



Article

Silicon Fertilizer and Microbial Agents Changed the Bacterial Community in the Consecutive Replant Soil of Lilies

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Abstract: Crop replanting leads to soil degradation and soil productivity reduction, which is a challenge for sustainable agricultural development. We previously found that silicon fertilizers combined with additional microbial agents are an effective means to alleviate problems that occur in a variety of Chinese lily during replanting, but little is known about the changes in microbial structure during this process. In the present study, we applied four treatments: CK (control), SF (silicon fertilizer), MF (microbial agents), and SMF (combination of silicon fertilizer and microbial agents). We treated the soil constantly for three years and investigated the bacterial community structure and some specific microbial groups in the soil of the lily root zone using 16S rRNA high-throughput sequencing analysis. The results showed that silicon fertilizer and microbial agent treatment significantly improved the growth status of the plants and changed the diversity and structure of the bacterial community in the soil. The genus *Pseudomonas* significantly increased in the SF treatment, and the phylum Actinobacteria and the genera *Nordella*, *Devosia*, and *Rhodoplanes* significantly increased in the SMF treatment. The genera *Nordella*, *Pedomicrobium*, and *Chthoniobacter* correlated with the seedling index or available silicon content. In addition, the two genera *Gaiella* and *Nocardioideis* were the key species linking the bacterial community in the soil. The soil physicochemical properties played an important role in restoring the soil bacterial community structures. In conclusion, silicon fertilizer and microbial agents changed the diversity and structure of the bacterial community. Under the fertilizer supplement model, the enrichment of the phylum Actinobacteria and the genus *Pseudomonas* played an important role in improving soil health and alleviating CRPs in lilies. In addition, organic matter, available phosphorus, available potassium, and available silicon were found to be the most important factors that have a great impact on the restoration of bacterial community structures.

Keywords: edible lily; soil; bacterial community; high-throughput sequencing; silicon fertilizer; microbial agent



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1. Introduction

Crop replanting leads to soil degeneration and soil productivity loss, which is a challenge for sustainable agricultural development. Therefore, there is the need, in order to find safe and effective technologies, to solve the problems of replanting. In recent years, microbial agents and the medium element silicon have increasingly attracted attention in plant nutrition. Microbial agents contain a large number of beneficial microorganisms, which not only provide beneficial bacteria to improve the soil microenvironment, but also inhibit pathogenic microorganisms and alleviate crops consecutive problems (CRPs) [1]. For example, microbial agents increased the abundance and diversity of soil bacterial in *Nicotiana* and *Benincasa*, inhibited the occurrence of *Meloidogyne* species, and finally promoted the growth and quality of crops [2,3]. Silicon is one of the essential microelements of plants. It is involved in morphological and physiological regulation and the

response to various plant genetic responses [4,5]. Silicon fertilizer has been reported to increase soybean root diameter, photosynthetic rate, and root nodule area [6], change soil properties, and increase the content of available silicon in soil [7], inhibiting the occurrence of *Plasmodiopyra brassicae* Wor [8] and, by inducing special beneficial bacteria in soil increasing, heavy metal resistance [9].

The Lanzhou lily (*Lilium davidii* var. *unicolor*) is the only edible sweet lily consumed as food in China. The lily is an endemic species with a narrow range, suitable only for the arid region at the altitude of 2000–2600 m in Gansu Province, Western China [10]. Lily reproduces asexually and is cultivated perennially, so it is usually grown in a long-term continuous monoculture, which results in serious CRPs, such as severe soil degradation and significant yield and quality losses. In addition, CRPs in lilies cause an estimated loss of 50 million dollars to farmers in the area. To combat CRPs, we conducted a field test of silicon fertilizer and microbial agents in 2019 and found that this practice enhanced the growth of the plant and bulb, changed the physiochemical and biological properties of the soil, increased the number of culturable bacteria, and decreased the number of culturable fungi [11]. There are many types of microorganisms in soil. The culturable microorganisms account for only a small proportion, and most of these bacteria and fungi cannot be cultured in vitro. Therefore, we know little about the changes in the overall microbial structure during the process.

Soil bacteria play an important role in nutrient uptake, resistance to soil-borne diseases, and the activation of the plant defense system against pathogens [12–14]. We used NGS technology to analyze the bacterial structures in the rhizosphere of the Lanzhou lily under continuous cropping, and we found that the phylum Proteobacteria and the related genus *Sphingomonas* can be regarded as biomarkers in the system of lily transplantation [15]. Currently, there are many reports showing the role of microbial agents in regulating soil microbial community, but fewer reports focus on the effects of silicon fertilizer on soil microbial community. Therefore, it is necessary to study all microorganisms to reveal the mechanism of soil biological properties under silicon fertilizer and microbial agent treatment.

On this basis, we hypothesize that the silicon element and microbial agents impressively influence the community of microorganisms in the soil. To clarify how the silicon element and microbial agents change the biological properties of the soil and alleviate the CPRs of the lily, we collected the data on the bacterial community structure in the soil of the root zone of the lily in four treatments using high-throughput DNA sequencing techniques (Miseq). The objectives of this study are to determine whether the silicon fertilizer and microbial agent treatments change the structure and diversity of the microbial community in the soil and to investigate the specific microorganisms involved in soil health under this fertilizer model.

2. Materials and Methods

2.1. Field Description and Soil Sample Collection

The field is located in Jiangjiashan village, Zhongpu town, Lintao county, Gansu Province, Western China (103°53'12"~103°53'14" E, 35°49'11"~35°49' 13" N, 2330 m elevation). It is an arid zone on the loess plateau. The soil is locally known as Huang-mian soil (a deep soil layer with a high water holding capacity, a pH of 7.8, and 1.3% organic matter). The Lanzhou lily has been cultivated as food in this area for over 140 years.

The experiment was conducted from March 2019 to March 2022. The Lanzhou lily was planted in the experimental field for 9 years (at a 0–30 cm soil depth, with 11.60 g/kg organic matter, 32.58 mg/kg alkali-hydrolyzable nitrogen, 180.98 mg/kg available potassium, 19.63 mg/kg available phosphorus, 1.22 s/cm EC, and a pH of 7.97). We laid out the experiment with four (4) treatments: CK, no treatment; SF, silicon fertilizer (SiO_2 : 70% $\pm$ 3%, Langfang Wuhe Agricultural Science and Technology Co., LTD, Langfang city, Hebei province, China); MF, Special 8TM microbial agent supplement (Special 8TM with 22 types of bacteria, with a total of 15,000 cfu/g and organic matter content $\geq$ 70%, produced

by Qingdao Yuanhui Biological Environmental Protection Technology Co., Ltd., Qingdao city, Shandong province, China); SMF, Special 8TM microbial agent and silicon fertilizer supplement. Three replicates were set for each treatment, and the plot area was 10 m² (5 × 2 m).

First, we applied the Special 8TM microbial agents (67.5 L/ha) to the trenches in all treatments and sowed the lily bulb seeds. The lily cultivar was sown on 18 April 2019 at a density of 0.30 × 0.15 m per plantlet (the bulb seeds had a weight of about 17 ± 2 g). On 10 August 2019, the microbial agents (67.5 L/ha) and silicon fertilizer (30 kg/hm²) were applied in different treatments. While the lily grew for 3 years, we repeated the application of microbial agents and silicon fertilizer in different treatments on 14 July 2020 and 22 June 2021. The field test was managed with the same agronomic management and fertilization regime based on traditional agricultural practices in this region with an organic fertilizer (11,250 kg/ha) and without irrigation.

Soil samples were collected at the seedling flowering stage (28 July 2020). The 5-point sampling method was selected for each plot, with 4 plants selected for each point and a total of 20 plants within each plot. Soil samples were collected at a depth of 20 cm below the soil and 10 cm from the root. The zone soils of the 20 plants were mixed to obtain one soil sample; all 12 soil samples were collected in the same way. Each soil sample was divided into 2 subsamples: one was brought to the laboratory on dry ice and stored at −80 °C for downstream applications (DNA extraction), and the other sample was air-dried to study the soil properties.

2.2. Determination of Soil Physiochemical Properties and Plant Growth

Six indexes of soil physiochemical properties were determined (pH, alkaline-hydrolyzed nitrogen, available phosphorus, available potassium, organic matter, and available silicon). After soil samples were collected from plant roots, these 20 plants for each plot were taken to the laboratory to determine seedling indexes and evaluate plant growth status. The data on the physiochemical properties of the soil and seedlings were published [11]. After 3 years of cultivation, we harvested the bulbs and tested the bulb yields for each plot on 28 March 2021.

2.3. 16 SrRNA High-Throughput Sequencing

Soil DNA was extracted using the PowerSoil DNA Isolation Kit (MoBio Laboratories, Carlsbad, CA, USA), and the quality and purity of the extracted DNA were tested using Nanodrop.

The V₃–V₄ hypervariable region of the 16S rRNA gene in the total soil DNA was amplified by PCR using KAPA 2G Robust Hot Start Ready Mix and appropriate primers. The common primer sequences are 338-F (5'-ACTCCTACGGGAGGCAGCAG-3') and 806-R (5'-GGACTACHVGGGTWTCTAAT-3'). The 25 µL PCR amplification system composition was as follows: 12.5 µL of 2 × Taq Plus Master Mix, 3 µL of BSA (2 ng/µL), 7.5 µL of ddH₂O, 1 µL of Forward Primer (5 µM), and 1 µL of Reverse Primer (5 µM). The cycling parameters were 94 °C for 5 min, followed by 32 cycles of 94 °C for 30 s, 55 °C for 30 s, and 72 °C for 60 s, with a final extension at 72 °C for 7 min. PCR amplification products were detected by 1% agarose gel electrophoresis, and the PCR products were automatically purified by a magnetic bead method. The Miseq library was then created and purified, and the library was finally deep sequenced on the Illumina Miseq platform from the Allwegene Company (Beijing, China).

2.4. Data Analysis

Data analysis is based on the cloud services of the Beijing Allwegene company (<https://www.allwegene.com>, accessed on 25 August 2020). The obtained high-quality sequences were extracted and leveled according to the “minimum sample sequence number” before analysis. The effective sequences of the soil samples under different fertilizer treatments were clustered into operational taxonomic units (OTUs) with a similarity de-

gree of 97% using Uparse [16]. The Venn diagram [17] uses R tools for the statistics and plotting of the OTU clustering results. To determine if the amount of sequencing data from the samples was appropriate and sufficient to reflect the microbial information, rarefaction [18] and Shannon-Wiener [19] and alpha diversity index analysis [20] were calculated with the Mothur software (version 1.45.3). Heat map [21] was created with R language. (version 3.6.0).

To examine the statistical significance of the structural similarity among communities in different treatments, PCoA (principal coordinate analysis) was performed using the R package (version 3.6.0). The LDA Effect Size [22] was carried out to detect species with significant differences in abundance among fertilizer groups: Wilcoxon rank-sum test was used to analyze the difference between groups, and the threshold was set at 0.05. Linear discriminant analysis (LDA) was used to reduce the data and evaluate the influence of species with significant differences, and the threshold was set at 2. To reveal the interaction within the different bacterial communities, network analysis was performed by using CYTOSCAPE (version 3.7.0). We selected the top 15 phyla and top 20 genera to perform the analysis with the Spearman inspection method and used the corresponding phylum as the legend ($p < 0.05$ and $|R| > 0.4$). Redundant analysis (RDA) was performed for the bacterial horizontal community and physicochemical parameters of the Lanzhou lily soil by using CANOCO5 (version 5.0). Pearson correlation was carried between soil bacteria (relative abundance $RA > 0.2\%$) and the seedling index and the available silicon content in soil, respectively.

2.5. Accession Numbers

The sequences obtained in this study were submitted to the NCBI Sequence Read Archive (SRA) under the Bioproject ID PRJNA842155.

3. Results

3.1. Quantity of the Microorganism Diversity in Root Zone Soil

Sequencing of the V3–V4 hypervariable regions of the 16S rRNA genes resulted in a total of 447,477 high-quality, chimeric-free reads with a dominant length of 400–440 bp. Among the reads, 10,3554, 10,6567, 112,558, and 124,798 sequences were obtained for each of the CK, SF, MF, and SMF soil samples, respectively. To normalize and standardize the read sequencing depth, all samples were randomly selected to 27,524 reads/samples. The OTU distribution revealed a total of 3273 OTUs and 38, 63, 38, and 34 unique OTUs in CK, SF, MF, and SMF, respectively (Figure 1A). Compared to CK, SF had the highest OTUs, while SMF had the lowest. The rarefaction (Figure 1B) and Shannon-Wiener (Figure 1C) tended to be flat, indicating that the amount of sequencing data was large enough to comprehensively reflect the status of the bacterial community of the lily soil in continuous cropping under different treatments.

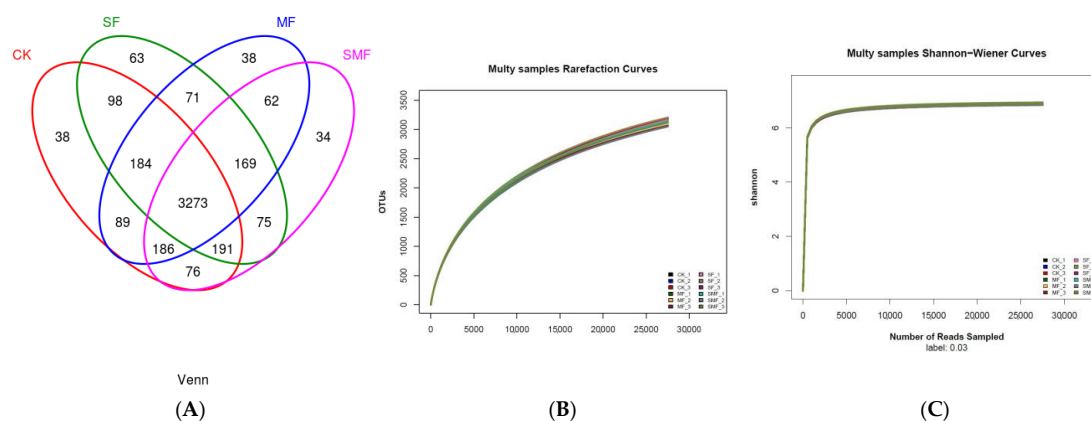


Figure 1. Venn diagram (A), dilution curve (B), and Shannon-Wiener curve (C) of soil bacterial community treated by silicon fertilizer and microbial agents.

Alpha diversity indices were evaluated based on OTUs. The results showed that the observed species shifted significantly in different treatment soil samples (Figure 2A). Beta diversity analysis based on PCoA showed that, although there was some overlap between replicates of individual treatments, most of the replicates were grouped together. The first principal coordinate axis (PCoA1), which contributed 27.45% of the total variation, and the second principal coordinate axis (PCoA2), which contributed 10.79% of the variation, explained 38.24% of the variation (Figure 2B).

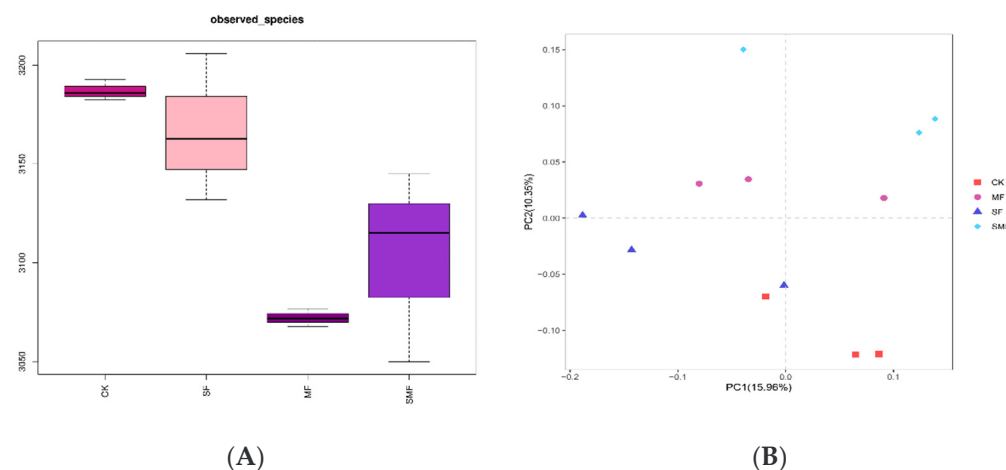


Figure 2. Bacterial diversity analysis of soil bacterial community treated by silicon fertilizer and microbial agents: (A): observed species ($p < 0.05$); (B): principal coordinate analysis (PCoA).

3.2. Taxonomic Distribution of Bacteria under Silicon Fertilizer and Microbial Agent Treatments

A large number of bacterial groups were identified at all taxonomic levels based on the results of species annotation. A total of 36 phyla were identified, with the dominant phyla being Proteobacteria, Acidobacteria, Actinobacteria, Chloroflexi, and Gemmatimonadetes (average RA > 5%). Among them, Acidobacteria was the optimal phyla in SF and MF, with RA values of 30.76% and 28.02%, respectively, while Proteobacteria was the optimal phyla in SMF, with a relative content of 29.98% (Figure 3). Among them, 104 classes were identified, and the dominant classes were Alphaproteobacteria, Betaproteobacteria, Blastocatellia, Gemmatimonadetes, and Subgroup 6 (average RA > 5%). A total of 126 orders were identified, and the most abundant orders (average RA > 5%) were Blastocatellales, Gemmatimonadales, and Rhizobiales. There are 232 families in total, mainly Blastocatellaceae Subgroup 4 and Gemmatimonadaceae (average RA > 5%).

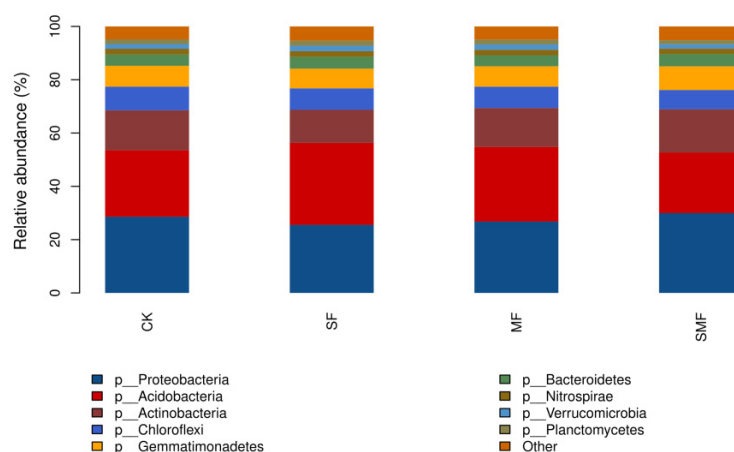


Figure 3. Barplots of soil bacterial community under silicon fertilizer and microbial agent treatment at the phylum level.

At the genus level, a total of 309 genera were detected. According to the OTU and its taxonomic heatmap analysis, cluster analysis was performed and a heatmap was created for the 20 most common genera (Figure 4). The identified genera were classified into low abundance, medium abundance, and high abundance groups. The most enriched genera were *Blastococcus*, *Haliangium*, *Pseudarthrobacter*, *Sphingomonas*, and RB41 (average RA > 1%).

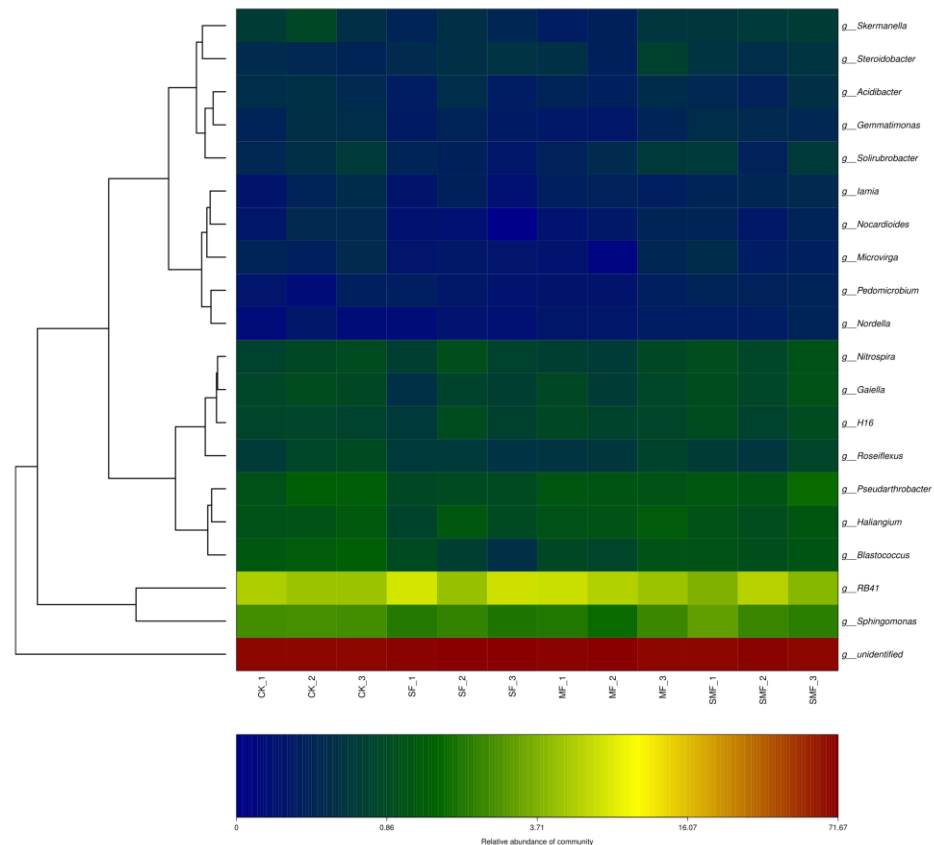


Figure 4. Heat map of soil bacterial community under silicon fertilizer and microbial agent treatment at the genus level.

3.3. LEfSe Analysis of Bacteria under Silicon Fertilizer and Microbial Agent Treatments

LEfSe analysis showed the changes in soil bacterial community at different taxonomic levels under different treatments (Figure 5). The results showed that some important bacterial groups significantly dominated in the CK, SF and SMF treatments, and we list several groups as follows: (I) in CK: the genera *Blastococcus*, *Pseudonocardia*, *Lautropia*, and *Rhizobium* were significantly dominant, as well as *Flavisolibacter* and its species *Clostridium butyricum*. (II) in SF: Pseudomonadales and its family Pseudomonadaceae and its genus *Pseudomonas* were significantly increased. (III) in SMF, Actinobacteria and the associated genera *Rhodoplanes* and *Streptosporangium* were significantly increased, along with *Nordella*, *Devosia*, and *Roseococcus*.

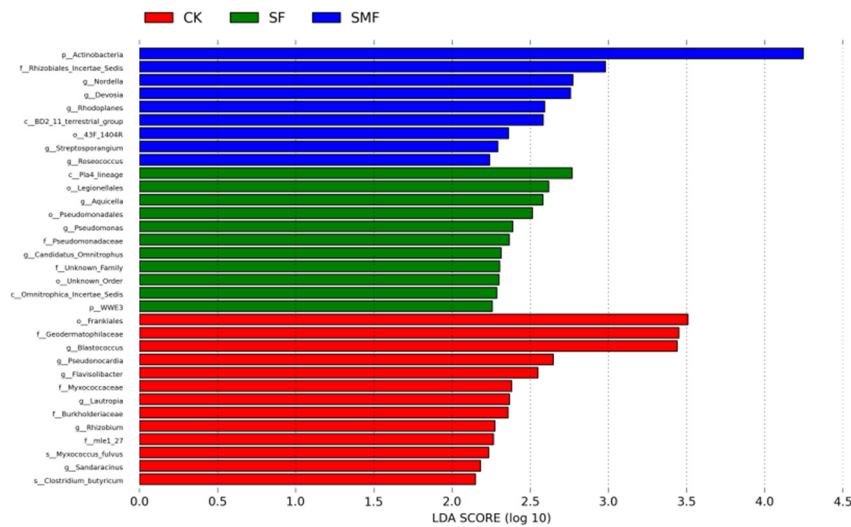


Figure 5. LDA obtained from LEfSe analysis showing changes in dominant bacterial communities at different taxonomic levels among different treatments.

3.4. The Lily Status Analysis and the Specific Bacterial Groups under Silicon Fertilizer and Microbial Agent Treatments

The treatments with silicon fertilizer and microbial agents improved the growth status of the lilies. In the first year after applying the treatments, the seedling index improved significantly compared to CK. After three years of constant application of silicon fertilizer and microbial agents, bulb yield increased by 13.48%, 10.78%, and 27.71% in SF, MF, and SMF, respectively, compared to CK (Table 1).

Table 1. Growth status of the Lanzhou lily over three years of constant application of silicon fertilizer and microbial agents: the significance is 0.05 for lower letters (a, b, c) presented in table.

Treatment	Seedling Index	Bulb Yield (kg/hm ²)
CK	90.77 ± 2.72 ^c	13,847.26 ± 281.01 ^c
SF	105.53 ± 0.98 ^b	15,713.66 ± 410.30 ^b
MF	110.03 ± 1.65 ^{ab}	15,339.85 ± 505.80 ^b
SMF	115.17 ± 2.44 ^a	17,684.44 ± 550.73 ^a

We studied the correlation between 22 dominant genera (RA > 0.2%) and the seedling index as well as the available silicon content in the soil. The results showed that the genus *Nordella* was positively correlated with seedling index and available silicon content, the genus *Pedomicrobium* was positively correlated with the seedling index, and the genus *Chthoniobacter* was negatively correlated with available silicon content (Table 2).

Table 2. The special bacterial groups (RA > 0.2%) correlated significantly with the seedling index and the available silicon content in the soil.

Bacteria Taxa	Correlation with Seedling Index (r_{si})	Correlation with Available Silicon (r_{as})	Relative Abundance (RA)
<i>g_Nordella</i>	0.79 **	0.63 *	0.32%
<i>g_Pedomicrobium</i>	0.63 *	0.44	0.35%
<i>g_Chthoniobacter</i>	−0.75 **	−0.63 *	0.26%

A total of 22 genera (RA > 0.2%) were detected; * represents $p < 0.05$; ** represents $p < 0.01$ Network analysis of bacterial groups under silicon fertilizer and microbial agent treatments.

Seedling index refers to the index in the first year under the treatments. Bulb weight refers to the weight of the mother bulbs that developed from the seed bulb after three years of growth (except for the baby bulb that developed from the large bulb, as shown in Appendix A and it was evaluated for all the plants in a plot in 2022).

To show the interaction within different bacterial communities, a network was created (Figure 6). At the phylum level, Verrucomicrobia was negatively correlated with Latescibacteria and Acidobacteria. In addition, Latescibacteria, Acidobacteria, and Proteobacteria were the most closely connected phyla (Figure 6A). At the genus level, there was a positive correlation between most of the bacterial genera. Only *RB41* was negatively correlated with *Acidibacter* and *Nitrospira*. *Gaiella* correlated with *Iamia* and *Sphingomonas*, and *Nitrospira* was correlated with *H16*, *Roseiflexus*, and *Haliangium*. Both *Gaiella* and *Nocardioideis* are the most important key genera closely related to other bacterial genera and thus act as “hubs” (Figure 6B).

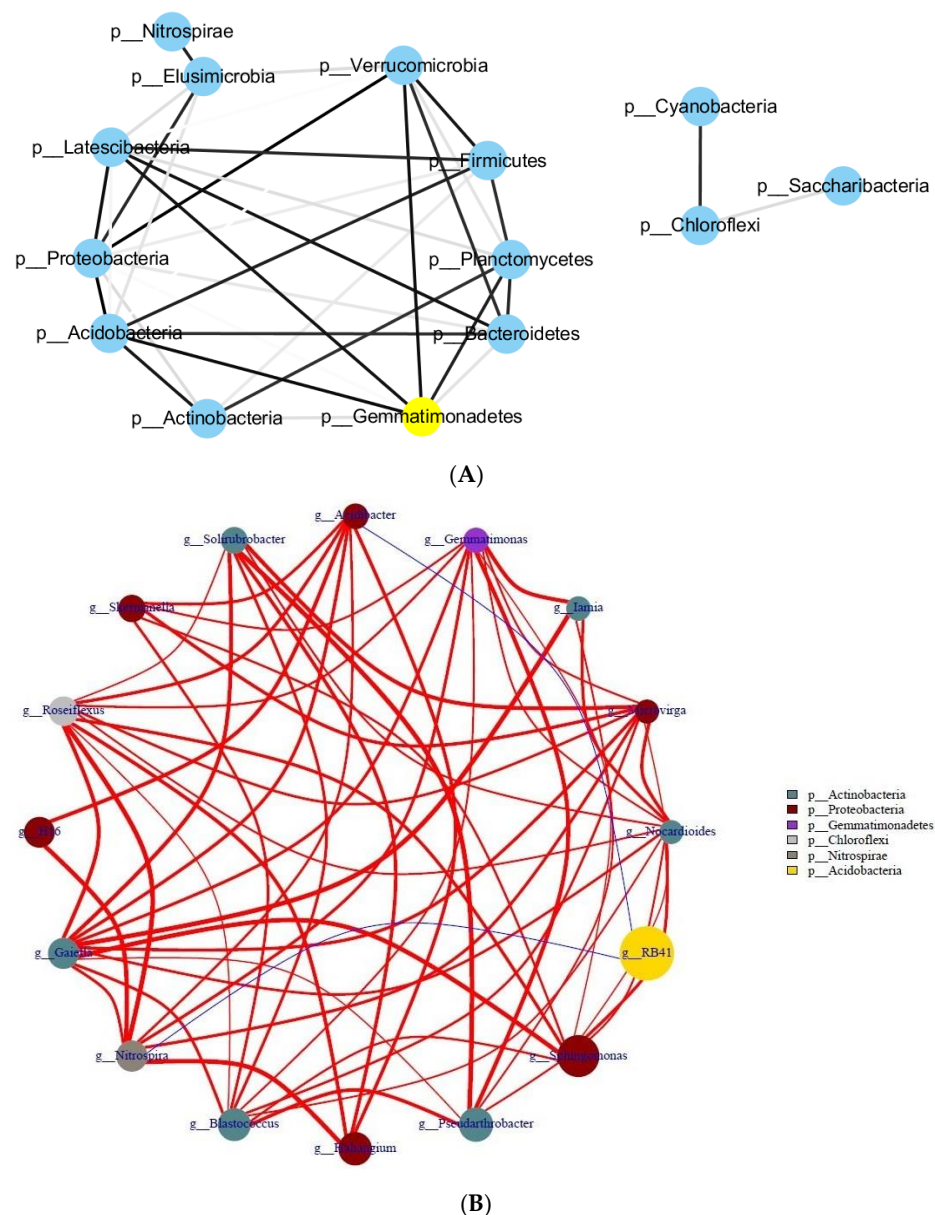


Figure 6. Network analysis of the 15 major bacterial phyla (A) and the 20 major bacterial genera (B) in soil treated with silicon fertilizer and microbial agents.

3.5. Links between Bacterial Community and the Soil's Physicochemical Properties

The silicon fertilizer and microbial agent treatments significantly changed the soil's physicochemical properties (Table S1). The RDA model showed that the six indexes of the soil's physicochemical properties contributed significantly to the restoration of the microbial community structure, and RDA1 and RDA2 explained 48.38% of the total variables (Figure 7). Among these indexes, the organic matter, available phosphorus, and available potassium were more important factors than the available silicon, which influenced the soil bacterial community structure. There was a strong positive correlation between soil pH and *RB41*. Available nitrogen and available potassium had a strong positive correlation with *Steroidobacter*, and available phosphorus had the strongest positive correlation with *Iamia*. Bacteria were negatively correlated with available silicon, available nitrogen, available potassium, and pH, but positively correlated with available phosphorus. RDA also showed that soil samples from CK, SF, MF, and SMF were clustered together, in different quadrants, and the differences among treatments were significant.

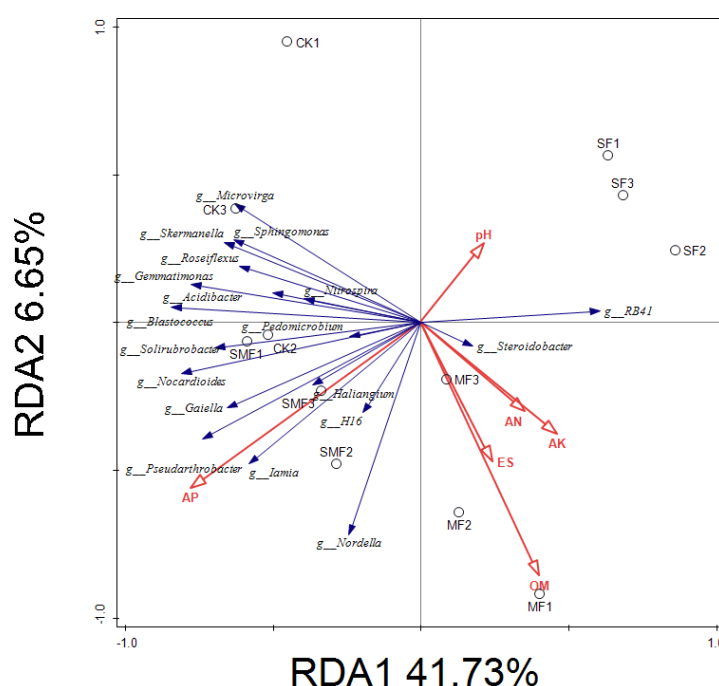


Figure 7. Redundancy analysis (RDA) of bacterial genera in soil and soil physicochemical properties: bacteria included top 20 genera; AP, AN, AK, ES, OM, and AP represented available phosphorus, alkali-hydrolyzable nitrogen, available potassium, available silicon, and organic matter, respectively.

4. Discussion

4.1. Bacterial Diversity and Some Special Bacterial Groups Related to Soil Health

In this study, the diversity of microorganisms in the differently treated soil samples significantly shifted (Figure 2A), and PCoA1 and PCoA2 explained 38.24% of the variation (Figure 2B). RDA also showed that the soil samples of CK, SF, MF, and SMF were significantly different from each other, and the RDA1 and RDA2 explained 48.38% of the total variables (Figure 7). All these results indicate that silicon fertilizer and microbial agents play a crucial role in rebuilding the microorganism structure.

The abundance of bacteria and the structure and diversity of the community influence the sustainable development of the soil and its productivity [23,24]. For example, the application of microbial agents in wheat soil can significantly change the diversity of functional microorganisms and the structure of the bacterial community [25], and the type of fertilization with *Bacillus subtilis* in benincasa soil can enrich soil bacterial diversity and reduce some special bacterial species [3]. However, in this study, the results were partially consistent with the above conclusion: The bacterial community structure significantly changed under

different treatments, while the bacterial diversity decreased significantly. The soil microbial community is complex, and the characteristics of the microbial community are the result of the complex interaction of the microbial population. Soil bacteria are susceptible to different fertilization models [26], microbial agent types [27], and different management practices [28], resulting in varying degrees in the bacterial community structure. Thus, our results could be due to the different microbial agents and silicon fertilizers used, as well as the different fertilization practices.

Our results show that the phylum Actinobacteria plays an important role in maintaining soil health. A total of 36 phyla, 104 classes, and over 300 genera were identified in this study. The predominant phyla were Proteobacteria, Acidobacteria, Actinobacteria, Chloroflexi, and Gemmatimonadetes in the different fertilizer treatments (Figure 3), which have also been detected in the soil of muskmelon [29], ginger [30], and *Catalpa bungei* [31]. At the phylum level, Actinobacteria were significantly increased in the SMF treatment compared to the CK, MF, and SF treatments (Figure 5). Actinobacteria can produce a variety of substances (extracellular enzymes and secondary metabolites) that can promote the decomposition of animal and plant remains in soil and influence the structure and diversity of the soil bacterial community [32]. In addition, some Actinobacteria strains can secrete hormonal substances and stimulate the root system to release more secretions [27], which provide abundant energy for microbial growth and multiplication and promote the proliferation of beneficial bacteria in the soil. On the other hand, microbial agents contain a large number of amino acids, polypeptides, sugars, nitrogen, phosphorus, potassium, and other nutrients, and silicon is one of the microelements essential for plants, which significantly improves the physiological activity of the roots and promotes the uptake and transformation of nutrients. This is a possible explanation why the supplemental administration of bacterial agents and silicon fertilizer (SMF treatment) was more effective than the supplemental administration of bacterial agents (MF treatment) or silicon fertilizer (SF treatment) in maintaining soil health and alleviating CRPs of the Lanzhou lily.

The results also showed that the genus *Pseudomonas* plays an important role in maintaining soil health. *Pseudomonas* sp. is known as a beneficial bacterium for plant growth because it enhances sulfate uptake [33] and acts as an antagonist against pathogens. Compared to CK, *Pseudomonas* significantly increased in all fertilizer treatments, especially in SF (Figure 5). Some *Pseudomonas* spp. are widely used as important members of commercial microbial agents. Their secretions can form protective films in plant roots to prevent pathogen invasion and alleviate soil-borne diseases [34]. It has been reported that silicon fertilizer inhibited the occurrence of *Plasmodiophora brassicae* Wor [8] and, by inducing some special beneficial soil bacteria, increased heavy metal resistance [9]. In this sweet lily replanting system, wilt disease, a type of soil-borne disease, occurred seriously, and our previous study identified *F. oxysporum*, *F. tricinatum*, and *F. solani* as pathogens of Lanzhou lily wilt disease using the in vitro culture method [35]. Therefore, we believe that, this fertilizer input model, acting as an antagonist against some soil *Fusarium* pathogens, might be one of the main mechanisms of *Pseudomonas* in maintaining soil health.

Our results suggest that the genus *Nordella* may be another important member in maintaining soil health. The genus *Nordella* was reported to play a key role in shaping the microbial structure during the in situ phytoremediation of vanadium-titanium magnetite mine tailings dam using *Pongamia pinnata* [36]. In the SMF treatment, the genus *Nordella* was significantly dominant compared to the CK, MF, and SF treatments (Figure 5) and positively correlated with the available silicon content and seedling index in lily soil (Table 2). Therefore, we concluded it might be an important member that could play a positive role in restoring the soil for replanting. However, we did not find a description of its function on soil quality, so it needs to be explored in vitro culture. We also detected several genera whose RA was significantly increased in the SMF treatment, such as *Rhodoplanes*, *Streptosporangium*, and *Devosia* (Figure 5), and two genera *Pedomicrobium* and *Chthoniobacter*, whose abundance correlated with the seedling index (Table 2). However, their function was less reported in the literature.

4.2. Relationship between Soil Bacteria and Soil Environment

In this study, RDA analysis showed that soil physical and chemical properties constituted the soil bacterial communities, with pH, available phosphorus, and organic matter playing the most important roles. After two years of continued treatment, soil pH decreased in SMF, while available phosphorus and available silicon increased significantly (Table S1). Soil pH is considered an indicator of the diversity of the soil microbial community, and the closer the pH is to 7, the greater the diversity of bacteria [37]. Some studies reported that soil bacteria RA were negatively correlated with pH, available silicon, and organic matter, while they were positively correlated with available phosphorus. For example, in pakchoi soil fertilized with a silicon bacterial community structure was significantly correlated with soil electrical conductivity, pH, and available potassium [9]. In soil with rice-wheat rotation fertilized with straw, bacterial community diversity was significantly negatively correlated with pH [38]. Our previous study showed that soil pH increased during the 0–9 years of the Lanzhou lily cropping system, and soil salinization occurred [39], while the organic content and bacterial richness increased due to the continuous application of organic fertilizers to the soil, solving the lily CRPs under the traditional soil management in this lily production area [15]. Therefore, we concluded that the bacterial community structure in the soil significantly changed mainly due to silicon fertilizer and microbial agents, which prevented an increase in pH and a decrease in organic content.

The network showed that there are potential interactions among different bacterial communities. At the phylum and genus levels, there were several key species connecting the group of soil bacteria, implying that these groups play a key role in maintaining the information network among soil microbial groups and regulating the micro-ecological flora. However, in this study, we only discussed the functions of some dominant microbial groups, and there is a large number of unidentified sequences. Therefore, it is necessary to conduct more detailed classification and function research using in vitro culture techniques in the future.

5. Conclusions

Silicon and microbial agents can alleviate CRPs in lilies by changing the diversity and structure of the bacterial community. In this fertilizer supplement model, the phylum Actinobacteria and the genus *Pseudomonas* played an important role in improving soil health and alleviating the CRPs of lilies. In addition, organic matter, available phosphorus, available potassium, and available silicon are the most important factors that contribute greatly to the rebuilding of the bacterial community and are involved in promoting soil health and alleviating CRPs.

Supplementary Materials: The following supporting information can be downloaded at <https://www.mdpi.com/article/10.3390/agronomy12071530/s1>, Table S1: Summary of soil physicochemical properties of Lanzhou: the data have been published [11]: the significance is 0.05 for lower letters (a, b, c) presented in table.

Author Contributions: Y.Y. and G.S. designed the research, performed the experiments, analyzed the data, and wrote the paper. L.Z., Y.L., L.H. and H.Y. conducted the discussions and revised the manuscript. All authors have read and agreed to the published version of the manuscript.

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Data Availability Statement: The sequences obtained in this study have been submitted to the NCBI Sequence Read Archive (SRA) under the Bioproject ID PRJNA842155.

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Appendix A



Figure A1. The Lanzhou lily cultivation methods: the sweet lily is cultivated perennially; after 3 years of cultivation, the large bulb (the mother bulb after three years of growth) is consumed as food, and the baby bulbs are resown to produce seed bulbs after 2–3 years of growth.

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