Landscape and Urban Planning 177 (2018) 83–91

Contents lists available at ScienceDirect

Landscape and Urban Planning

journal homepage: www.elsevier.com/locate/landurbplan

Research Paper

# Composition and functional genes analysis of bacterial communities from urban parks of Shanghai, China and their role in ecosystem functionality

Xin Wang[a,b], Jiang Wu[c], Deepika Kumari[c,*]

[a] Shanghai Key Lab of Urban Regeneration & Spatial Optimization Technology, Tongji University, Shanghai 200092, China
[b] MOE Joint Laboratory for International Cooperation on Eco-Urban Design, Tongji University, Shanghai 200092, China
[c] College of Architecture and Urban Planning (CAUP), Tongji University, Shanghai 200092, China

ARTICLE INFO

*Keywords:*
Bacterial communities
Biogeochemical cycling
Social-ecological system
Urban microbiome
Urban parks

ABSTRACT

Urban park soil plays a vital part in urban ecosystems, which harbor a considerable microbial diversity. Those microbes regulate soil fertility, plant health, and biogeochemical cycling. The existing studies have hardly focused on microbial diversity from urban parks, especially from China. As Shanghai, the largest city of China has experienced extensive urbanization, the present study focused on bacterial community compositions and their functional genes collected from 24 urban parks soils to ensure soil health and microbial sustainability of major parks of this city. To elucidate the bacterial communities from all 24 urban parks, soils were analyzed by sequencing V3-V4 region of the 16S rRNA gene using Illumina MiSeq. At the taxonomic level, 12,67,055 16S rRNA gene sequences were secured from all the soil samples. Out of 43 classified phyla, all the urban park soils had higher relative abundances of *Proteobacteria* and *Acidobacteria* accounting for 33.01–45.49 and 18.7–30.12%, respectively. A total of 6909 bacterial functional genes showing high functional gene diversity for essential biogeochemical processes (including carbon, nitrogen, phosphorus and sulfur cycles) exist in Shanghai urban parks that could be helpful in maintaining fertility of park soils and thus greenery of city. This is the first extensive report on soil microbial diversity from urban parks of China. Our results provide a foundation or a guideline to urban planners and to compare future research related to urban parks soil biodiversity and ecosystem function.

## 1. Introduction

The most diverse natural environment on the Earth is soil that harbors prokaryotic and eukaryotic microorganisms, which involve in nutrient cycling. Soil microbes play role in growth of plants and ecosystem functioning (Singh, Millard, Whiteley, & Murrell, 2004). Microbial diversity of soil is important for agricultural sustainability from economic, social, and ecological points of view (Brussaard, de Ruiter, & Brown, 2007). In particular, bacteria are highly involved in various biogeochemical processes of soils (Buee, De Boer, Martin, Van Overbeek, & Jurkevitch, 2009). Nevertheless, the ecological attributes of many soil taxa remain poorly understood, and the complete biodiversity found in soil remains unknown (Decaëns, 2010).

Urban parks are considered as of primary importance in urban planning (Xiao, Wang, Li, & Tang, 2017). These are attractive places that provide visitors with many services for health and well-being (Pröbstl-Haider, 2015). The ability of nature or green spaces or parks in influencing human beings positively is demonstrated in terms of reducing stress (Ulrich, Zimring, Quan, & Joseph, 2006) and even in speedy recovery from surgery (Ulrich, 1984). Urban parks are great reservoirs for soil and because those parks are meant for human recreational activities, human activities put forward a great influence on bacterial communities of soil (Jangid et al., 2008). Urbanization could have adverse impacts on soil ecosystems. China where population is shifting drastically from rural to urban area and thus facing rapid urbanization, there is little known about soil microbial diversity from different soil ecosystems. Despite of creation of many urban parks throughout China that play a vital role in urban ecosystems, there are few reports on microbial diversity of urban soils (Xu et al., 2014). The microbiome of the indoor or built environment has already been studied in detail over the past decade (Hoisington, Brenner, Kinney, Postolache, & Lowry, 2015; Leung & Lee, 2016). Maintenance of microbial diversity and composition could influence ecosystem of soil and nutrient cycling in urban parks. As soil microbes are one of the most important components of urban parks (Roesch et al., 2007), and play a crucial role in all biogeochemical cycles and transformations of nutrients in the soil (Nacke et al., 2011), the study of bacterial diversity in urban park is very significant.

* Corresponding author.
*E-mail address:* deepikakumari@tongji.edu.cn (D. Kumari).

https://doi.org/10.1016/j.landurbplan.2018.05.003
Received 8 September 2017; Received in revised form 27 March 2018; Accepted 3 May 2018

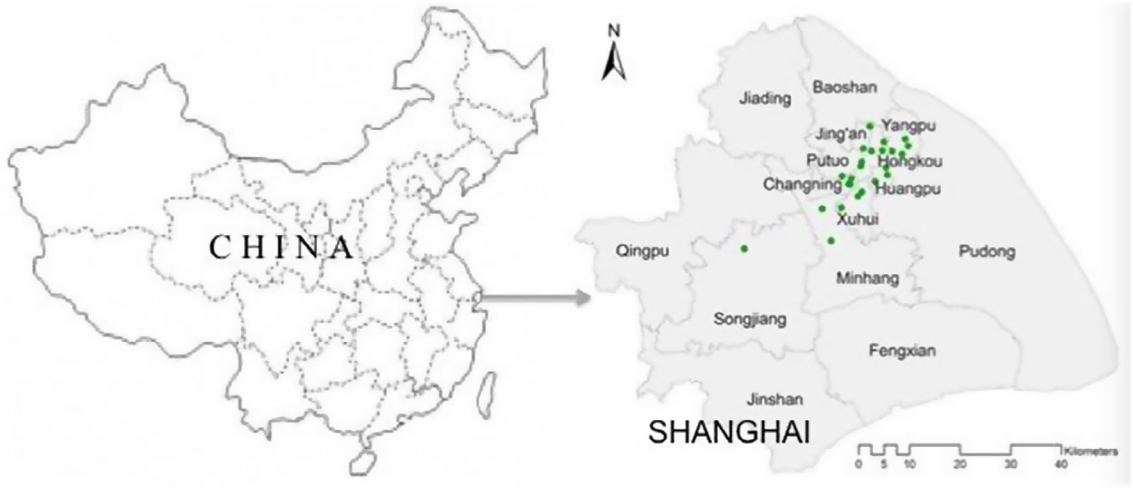


**Fig. 1.** A context map showing the study area in relation to the city of Shanghai and China.

The present study focused on soil bacterial diversity from urban parks of Shanghai, the most populous city in the world. Since China's economic reform in the late 1970s, Shanghai, has experienced fast pace expansion and urbanization (Zhao et al., 2006). Culture-independent molecular approach involving high-throughput Illumina sequencing opens a new perspective to characterize soil microbial diversity and community structure (Myrold, Zeglin, & Jansson, 2014). Therefore, Illumina MiSeq sequencing was utilized to analyze the 16S rRNA gene amplicons to elucidate complete bacterial communities in soils collected from 24 urban parks of Shanghai in present research. The principal objective of this work was to identify and analyze the bacterial diversity present in all main urban parks of Shanghai and their functional gene profiles.

## 2. Methodology

### 2.1. Study site and collection of soil samples

Shanghai is located on China's central eastern coast at the mouth of the Yangtze River (Fig. 1). Soils were sampled from 24 urban parks of Shanghai in this study. As shown in Fig. 2, these 24 parks are distributed across nine districts, out of which seven are referred to as urban areas including Putuo, Changning, Xuhui, Jingan, Huangpu, Hongkou, and Yangpu; while two districts away from the urban areas are Minhang and Songjiang (Table 1). The selected parks are main parks of chosen districts. They are situated in low to densely populated areas in 1 km and 2 km population buffer, based on the GIS model of the 6th national populations census in 2010 (Fig. 3).

The soil samples were collected from selected parks from top 10 cm of soil followed by removal of stones and roots by sieving using 2 mm mesh, and stored in iceboxes before taken to the laboratory. All the analyses of soils samples of urban parks were carried out within one week of collection.

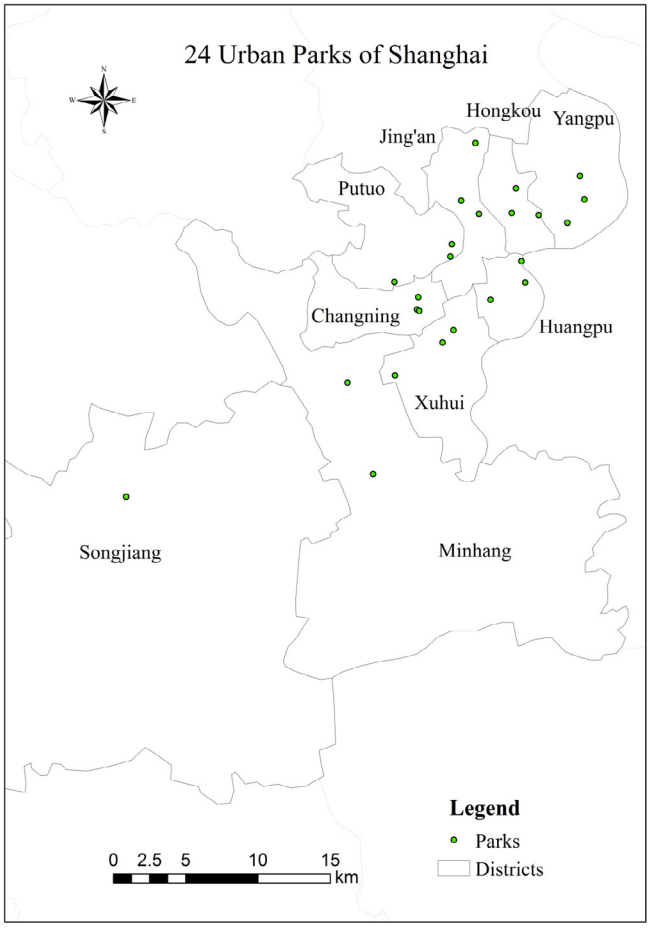


**Fig. 2.** Map of sampling points from 24 urban parks of Shanghai, China.

### 2.2. Genomic DNA extraction

The extraction of total soil DNA from soil samples (250 mg) was carried out with MoBio PowerSoil DNA Isolation Kit (MoBio, USA) as per manufacturer's protocol. The quantification of DNA was carried out using a Qubit 2.0 Fluorometer (Invitrogen, Carlsbad, USA). Initial PCR amplifications were performed on GeneAmp PCR System 9700 (Life Technologies, Rockville, USA). The final sequencing process was performed following the Illumina 16S Metagenomic Sequencing Library Preparation guide at Sangon Biotech Company, Shanghai. The V3 and V4 regions of the 16S rRNA gene were amplified using universal bacterial primers 341F (5′-CC TACGGGNGGCWGCAG-3′) and 805R (5′-GACTACHVGGGTATCTA ATCC-3′) that contained the required Illumina adaptors at the 5′ end of the primer sequences (5′-TCGTCGG CAGCGTCAGATGTGTATAAGA GACAG-3′ for the forward and 5′-GTC TCGTGGGCTCGGAGA TGTGTATAAGAGACAG-3′ for the reverse primers).