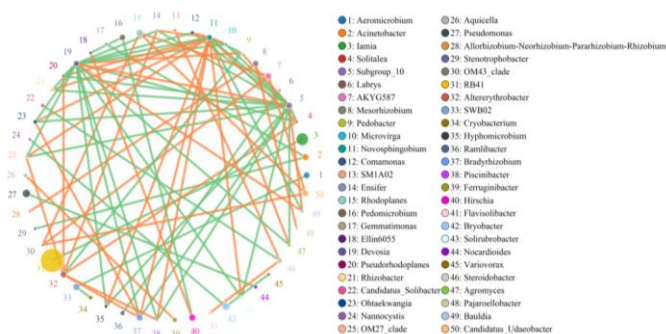


Figure 12. Species-related networks of soil sample bacteria at the genus level

Discussion

Interannual variation characteristics of soil bacterial community structure of Aralia continentalis Kitag.

There are many kinds of bacteria in soil. In different soil environments, the bacterial composition is similar and different, and the plants growing or planted in soil also have a certain degree of influence on the composition and structure of soil bacterial community, species richness, bacterial distribution uniformity and diversity (Dong et al., 2018; Zhu et al., 2019). At present, high-throughput sequencing technology is widely used to study plant rhizosphere soil microbial community, and the results obtained by high-throughput sequencing are more comprehensive and accurate than traditional sequencing technology (Wang et al., 2018). In this study, high-throughput sequencing technology was used to analyze the soil samples of *Aralia continentalis* Kitag. in different planting years. There were 25 phyla, 76 classes, 175 orders, 255 families and 423 species of soil bacteria in four different planting years. The dominant bacteria at phyla level were Proteus, Acidobacteria, Actinomycetes, Bacteroides and Curvularia, among which Proteus accounted for the largest proportion. This is similar to the related research results of selenium sand melon, cotton, ramie and wolfberry (Qiao et al., 2018; Zhu et al., 2018; Xiao et al., 2018; Yue et al., 2020). Proteus and Actinomycetes can participate in the carbon and nitrogen cycle of various organic matter. Nitrogen fixing bacteria play a certain role when crops absorb nitrogen from soil (Guo, 2019). Acidobacteria can degrade plant residues, carry out photosynthesis, participate in carbon metabolism, etc., and play a very important role in soil material cycle and ecological environment construction (Wang et al., 2016). In this study, the abundance of soil degenerative bacteria, actinomycetes and acidobacteria in different planting years of *Aralia continentalis* Kitag. showed the following trend: A4 < A3 < A2, indicating that continuous cropping may reduce the accumulation of soil beneficial bacteria and hinder soil material circulation and fertility renewal. Curvularia viridis is a kind of microbe that can produce energy through photosynthesis and CO₂ as carbon source. It also has strong competitiveness in soil with low organic matter and other nutrients (Kou et al., 2020). In this study, the dominant bacteria in soil of *Aralia continentalis* Kitag. were nitrifying Spirochetes, Sphingomonas, Proteus, Acidobacter and other beneficial bacteria, which had important value in the control of plant pathogens (Lalloo et al., 2010). With the extension of planting years, the abundance of flora increased, which indicated that the effective utilization of photosynthetic products in the process of planting *Aralia continentalis* Kitag. would be conducive to the growth of *Aralia continentalis* Kitag. (Zhu et al., 2016).

Interannual characteristics of soil bacterial community diversity of Aralia continentalis Kitag.

Soil bacterial nutrients mainly come from plant root exudates. The types and quantities of organic acids, inorganic ions, and other substances in plant root exudates at different growth stages are different, which affect the growth, distribution, abundance and diversity of soil bacteria, and soil bacteria also play a crucial role in soil physical and chemical reactions (Ding et al., 2018). In this study, we found that the diversity and evenness of soil bacterial community of *Aralia continentalis* Kitag. planted in different years were different. In terms of soil bacterial abundance, diversity and evenness, the soil bacteria of *Aralia continentalis* Kitag. planted for 1 year, 4 years and 10 years were significantly higher than those of *Aralia continentalis* Kitag. planted for less than 1 year, and with the increase of years, the abundance and diversity of bacterial species increased, and the increasing extent increased with the increase of years. Therefore, root exudates increased the abundance and diversity of soil bacterial community (Luo et al., 2019). In this study, we also found that there were 6 unique OTUs in soil bacteria of *Aralia continentalis* Kitag. planted for 4 years and 10 years, and 0 in soil bacteria of *Aralia continentalis* Kitag. planted within one year. Through the analysis of the effective sequence length distribution map and OTU number distribution map of each sample, it indicated that there were abundant soil bacteria species in *Aralia continentalis* Kitag. Most of the soil bacteria species planted in different years had great similarity with their distribution, but there were significant differences in the composition and distribution of a few soil bacteria. With the growth of *Aralia continentalis* Kitag. growing years increasing, the soil bacteria species of *Aralia continentalis* Kitag. growing in different years had great similarity with their distribution. The number of different kinds of soil bacteria showed the same or opposite changes, and some unique strains could also be produced, which may be affected by the physiological metabolism of *Aralia continentalis* Kitag. in different periods and the artificial cultivation and management measures in different periods (Zhou et al., 2018). There are many factors affecting soil bacterial diversity. To maintain soil bacterial diversity and richness, we should strengthen soil nutrient management and avoid soil acidification, so as to increase the quality and yield of *Aralia continentalis* Kitag. (Duan et al., 2012).

Conclusion

The soil bacterial community of *Aralia continentalis* Kitag. planted was significantly different from that of *Aralia continentalis* Kitag. unplanted. With the increase of planting years, the diversity of bacterial communities increases. In terms of community structure, the abundance of beneficial microorganisms such as *Proteobacteria*, *Acidobacteria*, *Actinomycetes*, *Bacteroides* and *Chloroflexus*, etc. decreases. This study has deepened the understanding of the microbial community structure and diversity in the rhizosphere of *Aralia continentalis* Kitag., combined with the environmental requirements of *Aralia continentalis* Kitag. growth and the factors of the physiological and metabolic activities of plant roots, it is speculated that there are other influencing factors and pathways in microbial regulation, these issues need to be further studied.

Funding. This research was funded by Project of Science and Technology Department of Jilin Province, China (20210601088FG).

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