

Article

Sustainability of Urban Soil Management: Analysis of Soil Physicochemical Properties and Bacterial Community Structure under Different Green Space Types

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Abstract: Soil bacterial communities play a key role in nutrient cycling and ecosystem functioning. This study aims to reveal how green space type impacts soil quality and the bacterial community, which finally contributes to suggesting strategies for managing sustainable environments in urban areas. For this purpose, urban green space soils in this study are divided into four different types; park green space (PARK), street green space (STREET), attached green space (ATTACH) and residential green space (RESID). Results showed that significant differences were observed for soil physicochemical properties. Soil organic matter, total nitrogen, soil moisture content and available nitrogen in the ATTACH and PARK soils were significantly higher than in the STREET and RESID soils. Across the four green space types, the structure of bacterial communities was dominated by Proteobacteria, Actinobacteria and Chloroflexi at the phylum level. The diversity and richness of bacteria were significantly higher in the PARK and ATTACH soils than in the RESID and STREET soils. Results of principal component analysis (PCoA) showed that soil bacterial communities could be clustered into four different groups according to different green space types. In addition, analysis of similarities (ANOSIM) also implied that soil samples differed significantly from others. Redundancy analysis (RDA) and Spearman correlation analysis both showed that the contents of soil organic matter, total nitrogen, soil moisture and pH had great influence on the structures of bacterial communities. In summary, these results suggest that soil physicochemical properties and bacterial communities can be strongly affected by green space types, and thus, objective assessment of a particular measure can be provided to land managers and policy makers for informed decision-making in urban development and sustainability.

Keywords: green space types; sustainable development; soil physicochemical properties; soil bacterial communities; high-throughput sequencing

1. Introduction

In recent years, ecological civilization and sustainable development were put forward by the Chinese government. The government had attached more importance to urban ecosystem sustainability and improvement since the Olympic Games held in Beijing in 2008. It is widely accepted that urban green space can provide important ecological, economic, and social benefits [1]. Environmental protection is the most beneficial way to build an eco-friendly city such as Beijing, which leads to the construction of natural resources and ecosystem stabilization. Soil quality of urban green space is one

of the most important indices in the ecological criterion system [2]. Soil is the main base for vegetation and is crucial for plant growth, particularly when a large number of green spaces are constructed over a short time period [3]. In addition, soil quality can be easily affected by green space types, soil bacterial community, nutrient cycles, decomposition of organic residues and pollutant degradation [4].

Soil bacterial community composition, structure and diversity are important indicators of urban ecosystem sustainability due to its strong correlation with overall green space quality and ecosystem environmental health [5]. Furthermore, soil bacterial communities can also play important roles in regulating soil nutrients and energy transformation by catalyzing numerous chemical, physical and biological reactions [3].

Numerous studies have reported that the composition of bacterial communities are affected by different land use types. Various land use patterns changed soil physicochemical properties, human maintenance, and then affected the soil nutrient supplying state, and microbial survival conditions, thus resulting in significant differences in soil nutrient transformation and soil microbial activity [6]. Huang et al. have examined changes in the soil microbial community after reductive soil disinfection and cucumber seedling cultivation suggesting that some nitrification, denitrification and nitrogen fixation genes could be affected by different land use types [7]. Mhuireach et al. have examined airborne microbial communities in parks and parking lots, indicating that different green space land uses can impact bacterial communities [8]. Guo et al. have analyzed the soil bacterial community composition from native broadleaf forests to mixed and bamboo forests, and observed that land use change can have a profound impact on soil bacterial composition [9]. Nacke et al. have analyzed soil bacterial community composition and the diversity of grasslands and forests, observing that different management types can affect soil bacterial communities significantly [10].

Previous studies have shown that development of urban green spaces has always been strongly affected by management practices. Management practices create and sustain urban habitat complexity over time, for example, the composition of soil microbial communities that are fundamentally important in providing ecosystem functions in urban environments are sensitive to disturbances, including management through litter removal or grass mowing, fertilization and irrigation, visitors' trampling, as well as changes in plant residue quality [1]. In addition, the land use system has given the planners significant power to regulate the development of cities in China [11]. In this case, the government has the absolute power to decide the use of urban land development by making planning policies. Management practices, as well as anthropogenic activities, may play an important role in regulating soil bacterial community structure by changing the soil characteristics.

Biotic and abiotic factors have proved to be critical drivers of composition and diversity of soil bacterial communities [12]. Fierer and Jackson demonstrated soil properties such as moisture content, pH and organic matter content were major drivers of bacterial community composition [13]. Hou et al. demonstrated that soil microorganisms were sensitive to soil disturbances and play crucial roles in soil ecosystem functions by regulating the cycling of nutrient elements and the decomposition of organic matter [14].

Although various previous studies have focused on the bacterial diversity and composition in different land use types, little is currently known concerning the detailed changes in soil bacterial communities that vary with urban green space types. To maintain the soil functions supporting the urban ecosystem, it is important to understand how soil nutrients and bacterial communities respond to anthropogenic disturbance, especially about management policies in urban soils. Therefore, we examined the responses to soil physicochemical properties and bacterial diversity in four major types of green spaces in this study. The main objective of this study is to investigate how different urban green space types affect the soil nutrients and bacterial community diversity using high-throughput 16S rRNA sequencing technology. Deeper understanding of such changes in soil nutrients and bacterial community structure in relation to green space types would greatly benefit urban ecological and environmental management or restoration and could also help to offer scientific guidance in urban sustainable development.

2. Materials and Methods

2.1. Study Area

The study area (Figure 1) is located in Chaoyang district inside the 5th Ring in Beijing (116.2745°–116.4895° E, 39.8252°–39.9816° N). The average annual temperature of study area is approximately 12 °C and the mean annual precipitation is 600 mm. The vegetation in the study area is composed of evergreen and broadleaf trees. The soil texture in both areas were characteristic of sandy silt and clay silt according to the USDA (United States Department of Agriculture) classification. In this study, urban anthropogenic disturbances mainly refer to trampling, mowing and raking, although some variation in, e.g., the level of air pollution might have existed. There are four main green space types in this study area, namely park green space (PARK), street green space (STREET), attached green space (ATTACH) and residential green space (RESID). PARK is the green space which is open to the public (including modern green parks and ancient royal parks) and provides space for education and recreation. STREET refers to the liner corridors between sidewalks, curbs or traffic islands (excluding street trees), which serves to buffer people from traffic, screen noise and solar radiation. ATTACH is the green space which is attached to industrial and commercial areas, providing an esthetic function as well as a venue for amenity-recreation. RESID is described as the green space which is maintained by the residential communities, providing leisure spaces for local residents [2]. Soils in the PARK and ATTACH areas have been intensively and extensively managed in Beijing, in contrast, soils in the green spaces such as STREET and RESID have seldom been managed. For green spaces such as PARK and ATTACH, management practices, such as planting, irrigation and fertilization with plant residues and inorganic fertilizers, have been frequent since their establishment. For green spaces such as STREET and RESID, leaf litter removal and mowing of lawns were the main management styles. In addition, accumulation of household garbage such as the plant ash and kitchen waste were also found when studying the residential quarter. Information concerning management practices was obtained from interviews with local park managers, field observations, published literature, policy documents and online information sources.

2.2. Soil Sampling and Analysis

Soil samples were collected from the surface horizon (0–30 cm) of urban green spaces in August 2016. In order to avoid destroying buried electric cables and other public network cables, we invited a local garden specialist to supervise soil sampling while maintaining a scientific sample distribution. Each type of green spaces was replicated at five plots, for a total of 20 plots. For each plot, a composite sample of soils was obtained, consisting of six soil cores obtained with a sampler (2.5 cm in diameter) at randomly selected locations. After visible plant fragments and large stones were removed, the subsamples were combined, and each sample was thoroughly mixed with a spade. Then, the soil samples were put into zip-lock bags and transformed to the lab on the ice. In the lab, soil samples were sealed and stored in a cold room (at –20 °C) until chemical analysis.

Each sample was mixed by sieving (mesh size 2 mm) and a subsample (approximately 2 g) of each composite sample was collected in a 2 mL Eppendorf tube and stored at –80 °C until DNA extraction [15]. DNA isolation was performed within five days, other properties were analyzed until the end of 2016.

The soil moisture (SM) content in each soil sample was determined after drying at 105 °C overnight [16]. Soil organic matter (SOM) content was estimated by loss on ignition at 550 °C [17]. Soil pH was measured in a 1:10 soil-water slurry with a digital pH meter (Elmetron, Poland). Total nitrogen (TN) content was determined by semi-micro Kjeldahl digestion using Se, CuSO₄ and K₂SO₄ as catalysts [18]. Available nitrogen (AN) was measured with an alkali N-proliferation method and available phosphorus (AP) was extracted with sodium bicarbonate [19]. The normal values of potassium concentration (AK) were extracted by ammonium acetate (NH₄AC) and determined by means of a flame photometer [16].

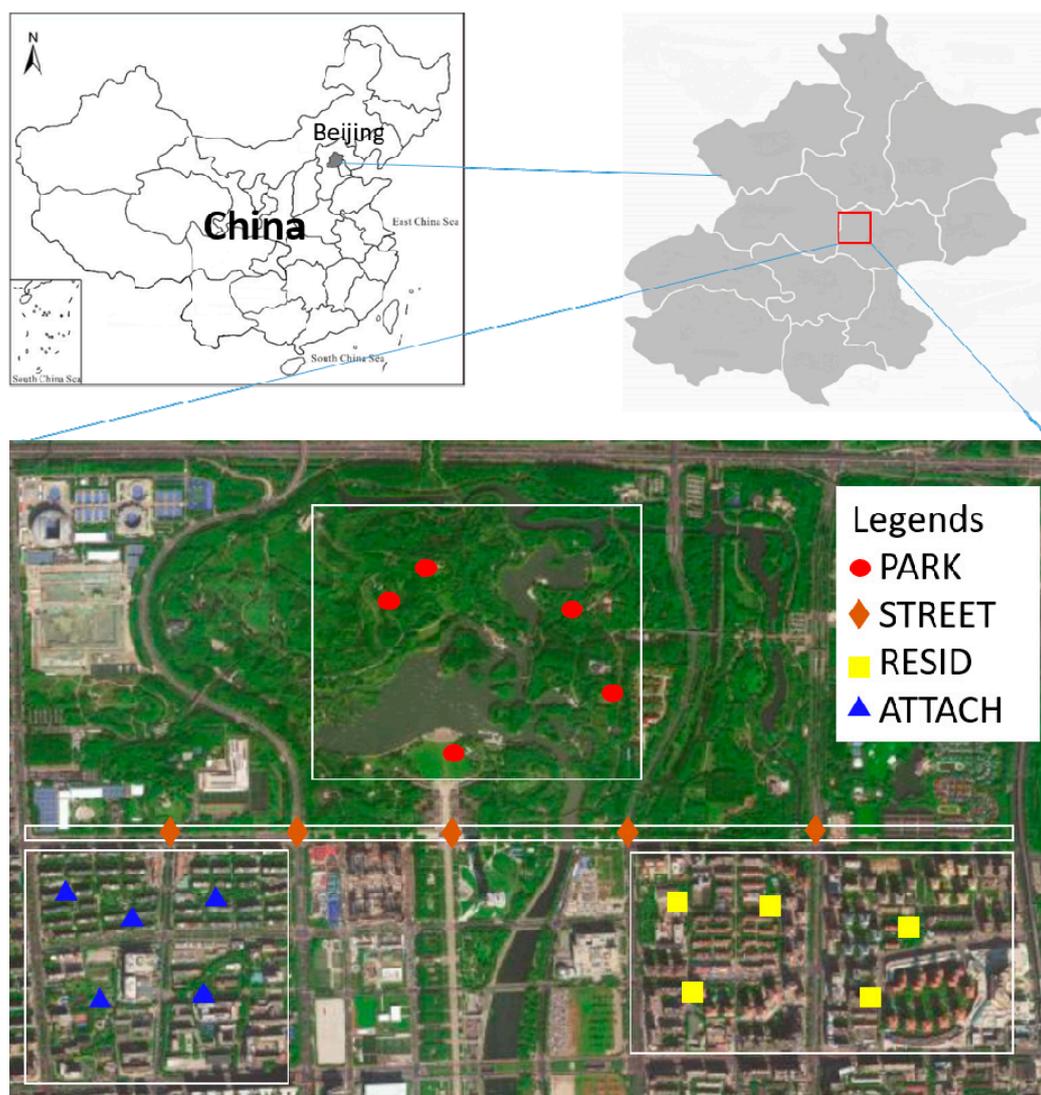


Figure 1. Location and sites of sampling points in the study area.

2.3. DNA Extraction and PCR Amplification

Microbial DNA was extracted from each of the 20 green space soil samples using the E.Z.N.A. [®]soil DNA Kit (Omega Bio-tek, Norcross, GA, USA) according to manufacturer's protocols [20]. The V4 region of the bacteria 16S ribosomal DNA gene were amplified by PCR using primers 338F (5'-ACTCCTACGGGAGGCAGCAG-3') and 806R (5'-GGACTACHVGGGTWTCTAAT-3') [21], where barcode was an eight-base sequence unique to each sample [22]. PCR reactions were performed in triplicate 20 μ L mixture containing 10 ng of template DNA, 0.8 μ L of each primer, 4 μ L of 5 \times FastPfu Buffer, 2 μ L of 2.5 mM dNTPs and 0.4 μ L of FastPfu Polymerase. The PCR amplification conditions were as follows: 95 $^{\circ}$ C for 3 min, 27 cycles at 95 $^{\circ}$ C for 30 s, 55 $^{\circ}$ C for 30 s, 72 $^{\circ}$ C for 45 s and a final extension at 72 $^{\circ}$ C for 10 min.

2.4. Illumina MiSeq Sequencing

The amplification products were purified using the AxyPrep DNA Gel Extraction Kit (Axygen Biosciences, Union City, CA, USA) according to the manufacturer's instructions, quantified using QuantiFluor[™]-ST (Promega, Wisconsin, USA), and the quality was confirmed by 2% agarose gel electrophoresis. Purified amplicons were pooled in equimolar and paired-end sequenced on an Illumina MiSeq platform according to the standard protocols.

2.5. Processing of Sequencing Data

Raw fastq files were de-multiplexed, quality-filtered using QIIME (version 1.7.0) [23]. The 300 bp reads were truncated at any site receiving an average quality score <20 over a 50 bp sliding window and the truncated reads shorter than 50 bp were discarded. Reads containing ambiguous characters were removed after two nucleotides mismatched in primer matching. Only sequences that overlapped longer than 10 bp were assembled according to their overlap sequence.

Operational taxonomic units (OTUs) were clustered with 97% similarity cutoff using UPARSE (version 7.1) [24] and chimeric sequences were identified and removed using UCHIME. The taxonomic classification was analyzed by RDP Classifier (<http://rdp.cme.msu.edu/>) against the SILVA (SSU115)16S rDNA database using confidence threshold of 70% [25].

2.6. Data Analysis

One-way analysis of variance (ANOVA) was carried out to compare physicochemical properties among soil samples from different green spaces using SPSS (version 19). Relationships among the bacterial community composition in different green space types were visualized using principal coordinate analysis (PCoA) of pairwise Bray–Curtis dissimilarity matrices based on 97% OTU similarity across different samples. The PCoA results were displayed using the WGCNA (Weighted Correlation Network Analysis) package, stat packages and ggplot2 package in R (Version 2.15.3). A similarity analysis (ANOSIM) was performed using 999 permutations and a Bray distance measure was used to test for differences in soil bacterial communities. Generally, an $R > 0.5$ indicates good separation, whereas $R \sim 0$ indicates no separation between the groups in ANOSIM. Redundancy analysis (RDA) was performed to visualize the relationships between soil physicochemical properties and bacterial communities. Spearman correlation coefficient between abundant phyla and physicochemical properties was also calculated. In all tests, a p value of <0.05 was considered statistically significant.

3. Results

3.1. Soil Physicochemical Characteristics

Table 1 shows that there were significant differences in the soil physicochemical properties among the samples. The samples from the four distinct green space types differed in terms of soil organic matter, soil moisture, pH and chemical elements. The SOM, TN, SM, AN in the PARK soils were obviously higher than in other three soil types and showed a significant difference ($p < 0.05$), whereas they did not show significant difference among ATTACH, STREET and RESID samples ($p > 0.05$). However, no significant differences were observed for the AK and AP values across all soil samples.

Table 1. Soil physicochemical properties in different green space samples of Beijing.

Types	SOM g/kg	TN g/kg	pH	SM %	AN mg/kg	AK mg/kg	AP mg/kg
PARK	33.95a	1.36a	7.19b	13.73a	80.11a	210.56a	17.75a
ATTACH	14.32b	0.75b	7.77a	11.54a	64.40b	128.06a	21.02a
STREET	12.29b	0.59bc	7.83a	6.66b	57.85b	128.85a	22.14a
RESID	10.09b	0.43c	7.85a	6.31b	54.56b	215.85a	22.36a

Notes: Values followed by same letters are not significantly different according to Duncan's test ($p < 0.05$).

Notably, the pH value was significantly lower in the PARK samples than in other three green space types. The pH value ranged from 7.19 to 7.85, indicating that it was slightly less alkaline in the PARK soils, whereas it was more alkaline in the other three types. Significantly higher soil moisture content was seen in the PARK (13.73%) and ATTACH (11.54%) soils than that in the STREET (6.66%) and RESID (6.31%) soils. The content of SOM and, particularly, TN were significantly higher in the PARK soils, reaching 33.95 g/kg (SOM) and 1.36 g/kg (TN). Overall, soil physical and chemical properties were strongly affected by green space types.

3.2. Analysis of 16S rRNA Sequencing Results

The Illumina Miseq sequencing platform was used to amplify and detect 16S rRNA gene product sequences from different urban green space soils. After performing a series of processing steps with the sequencing results, 31,739–43,477 valid sequences were obtained from each sample, for a total of 764,563 sequences (average length of 439.87 base pairs). A total of 4639 OTUs were obtained at a sequence-similarity level at 97%. The rarefaction curves for the OTUs detected in this study showed that the quantity of observed species (OTUs) increased as the sequencing depth increased. The ends of rarefaction curves taper off with increasing numbers of sequences per sample, as is commonly observed with sequencing data (Figure 2).

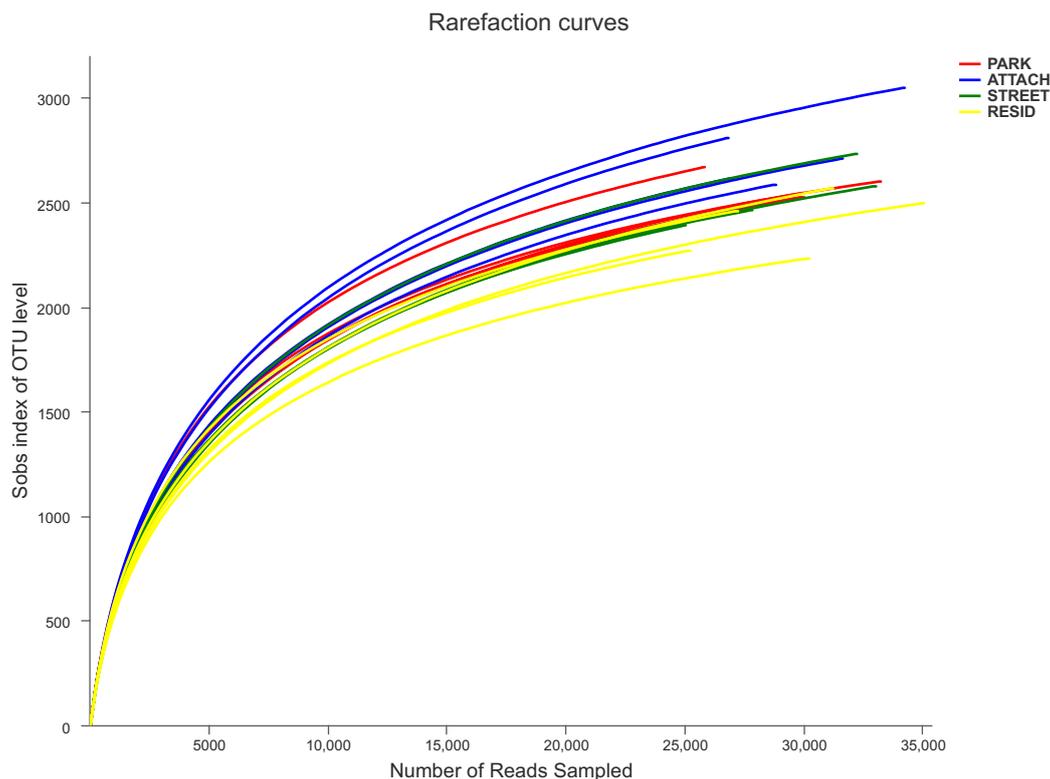


Figure 2. Rarefaction curves of each soil sample at cutoff level of 3%.

3.3. Richness and Diversity of Soil Bacterial Communities

In order to estimate the alpha diversity of the different bacterial 16S rRNA gene sequence libraries, we calculated diversity indices (Shannon, Simpson), richness estimators (Chao 1, ACE) and Good's nonparametric coverage estimator [26–28] (Table 2). Among all the samples, the average OTU density of the ATTACH samples was the highest, whereas that of the PARK soils was the lowest. For instance, the average number of observed bacterial OTUs was 3878, 4082, 3762 and 3640 for STREET, ATTACH, RESID and PARK samples (Figure 3). Sequencing integrity was measured using Good's coverage. The Good's coverage value in our study approached 95%, showing that most bacterial species in our samples were detected.

Table 2. The diversity estimates of bacterial community investigated by Miseq sequencing.

Sample	Shannon	Simpson	Ace	Chao1	Coverage
PARK	7.23ab	0.0018b	5434.58b	5461.76b	0.96ab
ATTACH	7.30a	0.0017b	6093.74a	6034.51a	0.95b
STREET	7.12b	0.0024a	5449.89b	5460.28b	0.96ab
RESID	7.13b	0.0023a	5131.49b	5183.30b	0.96a

Notes: Values followed by same letters are not significantly different according to Duncan's test ($p < 0.05$).

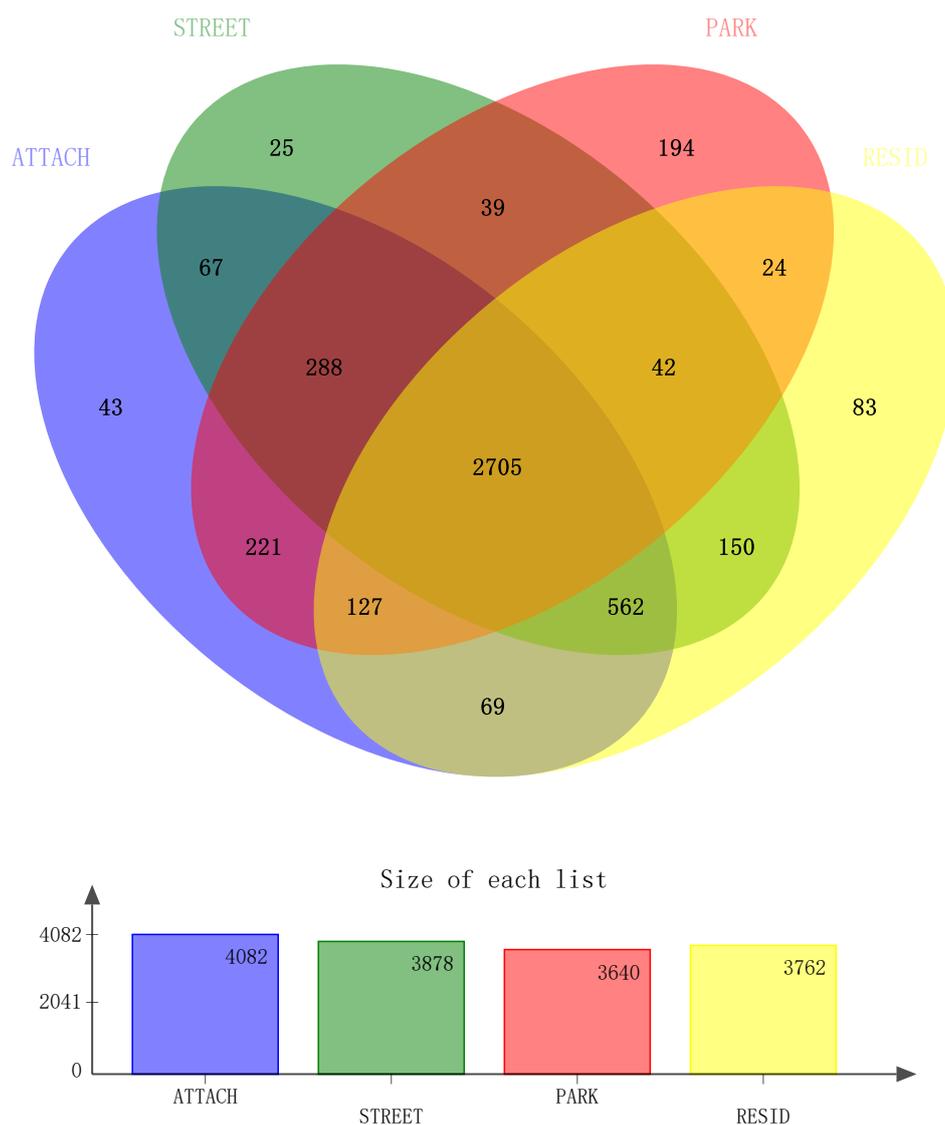


Figure 3. Venn diagram of the number of shared and unique OTUs (Operational Taxonomic Unit) under different green space types.

Both the observed and estimated total richness was higher in the ATTACH soils than other three soils. The results showed that PARK green space had less diversity and abundance in Shannon, Ace and Chao 1 than ATTACH green space, following by RESID and STREET green spaces, indicating that the bacterial diversity (Shannon and Simpson) and richness (Chao 1 and ACE) differed significantly among the four different green space types. The highest alpha diversities were found in the ATTACH green space (Shannon and Simpson indices of 7.30 and 0.0017, ACE and Chao 1 indices of 6093.74 and 6034.51,

individually), suggesting that management of the ATTACH green space increased the diversity of the soil bacterial community.

3.4. The Structure and Components of Soil Bacterial Community

On the phylum level, different phyla with a relative sequence abundance of at least 1% were identified (Figure 4). The dominant phyla across all samples were Proteobacteria, Acidobacteria, Chloroflexi, Actinobacteria, Gemmatimonadetes, Bacteroidetes, Nitrospirae, Planctomycetes, Saccharibacteria, Verrucomicrobia, Latescibacteria, Firmicutes and Cyanobacteria (the total relative abundances of each phylum >1%). However, across the different soil samples, the relative abundances of these bacterial phyla were significantly varied.

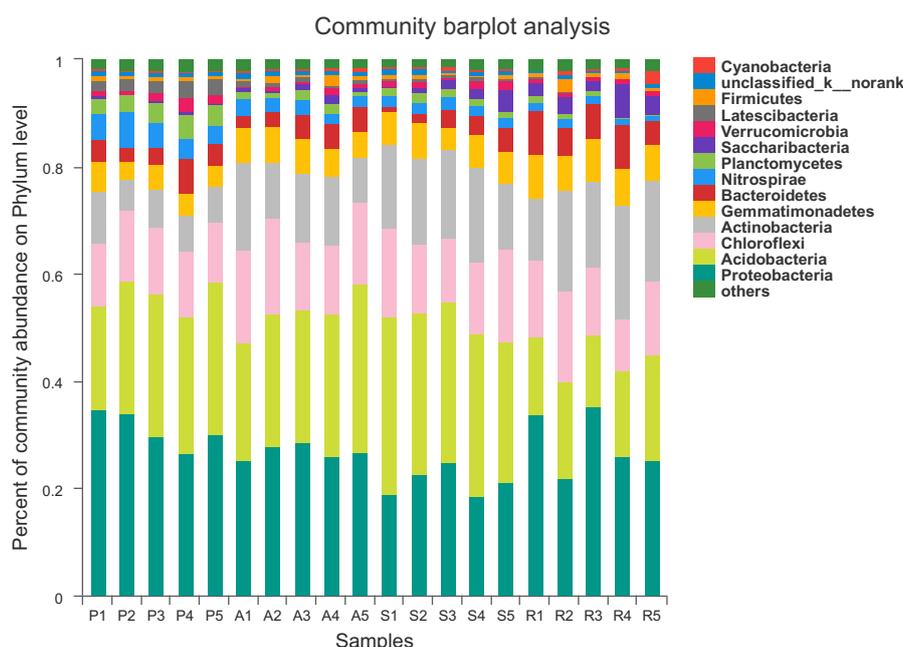


Figure 4. Relative abundance of bacterial phyla in the four green space soils (the bacterial phyla with relative abundance lower than 1% in all the soils were copolymerized in “others”).

Proteobacteria was the most abundant phyla in the PARK, ATTACH and RESID green space soils, while Acidobacteria was the most abundant phyla in the STREET green space soils. The bacterial diversity in PARK soils included a high relative abundance of Proteobacteria (26.46%–34.63%), followed by Acidobacteria (19.50%–28.59%), Chloroflexi (11.22%–13.25%) and Actinobacteria (5.54%–9.64%). In ATTACH soils, Proteobacteria (25.28%–28.57%) was also an important component of the bacterial community, followed by Acidobacteria (21.93%–31.35%), Chloroflexi (12.54%–17.80%) and Actinobacteria (5.54%–9.64%). The predominant phyla in the RESID soils were Proteobacteria (21.91%–35.32%), Acidobacteria (13.36%–19.61%), Actinobacteria (11.83%–21.40%) and Chloroflexi (9.71%–16.74%), whereas the predominant phyla in the STREET soils were Acidobacteria (26.18%–33.25%), Proteobacteria (18.55%–24.89%), Actinobacteria (12.16%–17.52%) and Chloroflexi (11.77%–17.49%). Overall, the composition at phylum level of the soil bacterial communities were similar among all the green space types, although the relative abundance of dominant phyla was different.

Analysis of bacterial community composition under different green space types showed that the 15 most abundant phylum accounted for 99.7% of the reads (Figure 5). Across all the different soil samples, the relative abundance of some bacterial phyla, such as Proteobacteria ($p < 0.01$), Acidobacteria ($p < 0.001$), Actinobacteria ($p < 0.001$), Gemmatimonadetes ($p < 0.01$), Bacteroidetes

($p < 0.05$), Nitrospirae ($p < 0.01$), Planctomycetes ($p < 0.001$), Saccharibacteria ($p < 0.05$), Latescibacteria ($p < 0.001$) and Armatimonadetes ($p < 0.001$), significantly varied.

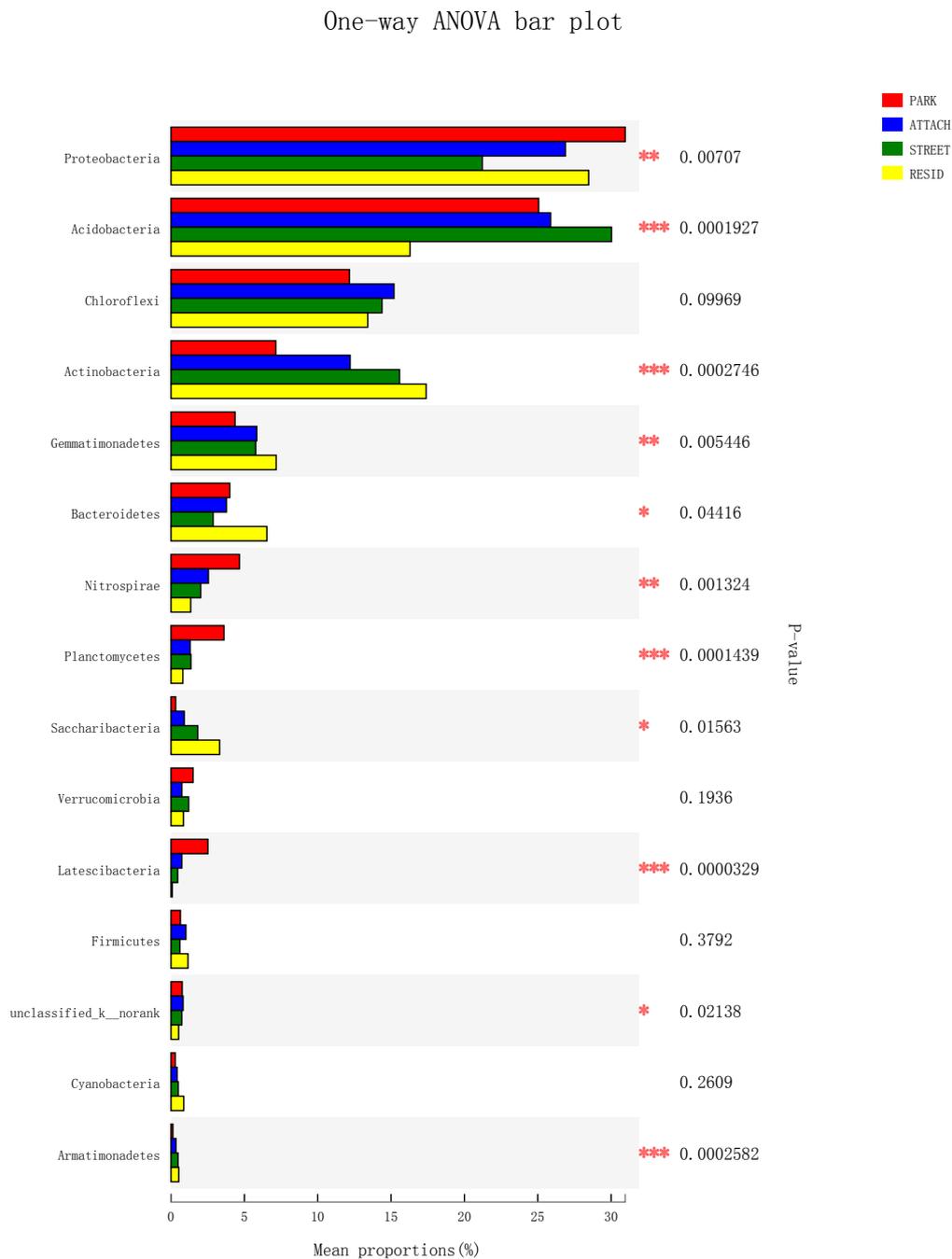


Figure 5. Changes in the relative abundances of bacterial phylum across the different green space types. Bars indicate one standard deviation. Asterisks show significant correlations (*** $p < 0.001$, ** $0.001 < p < 0.01$, * $0.01 < p < 0.05$).

3.5. The Dissimilarity of Soil Bacterial Community

The sample dots of all the four green space types in PCoA (Figure 6) were separated distinctly from each other. The first two components explained 44.88% of the total bacterial community variation among the individual samples across different green space types. Generally, the bacterial communities in the PARK, STREET, RESID and ATTACH soils were quite different and were scattered apart significantly from each other.

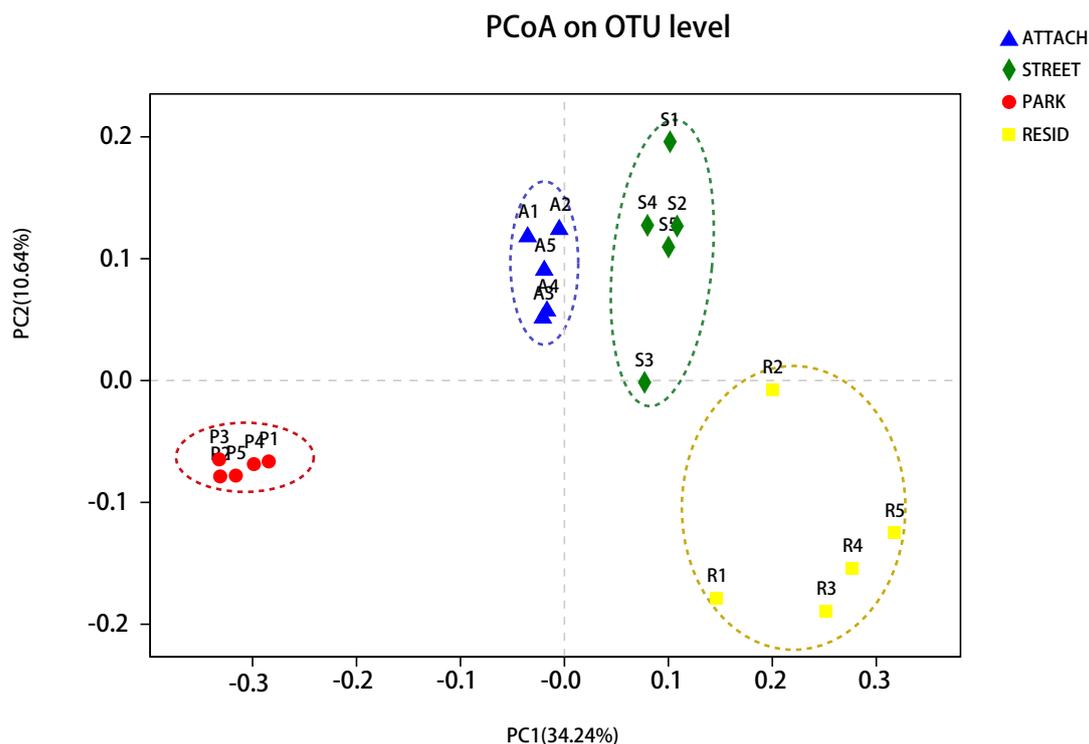


Figure 6. Principal component analysis (PCA) of bacterial communities based on OTUs at a distance of 3% for individual samples from different green space types. The first two components are 34.24% and 10.64%.

Analysis of similarities (ANOSIM) indicated that the OTU composition differed significantly ($R = 0.752$, $p = 0.001$) between the communities found in the four green space types. The results of the PCoA analysis, based on the similarity of the bacterial communities among the different green space types, were in agreement with those revealed results by the ANOSIM analysis.

3.6. Relationships between Bacterial Community Structure and Soil Physicochemical Properties

The redundancy analysis (RDA) clearly showed the relationship between soil physicochemical properties and the bacterial community structure. In this experiment, RDA analysis in Figure 7 was performed to determine the variable effects of soil physicochemical properties (pH, soil organic matter, soil moisture, total nitrogen, available nitrogen, available phosphorus and available potassium) on the OTU level. The first two axes of RDA explained 27.03% and 9.73% of the total variation in the data.

RDA analysis results showed that the four different green space types had different gathering positions, which meant green space types changed soil bacterial structure. As shown in Figure 7, influences of soil organic matter (SOM), soil moisture content (SM), total nitrogen (TN) and pH had great influences on bacterial community, whereas available nitrogen (AN), available potassium (AK) and available phosphorus (AP) had lower influence on bacterial community.

Spearman's correlation coefficient (Figure 8) was calculated to identify the correlations between the relative abundance of abundant phyla and soil physicochemical properties. Red color means higher correlation whereas green color signifies lower correlation. Stronger colors in the heat maps represent stronger correlations. It seems that pH, soil organic matter (SOM), soil moisture content (SM) and total nitrogen (TN) were the main contaminants which might have influenced bacterial communities.

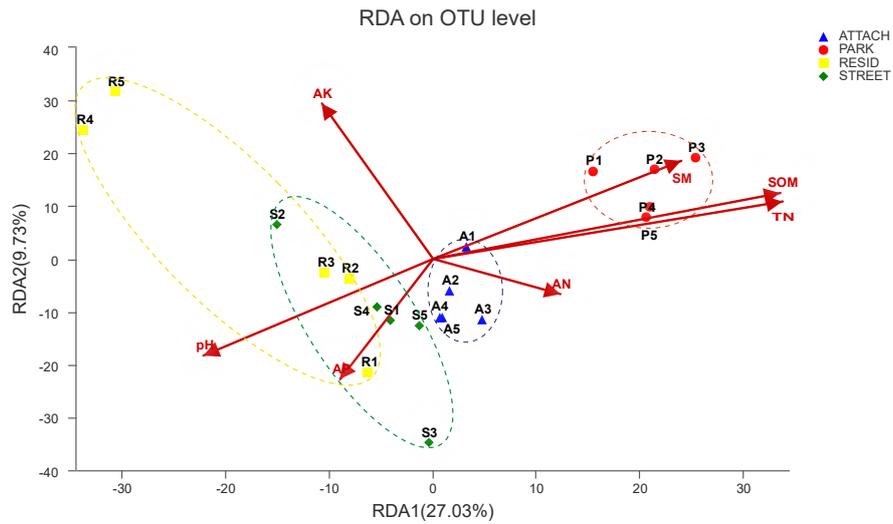


Figure 7. Redundancy analysis (RDA) of soil bacterial communities and soil physicochemical properties for individual samples from different green space types.

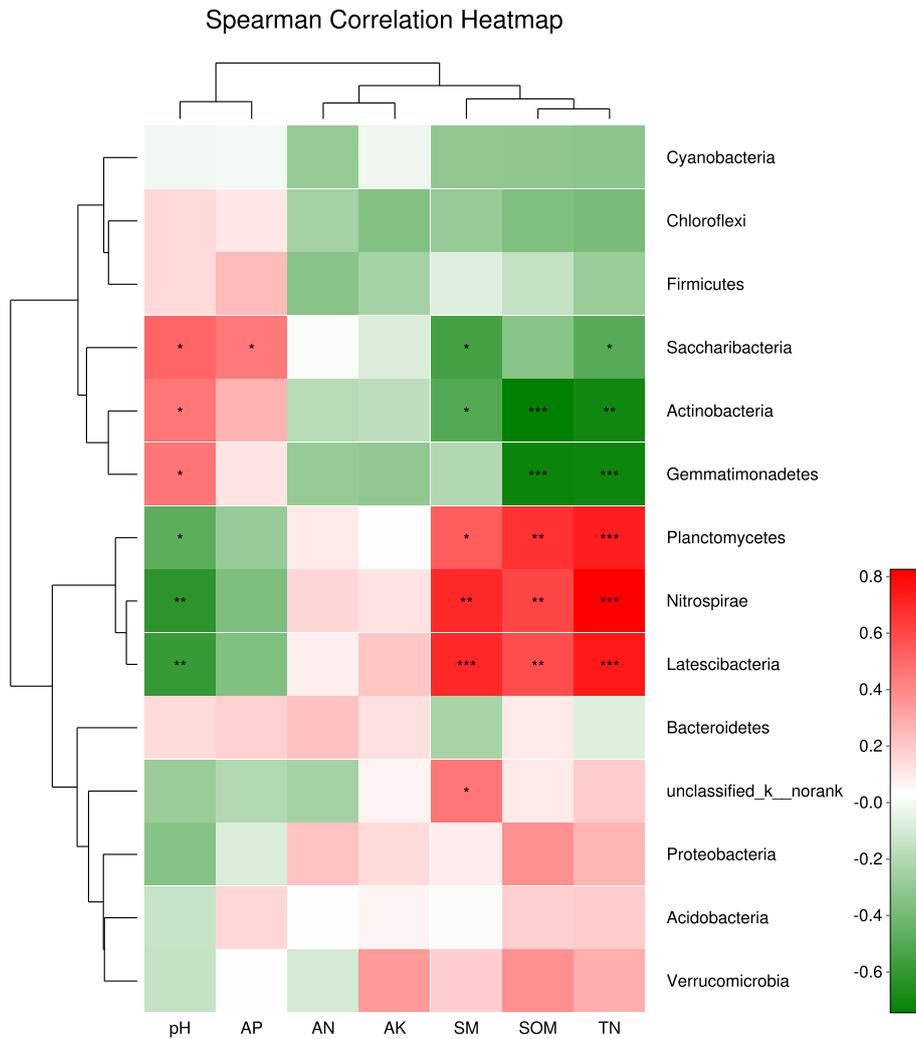


Figure 8. Spearman correlation heat map showing the correlations between bacteria phylum and physicochemical properties. Stronger colors (red is negative, green is positive) in the heat map represent stronger correlations. Asterisks show significant correlations (** $p < 0.001$, ** $0.001 < p < 0.01$, * $0.01 < p < 0.05$).

In the correlation analysis, we found that the relative abundances of Saccharibacteria ($p < 0.05$), Actinobacteria ($p < 0.05$) and Gemmatimonadetes ($p < 0.05$) were positively correlated with soil pH, while the relative abundances of Planctomycetes ($p < 0.05$), Nitrospirae ($p < 0.01$) and Latescibacteria ($p < 0.01$) were negatively correlated with soil pH. The relative abundance of Saccharibacteria had a positive correlation with soil AP ($p < 0.05$) and a negative correlation with SM ($p < 0.05$) and TN ($p < 0.05$). Gemmatimonadetes had a negative correlation with SOM ($p < 0.001$) and TN ($p < 0.001$), while Actinobacteria showed a negative correlation with SM ($p < 0.05$), SOM ($p < 0.001$) and TN ($p < 0.01$). In addition, Planctomycetes, Nitrospirae and Latescibacteria were positively correlated with SOM ($p < 0.01$), TN ($p < 0.001$) and SM ($p < 0.05$, $p < 0.01$, $p < 0.001$, respectively). For other measured variables, correlations were too weak or insignificant. These data suggested that the soil bacterial communities were influenced significantly by soil physicochemical properties.

4. Discussion

This study explored soil physicochemical properties and bacterial communities from different sites under different green space types in Beijing: PARK, RESID, ATTACH and STREET. It is well known that soil physicochemical properties can be affected greatly by land use types in agriculture and forests [9,29,30]. Similar findings were found in this study: green space types play critical roles in the maintenance of soil physicochemical properties especially in soil total nitrogen, pH value, soil organic matter and soil moisture content by affecting management practices. Consistent with our predictions and findings from previous studies, soil nutrients in the PARK soils were significantly higher than those in the other three green space types in this study [2]. Soil pH values of the different green space types were significantly different. Soil pH of the PARK soils was neutral to alkaline, and it was alkalinity in the STREET, ATTACH and RESID soils. This can be explained by the fact that extraneous materials, such as bricks and construction debris, included in the soils can cause an increase in the soil pH values. Human activities and street automobile emissions could also account for the higher pH values in the STREET and RESID soils. The higher soil moisture content in the PARK and ATTACH soils might have resulted from irrigation management (with more irrigation in these two green space types). Despite fleets of water trucks constantly spraying the streets, there is little effect for an urban watering system. Probable reasons may refer to evaporation and surface runoff of water in the STREET soils. The results showed that in the PARK and ATTACH soils, higher rates of plant coverage are able to increase soil infiltration and quickly reduce soil moisture in order to control surface runoff, which is also essential for organic matter accumulation in soil. In addition, soil organic matter could increase water holding capacity by enhancing the soil porosity [31]. PARK and ATTACH soils contained a higher abundance of nutrients, possibly because they are hardly influenced by anthropology and industry activities compared with the other two green space types [32]. STREET and RESID soils can be affected greatly by car emissions and human disturbance [33]. A previous study performed by Seddaiu et al. concluded that in more disturbed soils, lower amounts of total organic material were found [34]. A similar phenomena was also found in this study: the amount of soil organic matter and total nitrogen concentrations in the PARK and ATTACH soils were significantly higher than in the STREET and RESID soils. Management could be the main reason that caused the differences of soil nutrients among the different green space types [35,36]. On the one hand, it is well known that the PARK and ATTACH soils could get better fertilization and irrigation management, especially in classical imperial gardens which were constructed in Qing Dynasty [37]. Large amounts of high quality (rich in C and N) litter were produced by dry branches and fallen leaves from deciduous broad leaved trees, which then were broken down into humus, leading to increases in soil organic matter and nitrogen content [38]. Decomposition of plant material is a key ecosystem function determining the soil carbon and nitrogen cycles to a great extent. In the PARK and ATTACH soils, biological amendments including plant residues and sewage sludge can increase organic matter and soil porosity and then promote the accumulation of organic matter [2]. On the other hand, as for the RESID and STREET green spaces, a lower content of nutrients may be explained by management, e.g., leaf litter removal

and mowing of the lawns, both of which may lead to less input of labile C and N into the soil [39]. The lower content of organic matter in the RESID and STREET soils may be due to the destruction of the original surface organic horizon and a lack of accumulation of organic matter. In general, there is a strong positive relationship between soil organic matter and nitrogen, and the sequestration of soil organic matter can be affected by soil total nitrogen accumulation [40]. Although the amount of TN and SOM present in the RESID soils were low, the AP and AK concentrations were relatively higher than the other three types of green space soils. The comparatively higher concentrations of AK and AP in the RESID soils are the result of accumulation of household garbage especially the plant ash and kitchen waste. This finding can further confirm that soil properties would respond differently to types of urban green spaces.

Bacteria are the most abundant and diverse group of soil microorganisms and play multiple important key roles in soils. Although a large amount of knowledge regarding the response of soil bacterial communities to land use and soil properties has been assembled, the present understanding of how the interaction among different green space types affects the bacterial community is still poor. The present analysis indicates that green space types can affect the diversity and composition of soil bacterial communities significantly. Previous studies suggested that an open environment would help to thrive soil bacteria, but an opposite one would contain less diversity, which was consistent with the intermediate disturbance hypothesis [41], demonstrating that continuously disturbed soils benefit bacterial communities and allow more species to coexist [42]. However, contrary to former studies, results in the present study showed that there was much more bacterial diversity and abundance in the ATTACH and PARK soils among the four green space types, while the STREET and RESID soils had a significantly lower content in Shannon, Simpson, Ace and Chao1. Although the content of nutrients in PARK soils was the highest, the abundance and diversity of bacteria were significantly lower than those of ATTACH soils. Thus, the findings indicate that bacterial diversity depends not only on soil nutrients, but also on other factors such as management and anthropogenic activities. Natural or anthropogenic disturbances play a major role in influencing soil bacterial community structure. It can release nutrients from the breakdown of cells of organisms, provide available resources for primary productivity, and also lead to changes in the richness and diversity of species. In the present study, a lower alpha diversity in the STREET soils may lead to a less stable ecosystem, and in this sense lower nutrients and human trampling are not suitable for sustainable bacterial functions and processes.

In the present study, the total diversity indices showed significant variations, indicating that different green space types attribute to influence the bacterial diversity and alters the structure of the bacterial community. Therefore, these results suggest that green space types had an impact on soil bacterial communities that was greater than variation driven by soil properties observed in urban soils.

Based on the relative abundance of OTUs, significant differences were observed among all the four green space types according to ANOSIM analysis. The PCoA analysis showed an association among the soil samples from the four green space types, corroborating the differences found for the bacterial community composition. This indicated that the four green space types showed different relative abundances for dominant phylum, which was consistent with our former findings about soil physicochemical properties and bacterial community diversity, suggesting that bacterial communities are highly sensitive to different green space types.

Regarding the bacterial community composition, the predominant phyla were Proteobacteria (18.55%–35.32%), Acidobacteria (13.36%–33.25%), Chloroflexi (9.71%–17.80%) and Actinobacteria (5.54%–21.40%), which is similar to other observations [43]. Consistent with other studies, Proteobacteria was the most dominant phylum in all the samples in this study [44]. However, the relative abundance of Proteobacteria phylum identified varied between the four samples. Acidobacteria has also been identified as one of the most common phyla in soil [45]. The relative abundance of Acidobacteria were greater in the STREET soils, which probably implied that Acidobacteria prefer a less alkaline environment [46]. Actinobacteria played an important role in carbon cycling and were dominant in carbon-rich environments [47]. The reduced relative abundance

of Gemmatimonadetes might have been due to their preference for drier conditions [43]. Nitrospirae played an important role in nitrogen cycling, which was consistent with a previous study [46]. Verrucomicrobia were oligotrophic and able to grow under conditions of low carbon availability [48]. There were few variations of these dominant components of soil bacterial communities in the present study, indicating that the dominant phyla of soil bacterial communities were stable under different urban green space types, however, their relative abundance values were different.

Previous studies have demonstrated that environmental factors including SOM, available P, available K, available N and TN were identified to have important influences on bacterial communities [49]. According to Göransson et al., carbon was the most important resource for bacterial growth, nitrogen was the secondary limiting nutrient [50]. Our results demonstrated a strong relationship (both from RDA analysis and the Spearman correlation coefficients) between soil physicochemical properties and soil bacterial communities. Among the various environmental factors, SOM, SM, TN and pH were the most important factors for bacterial communities. Plant litter on the ground, roots and root exudates are major sources of soil organic matter and total nitrogen, which can impact the quality and content of soil nutrients, and can further affect the soil bacterial community diversity and structure. Shi et al. found that the content and composition of soil organic matter and total nitrogen were key factors that affected bacterial community composition and biological activities [51]. Soil pH is a critical soil factor as it determines the availability of soil nutrients and is a key driver of soil bacterial communities, therefore, pH changes will have subsequent impacts on soil biogeochemistry [52]. The phylum Actinobacteria showed a positive correlation with pH ($p < 0.05$), which was in accordance with previous results showing that Actinobacteria decreased at low pH [48]. Previous studies have shown that changes in soil properties could explain variations of soil bacterial communities under environmental changes [13,53]. In our study, the content of soil organic matter, total nitrogen and soil moisture content were closely related to green space management. Green space management could interact with these factors to significantly shape the overall composition of soil bacterial communities [1] and thus this study clarified how the different physicochemical properties related to green space management generally impacted the soil bacterial community structure across different green space types. On the regional scale, the variation of urban green space soil physicochemical properties mediated by human management can significantly alter the functional composition of soil bacterial communities in this study. This can be used to develop policy recommendations for the sustainable development of regional ecosystems in Beijing. On the national scale, the result may imply that such significant difference observed in this study are directly related to governmental urban planning policies and management practices. Thus, it is of paramount importance to apply these findings to other cities such as Shanghai and Guangzhou, which may help planners to regulate the development of eco-cities in China. On a global scale, development of urban soil ecosystems has always been strongly affected by state planning policies in Tokyo and Seoul [11]. In this case, the government has the absolute power to decide the planning and functional use of urban land development. Urban planning and management policies, as the most powerful means of government, promotes, guides, and regulates the processes of urban ecosystem development. However, the analysis of the impact of policies is not taken into consideration. Thus, this study can provide the necessary integrated information for government or urban land managers to improve their management practices and planning policies.

5. Conclusions

The physicochemical properties and bacterial diversity of urban soils reflected the condition of urban ecosystems in Beijing. Both soil physicochemical properties and bacterial diversity showed significant differences across different green space types in this study. Such a finding has potentially significant implications for deeper understanding of urban sustainable development and regional planning. The assessment results can provide a scientific basis for urban soil environmental assessment of changing processes and its influencing factors affected by management and urban green space

types. We believe that it is a useful tool for increasing the knowledge necessary for manage the urban ecosystems and, specifically, for a greater awareness of the urban ecosystem status in Beijing. Policymakers should therefore pay more attention to promoting development of soil irrigation and nutrients in street and residential green space types. Understanding the causes of variation of soil nutrients and bacterial diversity under different green spaces is a first step which allows for assessment of the sustainability of urban ecosystem management, which can help to not only increase resilience of urban soils regionally in Beijing, but also help address issues at the global scale, such as soil nutrient transformation and biodiversity conservation. In order to achieve sustainable development, urban soil management must be integrated into the regional planning and development strategies, making sustainability the fulcrum of an intelligent urban transformation towards a new model of the sustainable eco-friendly city.

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