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Soil Properties and Bacterial Communities in Relation to Vegetation Types and Park Ages in Yancheng, China

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Abstract: Urban parks are considered one of the most significant ecosystems when looking at urban green spaces, but ecological functions and the type of recreation space created can change depending on the park's age and its vegetation type. Therefore, the effects of the vegetation types present and urban park ages on soil properties and bacterial communities were tested in Yancheng, as it is a typical rapidly urbanizing city in China, and one of the most densely populated metropolises among the central cities of the Yangtze River Delta region. We found that the soil properties and bacterial community composition vary depending on vegetation type and park age. In addition, the pH value of soil planted with *Cynodon dactylon* is higher, and the available phosphorus concentrations in the old parks are at the highest levels, which are 1.20–2.66 times higher than in the middle-aged and young parks' soil. Gammaproteobacteria, Alphaproteobacteria, Acidobacteria_6, and Deltaproteobacteria are the predominant bacteria phyla in urban park soil. A higher level of bacterial operational taxonomic units (OTUs) are found in *Metasequoia glyptostroboides* soil (5479, 69.7%) and middle-aged park soil (5670, 72.2%). Saprospirae, Chloracidobacteria, and Alphaproteobacteria are negatively correlated with pH to a significant extent. Additionally, pH, available potassium, and soil organic carbon were positively correlated with saccharase activity. Available phosphorus and nitrogen are related to soil community composition. These results indicate that both park age and vegetation type contribute to the differences in soil pH, available phosphorus, soil organic carbon, available potassium, available nitrogen, alkaline phosphatase, and soil bacterial composition within urban parks in Yancheng.

Keywords: green space; urban park age; urbanization; bacterial diversity; soil environments



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1. Introduction

More than half of the world's human population lives in cities now, and this proportion continues to increase [1]. As of 2020, the urbanization rate in the Chinese mainland reached 63.89%, and the urban built-up area of the 687 main cities amounted to 61,000 km² (Ministry of Housing and Urban–Rural Development, PRC). As one of the most important land development trends in recent decades, urbanization can cause environmental concerns about the urban environment, undermine social sustainability, and threaten human health, which triggers landscape degradation [2]. Parks represent the largest green spaces in urban areas, playing a critical role in the urban ecosystem in relation to various aspects, such as biodiversity conservation [3,4], contaminants degradation [5], carbon fixation [6], nutrient cycling [7], hydrological cycles, and other soil processes [8]. All of these are also influenced by the landcover evolution associated with the park's age. Parks also provide open space for physical activities and social engagement, thus, improving the health of residents [9].

Soils are considered vital elements of global biodiversity. However, the rapid urbanization process has caused a series of environmental problems with relation to soil, such as

degradation, compaction, erosion, and contamination, which leads to deterioration in soil quality [10,11]. As a complex socio-ecological system, urban green space is home to a range of different ecological processes in the natural ecosystem [3]. Therefore, it is essential to thoroughly investigate the impact of vegetation cover (aboveground) and soil environment (belowground) on the urban green space ecosystem, and to reveal the mechanisms of their interaction with urbanization. This is beneficial in terms of preserving and managing urban green spaces [10,12].

According to some studies, plants are crucial for maintaining a healthy urban environment, as plant roots and leaf litter have a significant impact on soil properties [13,14]. Moreover, vegetation type is considered as a determinant of soil quality as it makes a noticeable difference to soil properties. Meanwhile, the relations between vegetation and soil environment are highly complex [15,16]. Time is another major factor that affects the soil ecosystem, especially microbial communities [17,18]. Park age can affect microbial community composition due to changing soil properties [19]. To a large extent, the changes in the soil ecosystem and its function result from the changes in vegetation during succession. Furthermore, park age and vegetation type are also affected by human disturbance, including park management and visits to urban areas [20]. A healthy soil environment can improve the recreation conditions for residents [21]. Therefore, it is essential to comprehensively evaluate how and to what extent park age and vegetation type affect the soil environment in urban parks [11,17]. This provides guidance on the management of park soil and vegetation.

Soil quality can be evaluated against different physicochemical properties, such as texture, pH value, organic matter, and nutrient elements. Various biological properties, such as microorganisms and enzymatic activities, have also been identified as the indicators of soil quality since they are sensitive and responsive to soil changes [22]. Almost all aerobic and facultative anaerobic microorganisms have catalase, which can decompose the hydroperoxide in the soil, thus, promoting the redox reaction in the soil [23]. Saccharase hydrolyzes sucrose to two reducing hexoses by breaking down glycoside bonds [24]. Phosphatase plays a vital role in mineralizing organic phosphorus in soils [25]. Anthropogenic activities can affect the soil environment as well, such as shaping the soil microbiome. Therefore, it is necessary to explore the changes in soil microbial communities and the influencing factors accordingly during the urbanization process. At present, there have been some studies conducted to examine the diversity and community composition of soil microbes in urban green spaces. Despite this, the urban park soils in urban ecosystems remain poorly understood [19,26]. For instance, urban park age (i.e., time since park construction) and vegetation type affect soil properties and bacterial communities.

A thorough investigation of how the quality of soil in urban parks evolves due to urbanization is crucial for establishing a scientific foundation for managing the ecological environment during the rapid urban expansion of cities. Understanding how these factors impact the physicochemical and biological properties of soil in urban parks is essential for devising effective strategies to mitigate their negative effects [17]. By managing the ecological environment in urban parks during rapid urbanization, we can ensure that these green spaces continue to provide vital ecosystem services that are essential for human health. We hypothesized that both urban park age and vegetation type may lead to significant differences in microbial community structure, which is correlated with soil physicochemical properties; the older parks are beneficial because they hold higher biodiversity. Herein, the urban parks of different ages (63a, 15a, and 3a) are selected to evaluate the effects of park age and vegetation type on soil properties and microbes in Yancheng City. The main objectives of this study are to (1) reveal the effects of vegetation type on soil properties and soil bacterial communities; (2) evaluate the association between park age, vegetation type, and soil properties; and (3) determine the critical factors affecting soil properties and the diversity and composition of bacterial communities in urban park soils.

2. Materials and Methods

2.1. Study Area and Soil Sample Collection

Yancheng (120.14° E, 33.38° N) (Figure 1a,b) is located on the east coast of the Yellow sea, Jiangsu province, China. It has a subtropical monsoon climate, with annual average temperature and annual precipitation of 13.7 °C and 1051 mm, respectively. The altitude of study area is about 8 m. It is a typical rapidly urbanizing city in China and one of the most densely populated metropolises among the central cities of the Yangtze River Delta region. By the end of 2021, Yancheng had an estimated population of 6.71 million, and 1.37 million people live in the area of the built district (Yancheng Bureau of Statistics, 2022). The created district area increased from 94.5 km² in 2012 to 173.11 km² in 2021, with urbanization rates of 55.4% and 64.75%, respectively (Ministry of Housing and Urban–Rural Development, PRC). The calculated total area of parks was about 10.39 km² (the average park size is 0.0630 km²).

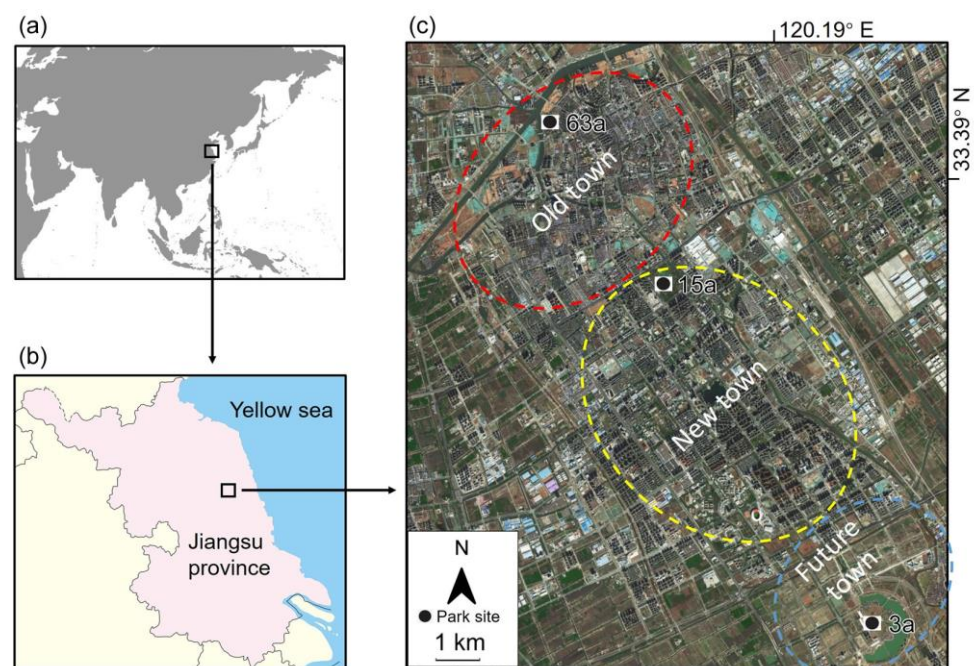


Figure 1. Location of urban park sampling sites in Yancheng, Jiangsu Province, China. (a) Eurasia; (b) Jinangsu Province; (c) Yancheng City.

In this study, a total of 45 soil samples were collected in the spring (May 2022), as the temperature in spring ranges from 10 to 25 °C, providing favorable conditions for the growth of both plants and microorganism. Nonrhizosphere soil samples were collected from different vegetation types (*Cynodon dactylon* (L.) Pers., *Photinia serratifolia* (Desfontaines) Kalkman, *Salix babylonica* L., *Metasequoia glyptostroboides* Hu and W. C. Cheng, and *Platanus acerifolia* (Aiton) Willd.) in the urban parks of different ages in Yancheng Jiangsu Province (Figure 1c). The five species of vegetation belong to three types: perennial grass (*Cynodon dactylon*), evergreen shrub (*Photinia serratifoli*), and deciduous tree (*Salix babylonica*, *Metasequoia glyptostroboides*, and *Platanus acerifolia*). These plants were selected as they were commonly found in parks in eastern China, and play an important role in park greening. The soil texture at the depth of 0–10 cm was mainly loam in urban parks in Yancheng. Plantations were set apart from each other by at least 5 m in each park, and the soil samples were taken within each plantation with a distance of at least 3 m for each. These parks were distributed along an urbanization gradient from the center to the edge of the built-up area of the city. The codes “63a”, “15a”, and “3a” represent a 63-year-old park (old park), a 15-year-old park (middle-aged park), and a 3-year-old park (young park), respectively. These three parks are all classed as representative parks.

Three soil cores (0–10 cm depth) for each vegetation type selected were collected using an aseptic plastic shovel, loaded into sterile ziplock bags, and taken to the laboratory using ice boxes. After the soil samples were thoroughly mixed, part of the soil was stored at 4 °C to measure the enzyme activities, part of the soil was stored at −80 °C for DNA extraction, and the remaining soil samples were air-dried and sieved with a 2 mm sieve to remove roots, large particles of gravel, and litter for analysis of the physicochemical characteristics in the laboratory.

2.2. Soil Physicochemical Properties

Soil pH was measured using a suspension of 5 g soil and 25 mL distilled water using a pH meter (Mettler-Toledo FE28, Schweiz, Switzerland). Soil organic carbon (SOC) content was determined using the external heating potassium dichromate volumetric method. Soil available phosphorus (AP) was extracted using NaHCO₃ and measured using the molybdenum blue method (UV-5550, Metash Instruments Co., Ltd., Shanghai, China). Soil available potassium (AK) was extracted with 1 mol/L NH₄Ac, and then measured by an atomic absorption spectrometer, and available nitrogen (AN) was measured by alkaline hydrolysis diffusion based on the methods of Avery and Bascomb [27].

2.3. Soil Enzyme Activities Assays

Catalase (EC 1.11.1.6), saccharase (EC 3.2.1.26), and alkaline phosphatase (ALP) (EC 3.1.3.2) activities were measured using the soil enzyme kit provided by Solarbio Science & Technology Co. (Beijing, China) and determined according to the manufacturer's specifications [28]. Catalase was analyzed using H₂O₂ as the substrate and determined with a spectrophotometer (UV-2450, SHIMADZU, Kyoto, Japan) at 240 nm. Saccharase was determined using sucrose as the substrate and quantified at 508 nm. ALP was determined based on *p*-nitrophenol release, and quantified at 400 nm.

2.4. DNA Extraction and 16S rRNA Gene Sequencing

The total genomic DNA of each sample was extracted from 0.5 g of wet soil with the PowerSoil® DNA Isolation Kit for soil (Mo Bio Laboratories, Inc., Carlsbad, CA, USA), following the manufacturer's specifications. Then, the amount of extracted DNA was determined by NanoDrop™ 2000 spectrophotometer (Thermo Scientific, Waltham, MA, USA) prior to PCR. The V4-V5 region of the bacterial 16S rRNA genes was amplified using the universal primers F515 (5'-GTGCCAGCMGCCGCGGTAA-3') together with R907 (5'-CCGTCAATTCMTTTRAGTTT-3') with the barcode. The thermal cycling parameters were as follows: 1 min at 98 °C, 30 cycles of 10 s at 98 °C, 30 s at 50 °C, and 60 s at 72 °C, followed by a final extension at 72 °C for 5 min. The PCR products were verified with 2% agarose gel, and purified using the DNA purification Kit (TIANGEN, Beijing, China). The paired-end sequencing was performed using the Illumina MiSeq platform (Shanghai Majorbio BioPharm Technology Company, Shanghai, China).

2.5. Statistical Analysis

Two-way ANOVA was conducted to determine the soil properties and the bacterial diversity, which varied depending on vegetation type and park age. Non-metric multidimensional scaling (NMDS) was performed to demonstrate the differences in soil environment based on the environmental data and Bray–Curtis dissimilarity. Based on the data for the top 10 genera, differences in overall bacterial community composition were explored using SIMPER test to detect the dissimilarity and the taxon contribution for the dissimilarity. Pearson's matrix analysis was carried out to reveal potential correlation between soil properties and bacterial composition. Redundancy analysis (RDA) was conducted to analyze the relationship between soil bacterial communities (top ten taxa) and soil properties (averaged for each site by taking three samples), and to identify the potential environmental factors affecting soil bacterial communities. All these statistical

analyses were conducted using software R 4.2.1 (R Core Team, 2022), PAST 4.03 [29], and SPSS 18.0 (SPSS Inc., Chicago, IL, USA).

3. Results

3.1. Soil Properties in Different Parks

The soil physicochemical properties of urban parks with different vegetation types are shown in Table 1. Among various soil properties, the pH value of soil planted with *Cynodon dactylon* was higher compared to other soils. AP concentrations in the old park were significantly higher than in the middle-aged and young parks' soil planted with the same vegetation type. Both vegetation type and park age affected soil SOC, AN, and AK. However, there was no regular trend detected (Table 1). Vegetation type had a significant effect on the catalase and ALP activities (Table 1). The soil planted with *Cynodon dactylon* and *Platanus acerifolia* had a higher level of ALP activity, while this level was the lowest in the soil planted with *Metasequoia glyptostroboides*. Catalase and sucrase activities were at the highest levels in the soil planted with *Salix babylonica* ($p < 0.05$). Park ages affected soil sucrase activity, which was at a higher level in the young park's soil than in the older park's soil with the same vegetation type (Table 1). Additionally, the stress value of the NMDS was $0.046 < 0.050$, suggesting an excellent representation in reduced dimensions (Figure 2). The plots of habitats planted with *Salix babylonica* were concentrated, as were those planted with *Photinia serratifolia*. To some degree, the plots gathered together by park age in the graph of NMDS.

Table 1. Soil physicochemical properties and enzyme activities in urban parks with different vegetations.

Properties	Parks	<i>Cynodon dactylon</i>	<i>Photinia serratifolia</i>	<i>Salix babylonica</i>	<i>Metasequoia glyptostroboides</i>	<i>Platanus acerifolia</i>
pH	3a	6.99 ± 0.07^a	6.68 ± 0.03^{def}	6.92 ± 0.09^{ab}	6.90 ± 0.02^{abc}	6.63 ± 0.05^f
	15a	6.99 ± 0.10^a	6.70 ± 0.05^{cdef}	6.67 ± 0.10^{ef}	6.68 ± 0.10^{ef}	6.86 ± 0.01^{abcde}
	63a	6.96 ± 0.02^a	6.94 ± 0.03^{ab}	6.88 ± 0.05^{abcd}	6.71 ± 0.12^{cdef}	6.74 ± 0.11^{bcdef}
SOC (g/kg)	3a	6.24 ± 0.82^{de}	8.00 ± 1.25^a	7.91 ± 0.52^a	7.64 ± 0.88^{abc}	7.32 ± 0.44^{abcd}
	15a	6.54 ± 0.79^{bcde}	6.78 ± 0.36^{abcde}	6.35 ± 0.64^{cde}	6.91 ± 0.23^{abcde}	6.93 ± 0.21^{abcde}
	63a	7.48 ± 0.69^{abcd}	5.83 ± 0.72^e	7.22 ± 0.57^{abcd}	7.58 ± 0.62^{abc}	7.82 ± 0.57^{ab}
AN (mg/kg)	3a	14.36 ± 2.29^{def}	14.31 ± 0.55^{def}	16.87 ± 0.79^{bcde}	18.49 ± 3.15^{abc}	15.56 ± 2.19^{cdef}
	15a	16.72 ± 3.27^{bcde}	12.02 ± 0.30^f	18.25 ± 0.72^{abcd}	13.83 ± 0.91^{ef}	19.66 ± 1.20^{ab}
	63a	21.24 ± 2.55^a	18.81 ± 2.77^{abc}	20.72 ± 3.00^{ab}	15.55 ± 2.52^{cdef}	17.19 ± 1.17^{bcde}
AP (mg/kg)	3a	24.09 ± 2.23^c	23.14 ± 2.55^{cd}	23.49 ± 0.51^{cd}	23.92 ± 2.92^c	18.41 ± 1.61^e
	15a	14.28 ± 1.13^f	23.39 ± 1.40^{cd}	20.61 ± 1.15^{de}	18.66 ± 1.21^e	24.79 ± 0.59^c
	63a	38.05 ± 0.99^a	27.70 ± 1.96^b	28.09 ± 2.93^b	25.54 ± 0.86^{bc}	23.13 ± 0.10^{cd}
AK (mg/kg)	3a	128.29 ± 0.88^{cde}	150.03 ± 9.68^{ab}	156.58 ± 12.52^a	148.38 ± 10.80^{abc}	68.05 ± 8.10^i
	15a	86.30 ± 11.19^{hi}	89.20 ± 7.08^{gh}	119.62 ± 10.49^{def}	123.49 ± 1983^{de}	100.90 ± 6.39^{fgh}
	63a	153.53 ± 19.63^{ab}	93.73 ± 5.79^{gh}	132.49 ± 8.04^{bcd}	139.22 ± 6.33^{abcd}	109.09 ± 4.03^{efg}
Catalase (U/g)	3a	7.81 ± 1.83^{cdef}	6.97 ± 0.48^{efg}	9.91 ± 1.22^a	5.59 ± 0.40^{gh}	6.49 ± 0.59^{fgh}
	15a	7.43 ± 0.63^{def}	8.81 ± 0.85^{abc}	9.65 ± 0.53^a	6.02 ± 0.23^{gh}	6.82 ± 0.60^{fg}
	63a	8.59 ± 0.28^{abcd}	8.23 ± 0.33^{bcde}	9.41 ± 0.37^{ab}	5.32 ± 0.41^h	6.56 ± 0.61^{fgh}
Alkaline phosphatase (U/g)	3a	34.69 ± 0.14^a	33.17 ± 0.32^{de}	33.29 ± 0.14^{de}	32.34 ± 0.38^g	34.65 ± 0.21^{ab}
	15a	34.43 ± 0.26^{ab}	33.47 ± 0.17^{de}	33.25 ± 0.10^{de}	32.51 ± 0.14^{fg}	34.11 ± 0.64^{bc}
	63a	34.19 ± 0.15^{ab}	33.03 ± 0.35^{ef}	30.65 ± 0.17^h	29.55 ± 0.66^i	32.78 ± 0.76^{bc}
Saccharase (U/g)	3a	25.63 ± 4.34^d	30.86 ± 0.98^{bcd}	38.36 ± 1.06^a	34.23 ± 0.27^{ab}	30.84 ± 4.50^{bcd}
	15a	24.78 ± 1.29^d	29.38 ± 4.43^{bcd}	34.13 ± 2.79^{ab}	30.42 ± 2.32^{bcd}	26.45 ± 1.16^{cd}
	63a	29.55 ± 0.68^{bcd}	24.59 ± 1.83^d	34.11 ± 2.60^{ab}	33.10 ± 0.75^{abc}	28.26 ± 1.61^{bcd}

Notes: values are means $\pm$ S.D. (n = 3); in each row, the different small letters within each soil property stand for statistical significance ($p < 0.05$) among different vegetation types and park ages; SOC, soil organic carbon; AN, available nitrogen; AP, available phosphorus; and AK, available potassium.

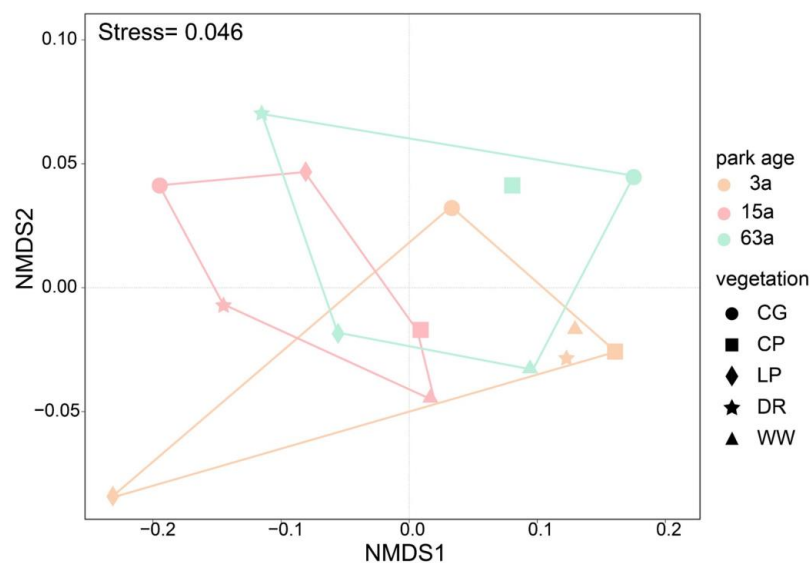


Figure 2. Non-metric multidimensional scaling plots based on the environmental data by Bray–Curtis dissimilarity. Notes: 63a, old park; 15a, middle-aged park; 3a, young park; LP, *Platanus acerifolia*; DR, *Metasequoia glyptostroboides*; CP, *Photinia serratifolia*; WW, *Salix babylonica*; and CG, *Cynodon dactylon*.

3.2. Bacterial Community Composition and Diversity

Operational taxonomic units (OTUs) were clustered based on 97% sequence identity in the qualified sequence. The bacterial differences were found to be more significant in *Metasequoia glyptostroboides* soil and middle-aged park soil (Figure 3). A total of 7856 OTUs were found in the bacterial communities. Among them, 2811 (35.8%) bacterial OTUs were found in all three park soil samples (Figure 3a). Compared to the abundance of OTUs in the urban parks of different ages, the middle-aged park (15a) contained the highest number of OTUs (5670, 72.2%), followed by the young park (3a) with 5286 (67.3%) OTUs, and the old park (63a), which contained the lowest number of OTUs (4688, 59.7%). It is suggested that soil bacterial communities increase and then decrease with the urban park age (Figure 3a). There was a relatively large core microbiome regardless of vegetation type. The park soil planted with *Metasequoia glyptostroboides* had the highest number of OTUs (5479, 69.7%), followed by *Photinia serratifolia* with 4528 (57.6%) OTUs, *Cynodon dactylon* with 4330 (55.1%) OTUs, *Platanus acerifolia* with 4296 (54.7%) OTUs, and the park soil planted with *Salix babylonica*, which had the lowest number of OTUs (3413, 43.4%) (Figure 3b).

The diversity of bacterial communities in the urban park soils under investigation was high, and the dominant bacteria were found to be Gammaproteobacteria (11.9–28.8%) and Alphaproteobacteria (16.5–18.7%), followed by Acidobacteria_6 (6.5–12.4%) and Deltaproteobacteria (5.4–9.5%) (Figure 4a). There were also a lot of unknown bacteria detected in the urban parks' soil. Gammaproteobacteria, Acidobacteria_6, and Deltaproteobacteria showed the most significant variation in relative abundance, and Gammaproteobacteria decreased sharply from 31.48% in the old park's soils to 9.28% in the middle-aged park's soils. In contrast, Acidobacteria_6 and Deltaproteobacteria were increased from 6.97% and 5.61% in the old park's soils to 12.02% and 13.12% in the middle-aged park's soils, respectively (Table S1). Additionally, the relative abundance of Alphaproteobacteria increased with park age, while the relative abundances of Gammaproteobacteria and Acidimicrobiia decreased first and then increased (Figure 4b). The relative abundance of Gammaproteobacteria given different vegetation types is in the following order: *Photinia serratifolia* > *Cynodon dactylon* > *Metasequoia glyptostroboides* > *Salix babylonica* > *Platanus acerifolia* (Figure 4c). The top 10 genera accounted for 72.66%, 77.05%, and 73.34% of the microbial communities in the sample soil from the old park (63a), the middle-aged park (15a), and the young park (3a), respectively (Table S1). Meanwhile, the top 10 genera accounted for 74.37%, 80.42%, 69.99%, 76.58%, and 70.97% of the microbial communities in the soils planted with *Cynodon dacty-*

lon, *Photinia serratifolia*, *Salix babylonica*, *Metasequoia glyptostroboides*, and *Platanus acerifolia*, respectively (Table S2).

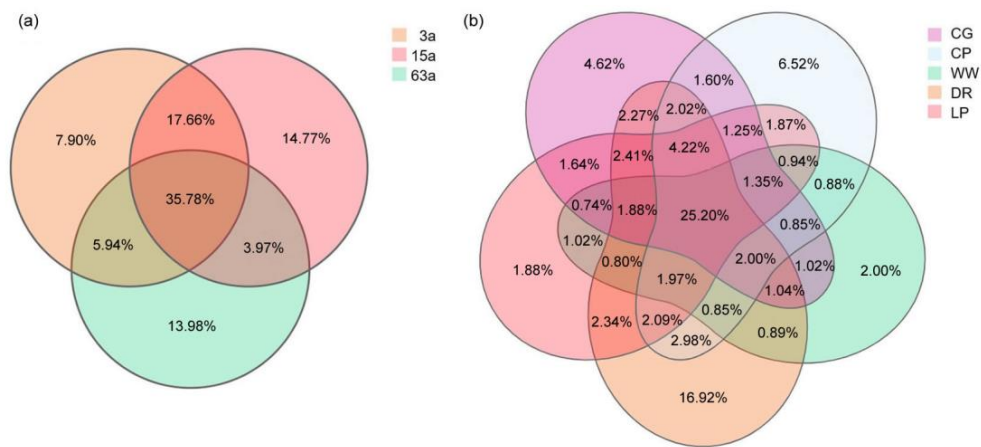


Figure 3. Percentage of operational taxonomic units (OTUs) with different categories in urban parks' soil samples: (a) urban parks and (b) vegetation types. Notes: 63a, old park; 15a, middle-aged park; 3a, young park; LP, *Platanus acerifolia*; DR, *Metasequoia glyptostroboides*; CP, *Photinia serratifolia*; WW, *Salix babylonica*; and CG, *Cynodon dactylon*.

Most of the dissimilarity in community structure between the parks with different ages was contributed by Gammaproteobacteria, Deltaproteobacteria, and Alphaproteobacteria with 43.70%, 12.07%, and 11.66% dissimilarity, respectively (Table 2). Similarly, the dissimilarity between communities in different vegetation types was caused by Gammaproteobacteria, Alphaproteobacteria, and Deltaproteobacteria with 43.08%, 12.51%, and 11.61% dissimilarity, respectively (Table 3). The dissimilarity was the lowest in the comparison of bacterial communities in parks “15a vs. 63a” (with Gammaproteobacteria, Deltaproteobacteria, and Alphaproteobacteria contributing more than 10% dissimilarity for each) compared with other comparisons including “3a vs. 15a” (with Gammaproteobacteria, Deltaproteobacteria, Alphaproteobacteria, and Acidobacteria-6 contributing more than 10% dissimilarity for each) and “3a vs. 63a” (with Gammaproteobacteria and Alphaproteobacteria contributing more than 10% dissimilarity for each). The dissimilarity was the lowest in the comparison of bacterial communities in the vegetation “*Salix babylonica* vs. *Platanus acerifolia*” (with Gammaproteobacteria and Deltaproteobacteria contributing more than 10% dissimilarity for each), and the highest in the vegetation “*Cynodon dactylon* vs. *Photinia serratifolia*” (with Gammaproteobacteria and Alphaproteobacteria contributing more than 10% dissimilarity for each) (Table S3).

Table 2. Dissimilarity percentages (SIMPER) with the taxon contributions based on park age (overall average dissimilarity = 34.43).

Taxon	Av. Dissim	Contrib. %	Cumulative %	3a Av. Abund	15a Av. Abund	63a Av. Abund
Gammaproteobacteria	15.050	43.700	43.70	0.315	0.093	0.245
Deltaproteobacteria	4.156	12.070	55.77	0.056	0.131	0.054
Alphaproteobacteria	4.016	11.660	67.43	0.183	0.178	0.153
Acidobacteria-6	3.414	9.914	77.34	0.070	0.120	0.101
Betaproteobacteria	2.468	7.168	84.51	0.069	0.092	0.069
Actinobacteria	1.388	4.032	88.54	0.018	0.026	0.036
Nitrospira	1.206	3.501	92.05	0.010	0.027	0.020
Chloracidobacteria	1.081	3.140	95.19	0.016	0.028	0.025
Saprospirae	0.933	2.708	97.89	0.018	0.022	0.016
Acidimicrobiia	0.725	2.107	100.00	0.017	0.019	0.024

Notes: 63a, old park; 15a, middle-aged park; and 3a, young park.

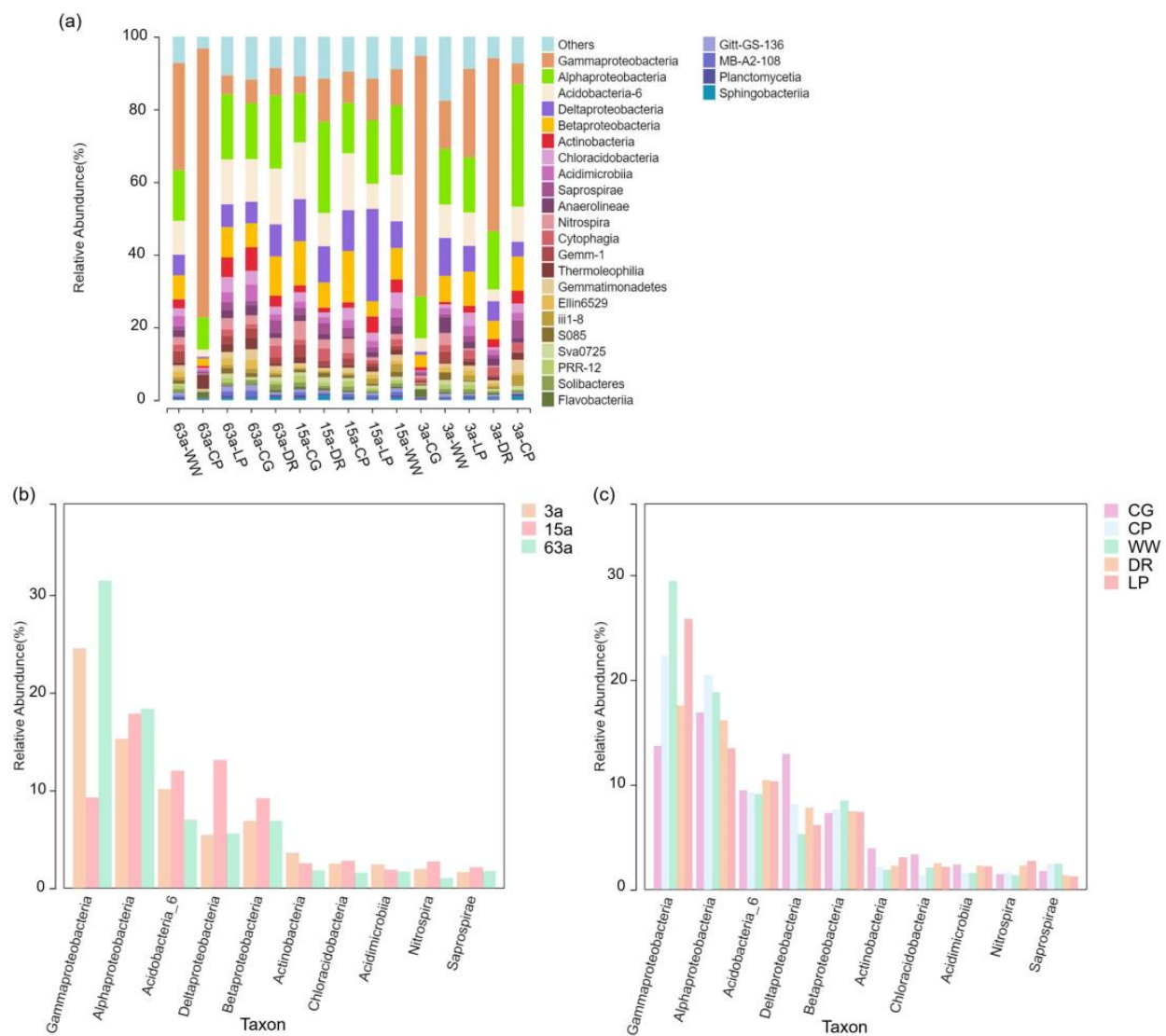


Figure 4. Relative abundances of bacterial community at the phylum level in urban park soils with different vegetation types (a), dominant bacterial community abundance based on urban parks (b), and vegetation types (c). Notes: 63a, old park; 15a, middle-aged park; 3a, young park; LP, *Platanus acerifolia*; DR, *Metasequoia glyptostroboides*; CP, *Photinia serratifolia*; WW, *Salix babylonica*; and CG, *Cynodon dactylon*.

Table 3. Dissimilarity percentages (SIMPER) with the taxon contributions based on vegetation type (overall average dissimilarity = 33.27).

Taxon	Av. Dissim	Contrib. %	Cumulative %	CG Av. Abund	CP Av. Abund	WW Av. Abund	DR Av. Abund	LP Av. Abund
Gammaproteobacteria	14.330	43.080	43.08	0.258	0.295	0.176	0.223	0.137
Alphaproteobacteria	4.163	12.510	55.60	0.135	0.188	0.162	0.205	0.169
Deltaproteobacteria	3.862	11.610	67.20	0.062	0.053	0.078	0.081	0.129
Acidobacteria-6	3.219	9.675	76.88	0.103	0.091	0.104	0.092	0.095
Betaproteobacteria	2.458	7.389	84.27	0.074	0.085	0.075	0.076	0.073
Actinobacteria	1.355	4.073	88.34	0.031	0.019	0.023	0.022	0.039
Nitrospira	1.148	3.451	91.79	0.027	0.014	0.023	0.016	0.014
Chloracidobacteria	1.078	3.241	95.03	0.021	0.021	0.025	0.014	0.033
Saprospirae	0.929	2.791	97.82	0.012	0.025	0.014	0.024	0.017
Acidimicrobiia	0.724	2.176	100.00	0.022	0.016	0.023	0.015	0.024

Notes: CG, *Cynodon dactylon*; CP, *Photinia serratifolia*; WW, *Salix babylonica*; LP, *Platanus acerifolia*; and DR, *Metasequoia glyptostroboides*.

3.3. Redundancy Analysis

The bacterial communities were clustered in terms of pH and SOC based on RDA, and the eigenvectors of RDA 1 and RDA 2 contributed to 50.63% and 23.03% of the variance, respectively. Thus, the cumulative contribution to variance based on RDA 1 and RDA 2 was 73.66% (Figure 5). Soil bacterial communities were classed with the SOC gradient in RDA 1 at a smaller angle with RDA 1. AN ($r^2 = 0.518$, $p = 0.012$) and AP ($r^2 = 0.455$, $p = 0.025$) were identified as the significant environmental factors causing the variation between different bacterial communities because of the longest vectors among the soil properties investigated.

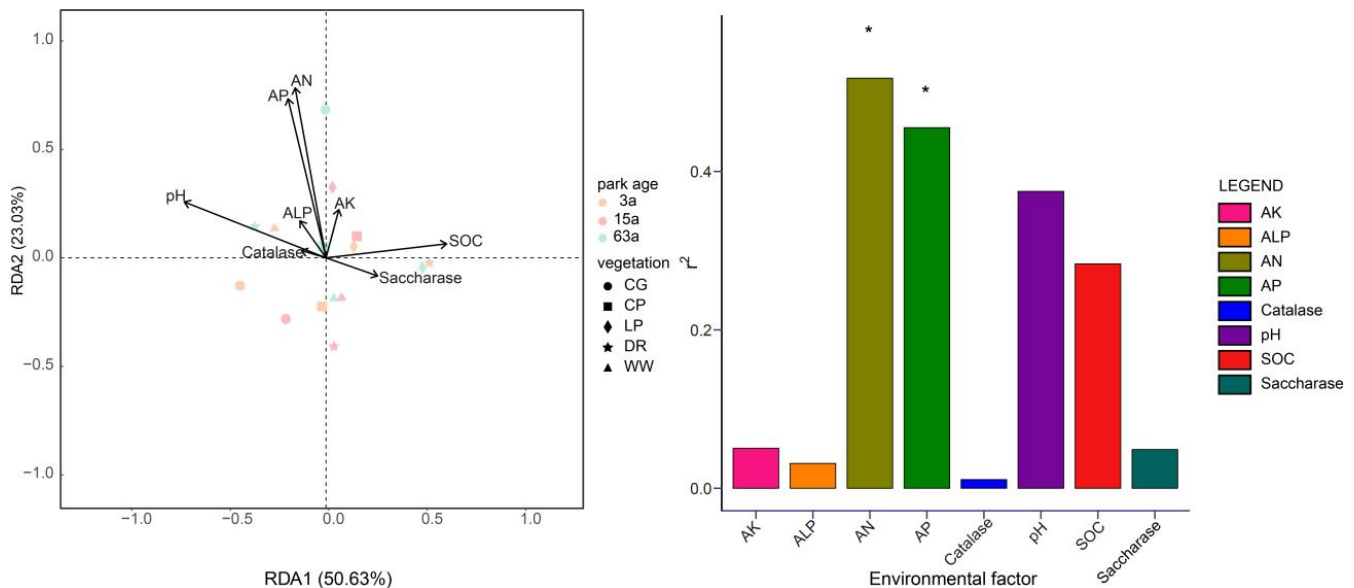


Figure 5. RDA biplot showing the relationship between soil bacterial communities and soil properties (a) and the environmental factors explaining the variations among soil bacterial communities (b). Note: 63a, old park; 15a, middle-aged park; 3a, young park; LP, *Platanus acerifolia*; DR, *Metasequoia glyptostroboides*; CP, *Photinia serratifolia*; WW, *Salix babylonica*; CG, *Cynodon dactylon*; ALP, alkaline phosphatase; SOC, soil organic carbon; AN, available nitrogen; AP, available phosphorus; and AK, available potassium. * Means the correlation with $p < 0.050$.

3.4. Correlations among Soil Properties and Bacterial Community

According to the soil properties determined, the soil pH had a more significant impact on the relative abundance of soil bacterial communities, showing a significantly negative correlation with Nitrospira, Betaproteobacteria, and Acidobacteria_6 ($p < 0.01$) (Figure 6). In addition to pH, AN was also negatively correlated with Nitrospira. AP exhibited a significantly positive correlation with Deltaproteobacteria. Compared to other soil factors measured, SOC and AK showed a significantly positive correlation with the activity of saccharase. Alkaline phosphatase activity showed strong negative correlations with Alphaproteobacteria (Figure 6). Moreover, we found that the investigated soil properties had no significant correlations with Saprospirae, Acidimicrobiia, Chloracidobacteria, Actinobacteria, and Gammaproteobacteria.

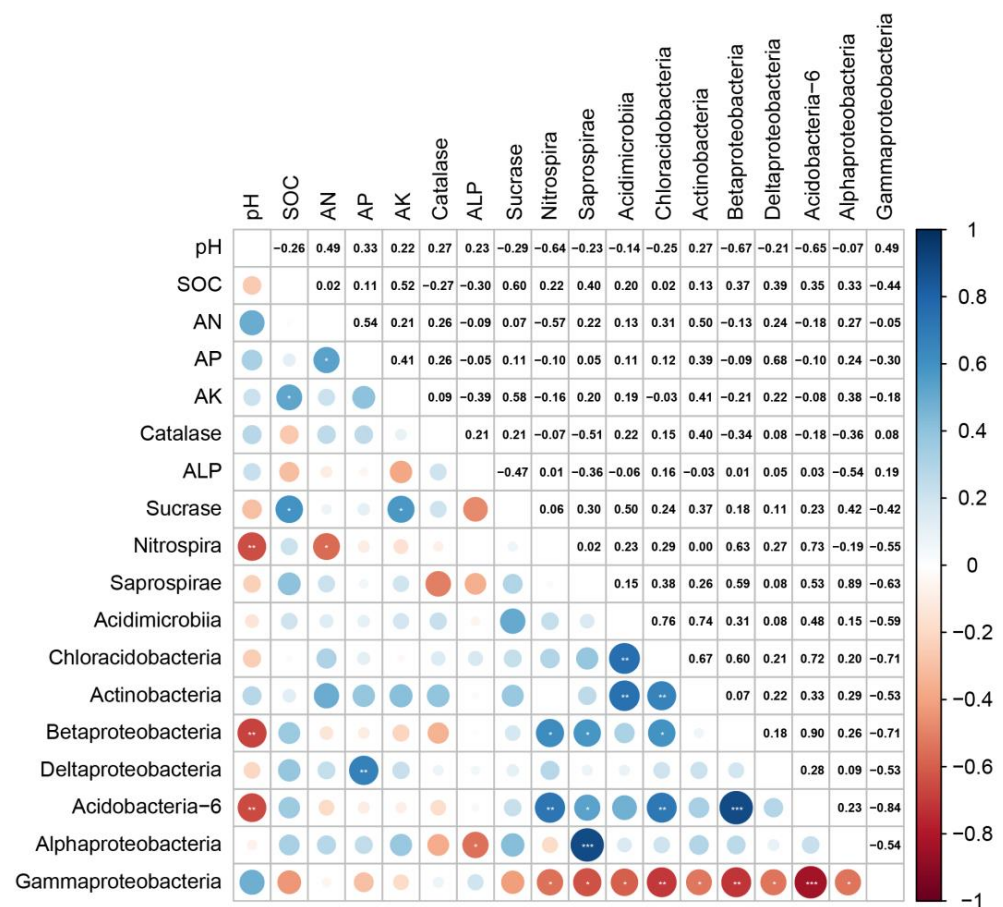


Figure 6. Correlation of soil properties and relative abundance of bacterial communities. Note: the color gradient in the box indicates Pearson's correlation coefficient, the magnitude of which is proportional to the r-value, and the number indicates the Pearson's r-value. * $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$; ALP, alkaline phosphatase; SOC, soil organic carbon; AN, available nitrogen; AP, available phosphorus; and AK, available potassium.

4. Discussion

Soil properties change in predictable ways with the development of urban green spaces like the nature system [30,31], and microbial communities vary with changes in soil properties constantly [19,32]. Most ecosystem services are primarily determined by the interactions between soil and plant systems, which are usually affected by vegetation type and age [17,33,34]. In this study, we investigated the potential influence of vegetation type and urban park age on soil physicochemical properties, enzyme activities, and bacterial community structures in nonrhizosphere soils. The microbial diversity in the nonrhizosphere was found to be more sensitive to the changes that came about with the successional stage than in the rhizosphere soil [35]. Our results revealed that the pH of soil planted with *Cynodon dactylon* was higher than that planted with *Photinia serratifolia*, *Salix babylonica*, *Metasequoia glyptostroboides*, and *Platanus acerifolia*. However, soil pH shows no regular trend as park age changes (Table 1). SOC is higher in the soil planted with *Platanus acerifolia* in the young and middle-aged parks compared to other vegetation types (Table 1). Vegetation types are able to significantly change soil physicochemical and biological properties [17,36]. Vegetation type (trees, herbs, and grasses) can be categorized as either evergreen or deciduous trees. As *Platanus acerifolia* is deciduous, the presence of litter is conducive to organic matter accumulation in the topsoil, which was consistent with other studies that reveal the increase in organic matter concentration with park age [20]. Urban green spaces are considered a C sink [37] and soil C accumulates in the presence of

vegetation [17]. Meanwhile, vegetation roots can change soil physicochemical properties through root exudation, as it accounted for about 11% of the net fixed C, and this percentage varied with plant species and age [38]. Root exudates are a mix of carbohydrates, amino acids, and organic acids, which can change soil pH, and, thus, cause a series of differences in soil properties [39]. The root exudation can be influenced by the vegetation type and the plant age [40]. However, according to NMDS in Figure 2, it is difficult to determine whether the effect of vegetation is caused by the differences in plant age or type [31].

Soil properties are regarded as the key contributor to soil microbial activity and the composition of communities in urban parks [41]. AK and SOC are positively correlated with saccharase activity (Figure 6). Since saccharase could hydrolyze sucrose to two reducing hexoses, it is crucial to meet the demand of soil microorganisms and plants for nutrients [42]. The relative abundance of Nitrospira, Acidobacteria_6, and Betaproteobacteria is negatively affected by soil pH to a significant extent regardless of the soil properties measured (Figure 6). Among these soil properties, pH may have an immediate impact, and is reported to be associated with bacterial community composition [12,22,26]. pH affects soil microbial composition as it can influence numerous essential soil properties, such as, salinity, metal solubility, nutrient availability, and organic carbon properties, that may change soil microbial communities, and it can also influence the physiological activity of soil bacteria [43]. In addition to pH, AP, AN, and ALP are also significantly related to soil community composition (Figure 6). Highly relevant to P, microbial community composition is a primary factor affecting the relative abundance of Proteobacteria [32]. No single parameter alone affects all soil properties, which may imply a correlation between bacterial community composition and the difference in environmental tolerance. The relative abundance of Gammaproteobacteria is higher in the soil planted with *Cynodon dactylon*, *Photinia serratifolia*, and *Metasequoia glyptostroboides* than in the soil planted with *Platanus acerifolia* (Figure 4c). In some studies, it has been demonstrated that various fast-growing plants, such as *Cynodon dactylon*, could produce a labile, easily decomposed litter that contributes to altering the biogeochemical characteristics of soil through variations in soil food webs [44].

The number of unique OTUs in the old and middle-aged parks was relatively larger than in the young park (Figure 3). The relative abundance of dominant phyla varies depending on the age of the urban park soil (Figure 4b). The changing time of soil properties and microbial communities caused by vegetation in the old parks is longer than in the younger parks [19]. In this study, the diversity of bacterial communities first increases and then decreases with park age (Figure 3), which is consistent with the previous study, indicating that bacterial diversity and evenness are more significant in the middle-aged park than in the young and old parks [19]. Soil bacterial community is highly correlated with the construction time of parks [45]. Middle-aged and old parks differ from young urban parks in terms of edaphic conditions [31]. However, some research illustrated that microbial diversity and richness increased with an urban park's age, as older parks generally have more beneficial soil properties (such as higher soil C, OM content, and nutrients' retention) than young parks [19]. The interaction between plant and soil is highly complex, which is likely to affect microbial communities as soil properties such as pH, total C, and total N change with plant age [46]. Plant roots affect microorganisms by releasing root secretions and influencing the flow of nutrients in the rhizosphere soil [47]. As a result, microbial communities in soil planted with different vegetation types varied [48]. In addition, urban areas are considered socio-ecological systems. The relationship between park age and bacterial community structure illustrates the presence of anthropogenic interference, which is also considered to be a critical factor affecting soil bacterial community composition [49]. This is because the effects of anthropogenic activity on urban parks of different ages vary, which may explain the variation in bacterial community composition depending on the age of urban parks.

The main phyla in different urban park soils include Gammaproteobacteria, Alphaproteobacteria, Acidobacteria, Deltaproteobacteria, and Betaproteobacteria (Figure 4). As

revealed by the studies on a wide range of soil types, Proteobacteria and Acidobacteria are the dominant phyla of the urban soil microbiome [26,50]. Most of the dissimilarity in community structure between the parks with different ages and vegetation types was caused by Gammaproteobacteria, Deltaproteobacteria, and Alphaproteobacteria, and the dissimilarity was low both in terms of park age and vegetation type (Tables 2 and 3). Soil microbial communities and diversity in New York City's Central Park are similar to those in global soil sample sets [51]. This may be due to the more stable nature of the soil microbiome than that of other habitats [52]. Moreover, land-use history is a more critical element than soil properties in determining a soil's biological community composition [53]. In the present study, the bacterial communities in those soils planted with the five different plants differ, and the prominent phyla in the soil planted with *Photinia serratifolia*, *Cynodon dactylon*, and *Metasequoia glyptostroboides* were Gammaproteobacteria and Alphaproteobacteria, while the dominant phyla in the soil planted with *Platanus acerifolia* are Gammaproteobacteria, Alphaproteobacteria, and Deltaproteobacteria. Meanwhile, the relative abundance of the bacterial communities varies (Figure 4c). Vegetation type appears to affect the communities of soil microbial in urban parks significantly and in different ways, such as the effects of soil pH and rhizodeposition (root exudates), which directly interact with root symbiotic microorganisms [47,54,55]. Differently, it is reported that bacterial community composition is not significantly affected by vegetation type [51]. The urban park soils are highly disturbed during park construction and this disturbance is still ongoing; whether plants can change soil properties and, thus, reshape soil function is unclear [17,56]. In our opinion, the impact of both vegetation type and park age on soil bacterial community composition in the young and middle-aged parks is more significant than in the old parks.

5. Conclusions

The present study contributes to improving the understanding of changes in soil properties and bacterial community composition during the urbanization process in urban parks with different vegetation types, which is beneficial in revealing the effect of urbanization on ecosystem function. Our results show no significant difference in the bacterial communities among the parks of different ages or vegetation types, despite the variation in the relative abundance of the bacterial taxa. There is no clear trend shown by soil SOC, AP, and AK concentrations, either according to vegetation type or park age. Among these soil properties, pH, AP, and AN are important soil properties in shaping bacterial community composition. Meanwhile, the complexity of soil bacterial community rises with park age and then declines. According to the values of soil properties and the bacterial communities, both park age and vegetation type contribute to the variation in soil properties and the diversity of bacterial community in urban park soils. Additionally, *Salix babylonica* planted in the middle-aged park had positive effects on soil properties. In the future, further research can be conducted to reveal the impact of ecological management and environmental risks on the soil and vegetation in urban parks. The bacteria in rhizosphere soil are also very interesting scientific issues that deserve further investigation.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/agronomy14061133/s1>. Table S1: The relative abundances of top 10 bacterial community at the phylum level in urban park soils with different park age and; Table S2: The relative abundances of top 10 bacterial community at the phylum level in urban park soils with different vegetation types. Table S3 Dissimilarity percentages (SIMPER) with the taxon contributions between different park age and plantation.

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