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Vegetation–soil microbiome linkages in urban green spaces: global patterns, methodological biases, and implications for urban ecosystem management

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Systematic Review

Keywords: Urban green spaces, systematic review, microbiome, vegetation

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Title - Vegetation–soil microbiome linkages in urban green spaces: global patterns, methodological biases, and implications for urban ecosystem management

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Abstract:

Urban green spaces (UGS) play a critical role in sustaining biodiversity and ecosystem functioning in cities, yet the influence of above-ground vegetation on below-ground soil microbiomes remains poorly synthesized. Urbanization changes land use, plant diversity, and soil properties, which influence soil microbiomes that can shape soil health and diversity. In this study, we conducted a systematic review of 148 studies published between 1990 and 2025 to evaluate how vegetation characteristics are associated with soil microbial communities in urban green spaces. Papers were collected from Web of Science, Scopus, and Google Scholar and systematically screened following PRISMA guidelines with a strict set of exclusion criteria. Across studies vegetation was commonly described using species richness, diversity, and land-use type, while microbial communities were mostly examined at the phylum level, with bacterial and fungal dominating reported outcomes.

We discovered a lack of studies across parts of Asia and Africa which may skew a global analysis and make representation uneven.More than 60% of the studies were conducted in temperate transition zones, with <10% representation from tropical and subtropical regions. Studies reported differences in the composition of the soil microbial community for different vegetation types and land use categories. However, the direct relationship between certain characteristics of the vegetation and the diversity of the microbial community was not often tested, and the representation of the vegetation-related variables was often low compared to the representation of the soil-related variables.

The present systematic review has identified knowledge gaps in the understanding of

the relationship between plants, soils, and microbes in urban ecosystems, thereby underscoring the need for more research to inform the management of these spaces in an evidence-based manner.These findings highlight the need to integrate vegetation design with soil microbiome considerations in urban green space planning and management.

Introduction:

According to the United Nations, by the year 2050, 70% of the Earth's population will live in cities, underscoring the rapid rate of global urbanization(Sun et al., 2023). This expansion affects biodiversity by intensifying anthropogenic activities within cities and adjoining rural and natural areas through sprawling(Filepné Kovács et al., 2024). Species responses to urbanization vary depending on their adaptability and have been classified in three categories: urban exploiters, urban adapters and urban avoiders. They exhibit differing capacities to persist in human-modified environments, with exploiters being the least vulnerable, adapters moderately vulnerable, and avoiders the most vulnerable to habitat changes (Simkin et al). As urban land use continues to expand—projected to cause significant habitat loss and fragmentation—species that depend on native habitats (i.e., avoiders) face disproportionate risks, contributing to the anticipated decline in terrestrial vertebrate diversity (~30,000 species) (Simkin et al., 2022). However, urban green spaces (UGS) within cities and towns provide crucial refuges for a diverse range of local biodiversity, including birds (Aronson et al., 2014), mammals (Bateman & Fleming, 2012), insects (Baldock et al., 2015), amphibians, and plants (Chollet et al., 2018). Studies have shown that UGS supports various species,

including endangered ones, by offering critical habitats amid urbanized landscapes (Soanes & Lentini, 2019). Moreover, UGS facilitates the movement of species across fragmented urban environments, enhancing ecological connectivity and promoting genetic diversity within urban landscapes (Beninde et al., 2015). However, research on below-ground biodiversity, particularly soil microbial communities in urban environments, remains limited and geographically uneven, with relatively few studies conducted in rapidly urbanizing regions of the Global South.

This may be attributed to the complex relationship that soil microbiome has with biodiversity and several other factors, many of which are elucidated in Fig.1. Several studies have now shown how microbial communities are interconnected with each other (Banerjee and van der Heijden, 2023). Additionally, healthy soil affects plant and animal productivity, water and air quality, thereby playing a crucial role in global air quality and water security (Banerjee and van der Heijden, 2023). Similarly, increased soil stress can eliminate organisms that aid in the discovery of new antibiotics, which is vital for a world hurtling toward antimicrobial-resistant diseases(Brevik et al., 2020). Urban soils (often called technosols) are frequently subjected to tampering, compaction, surface sealing, and change in above-ground vegetation structure and composition, all of which will affect soil microbial diversity(Fig. 1) (Fierer, 2017). Studies have shown that soil functionality depends not only on microbes but also on microbial community evenness, a lack of which affects nutrient cycling in soil, leading to soil stress (Mendes et al., 2015). A global survey on urban green spaces and natural systems in 56 cities spanning 6 continents identified several factors, such as park management practices and

environmental stress, that affect the soil microbiome(Delgado-Baquerizo et al., 2021)detailed comprehensively in Fig.1.

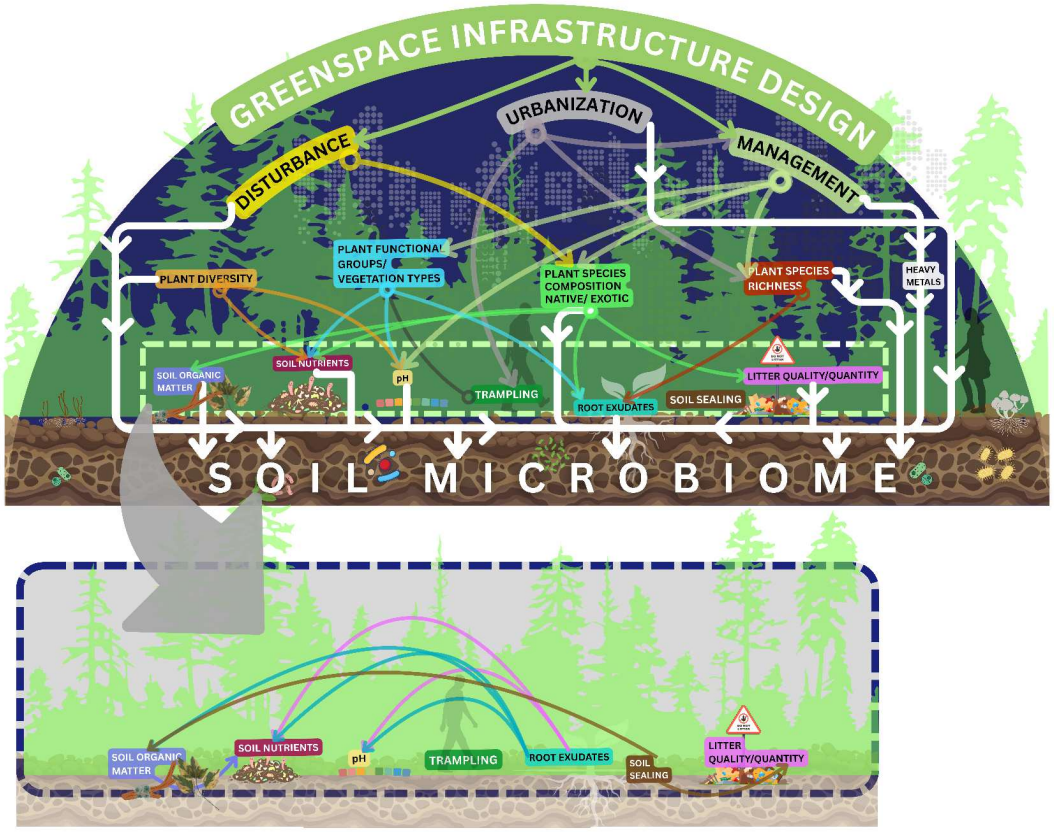


Fig. 1 : The flowchart depicts an intricate network of factors shaping the soil microbiome while highlighting the effect of above ground vegetation in the context of urban greenspaces. Most urban greenspaces face substantial disturbance and various management practices. Chosen studies have looked at different aspects of both, their effect on vegetation and hence, their effect on soil microbiome.

Although awareness has grown among urban space managers about the importance of preserving natural vegetation and biodiversity, there remains a prevailing tendency to prioritize the aesthetic appeal of planted vegetation (Zhao et al., 2024). This is significant since belowground soil microbiota are rarely considered important while

making such decisions, and yet they are affected by the management of land use systems (Mendes et al., 2015). It is crucial to prioritize the study of soil microbial communities as they play a fundamental role in biogeochemical cycles, support plant health, enhance soil fertility, and contribute to the overall sustainability of urban green spaces.

A study of 600 soil samples collected across Central Park, New York City, revealed a high level of below-ground microbial diversity, most of which was undescribed when compared to global microbiomes (Ramirez et al., 2014). A similar study from five urban green spaces in Adelaide, Australia, showed clear associations of soil fungal diversity with above-ground vegetation, such as areas with woody vegetation, which showed the most fungal diversity(Baruch, Liddicoat, Laws, et al., 2020). A follow-up to this study showed how plant species diversity correlates with soil bacterial diversity. Both high vegetation cover, non-native species and heterogeneity in the environment increase available nutrients, thus letting a wider array of bacteria thrive (Baruch, Liddicoat, Cando-Dumancela, et al., 2020b). Another study in Southern Finland also saw a distinct difference in microbial communities between urban parks and natural forests (Hui et al., 2017). The global study by Delgado-Baquerizo et al., that urban green spaces have distinct soil bacteria and protists from natural ecosystems. Along with global homogenization, urban green spaces are also hotspots of microbial activity, especially plant pathogens and fungal parasites.

Most of these studies were conducted to help city planners and urban managers plan the vegetation of the city, especially in green spaces. Based on studies so far, the soil physico-chemical properties, vegetation, and soil microbial communities are intricately

linked and affect each other greatly. However, there is limited research that focuses on the effect of above-ground vegetation on soil microbial communities in urban green spaces. This study thus aims to examine the gaps in our understanding of the role played by above-ground vegetation in shaping the below-ground microbial communities. We synthesized insights from over 148 studies to highlight the factors influencing soil health and their impact on human well-being in these environments. This systematic review focuses on the type of studies that have been conducted, the vegetation attributes noted, and the microbes that are examined. We have taken a comprehensive approach in bringing to light the different viewpoints of the studies and tried to map them to provide a better understanding of the factors that directly and indirectly affect soil microbial diversity in urban green spaces due to above-ground vegetation.These findings highlight the need to integrate vegetation design with soil microbiome considerations in urban green space planning.

Objectives:

The primary questions addressed in this paper are:-

What evidence exists for the role of above-ground vegetation on soil microbiomes in urban green spaces? What are the critical gaps in the available literature?

The secondary questions are:-

1. How much research has been conducted to describe the relationship between plants and the soil microbiome in urban green spaces?
2. Which geographical locations and climates are these studies primarily limited to, and do they adequately represent the climatic and economic variations across the

globe?

3. How does above-ground vegetation type and diversity affect soil microbial diversity, biomass, and functional traits in urban green spaces?
4. What types of microbes have been identified in these studies?
5. What patterns emerge linking vegetation attributes with microbial community structure across urban green spaces?

This review was conducted to address the above objectives. It is following a systematic approach, conforming to the PRISMA reporting standards to ensure comprehensive and unbiased coverage of literature (Page et al., 2020). This would also entail ensuring replicability in the methodology, allowing any academic to thoroughly understand this study and use it as a foundation for future research.

Methods:

Search for Articles:

We used three different bibliographic databases for this review: Web of Science (WOS), SCOPUS, and Google Scholar (GS). Each search string was adapted to suit each database. The search was conducted from December 2023 to Sep 2025. The number of records retrieved in each string is shown in Table 1.

Databases	Search Strings	Number of Records Retrieved

Web Of Science	(((TS=(Urban OR pocket OR remnant OR city OR urban-rural OR settlements)) AND TS=(green space OR park OR patch OR forests)) AND TS=((soil OR pedosphere) AND (microb* OR bacteria OR fungi OR prokaryote OR eukaryote))) AND TS=(plant AND (community OR diversity OR invasive OR richness OR ornamental OR exotic OR evenness OR composition) OR vegetation OR tree OR shrub)	895
	(((TS=(Urban OR pocket OR remnant OR city OR urban-rural OR settlements)) AND TS=(green space OR park OR patch OR forests)) AND TS=((soil) AND (microb* OR bacteria OR fungi OR prokaryote OR eukaryote))) AND TS=(plant AND (community OR diversity OR invasive OR richness OR ornamental OR exotic OR evenness OR composition) OR vegetation)	900
	(((TS=(Urban OR pocket OR remnant OR city OR urban-rural OR settlements)) AND TS=(green space OR park OR patch OR forests)) AND TS=((soil OR pedosphere OR turf) AND (microb* OR bacteria OR fungi OR prokaryote OR eukaryote))) AND TS=(plant AND (community OR diversity OR invasive OR richness OR ornamental OR exotic OR evenness OR composition) OR vegetation)	1122
	(((TS=(Urban OR pocket OR remnant OR city OR urban-rural OR settlements)) AND TS=(green space OR park OR patch OR forests)) AND TS=((soil OR pedosphere OR turf) AND (microb* OR bacteria OR fungi OR prokaryote OR eukaryote OR belowground biodiversity))) AND TS=(plant AND (community OR diversity OR invasive OR richness OR ornamental OR exotic OR evenness OR composition OR native) OR vegetation OR tree OR shrub)	1122
SCOPUS	TITLE-ABS-KEY((((Urban OR pocket Or remnant OR city OR urban-rural OR settlements)) AND (green space OR park OR patch OR forests)) AND ((soil OR pedosphere OR turf) AND (microb* OR bacteria OR fungi OR prokaryote OR eukaryote))) AND (plant AND (community OR diversity OR invasive OR richness OR ornamental OR evenness OR composition) OR vegetation OR tree OR shrub)	115
	TITLE-ABS-KEY((((Urban OR pocket Or remnant OR city OR urban-rural OR settlements)) AND (green space OR park OR patch OR forests)) AND ((soil OR pedosphere OR turf) AND (microb* OR bacteria OR fungi OR prokaryote OR eukaryote OR (belowground AND biodiversity)))) AND (plant AND (community OR diversity OR invasive OR richness OR ornamental OR exotic OR evenness OR composition OR native) OR vegetation OR tree OR shrub)	119
Google Scholar	Urban OR pocket OR remnant OR city OR urban-rural OR settlements AND green space OR park OR patch OR forests AND soil OR pedosphere OR turf AND microb* OR bacteria OR fungi OR prokaryote OR eukaryote AND plant AND community OR diversity OR invasive OR richness OR ornamental OR evenness OR composition OR vegetation OR tree OR shrub	199
	Urban OR pocket OR remnant OR city OR urban-rural OR settlements AND green space OR park OR patch OR forests AND soil OR pedosphere OR turf AND microb* OR bacteria OR fungi OR prokaryote OR eukaryote OR (belowground biodiversity) AND plant AND community OR diversity OR invasive OR richness OR ornamental OR exotic OR evenness OR composition OR native OR vegetation OR tree OR shrub	224

Table 1: The table consists of all the search strings used for each database and the number of records from each. The highlighted strings indicate the maximum number of records from that database.

We used Google Scholar to scope for articles, develop the search strings and the inclusion-exclusion criteria. The final search strings for each source used can be found below (Table 1). Web Of Science, SCOPUS, and Google Scholar were used as databases to obtain the studies for analysis. In the search string, we also used terms synonymous with cities, plants, diversity, soil, and microbiome, along with Boolean operators such as 'AND' and 'OR'. We identified additional articles by reviewing the bibliographies of the included studies after the primary screening. All results from each database were retrieved, and duplicate entries were removed.

The scoping exercise revealed that the majority of studies began around 1990, so we included research published from 1990 to 2025. Studies from all geographic affiliations were considered, with no restrictions on location. Only studies published in English were included.

We estimated the comprehensiveness of the search string by checking the overlap, in terms of the number of studies, among the three databases. We found a significant overlap, indicating that all three databases covered key articles published during the selected time frame.

Screening process:

Authors screened the articles based on the title and abstract of the papers. The agreement coefficient between reviewers came to 0.79. The coefficient was calculated using the formula shown in Fig. 2. This was followed by the full-text screening.

$$\kappa = \frac{(Po - Pe)}{1 - Pe}$$

$$P_o \text{ (observed agreement)} = \frac{Both\ AM, AS\ included + Both\ AM, AS\ excluded}{Total\ Number\ of\ Papers}$$

$$P_e \text{ (expected agreement)} = \left[\frac{(Studies\ included\ by\ AS) * (Studies\ included\ by\ AM)}{(Total\ number\ of\ studies)^2}\right] + \left[\frac{(Studies\ excluded\ by\ AS) * (Studies\ excluded\ by\ AM)}{(Total\ number\ of\ studies)^2}\right]$$

Fig. 2 : The figure shows the formula used to calculate the agreement coefficient, also called the kappa coefficient.

Table 2 below shows the inclusion and exclusion criteria and their rationale. Although initially studies of an experimental nature were only considered, upon realizing the variety as well as the importance of other study designs, observational studies, surveys and other reviews were also included.

Inclusion Criteria	**Rationale**
Urban green spaces	Studies conducted in green spaces of urban areas only, i.e., forests, cemeteries, residential campuses, parks, gardens
Soil microbes/microbiome/microbiota/bacteria/fungi/prokaryotes/eukaryotes	Studies involving microbes present in the soil can include bacteria, fungi, protists, microeukaryotes and symbiotic communities such as mycorrhizae and communities close to the roots, i.e., rhizosphere

Relevant ecosystem	Only terrestrial ecosystems
Vegetation characteristics studied	Community characteristics (Richness, evenness, diversity), Plant species type (exotic, invasive, ornamental)
Analytical modeling	Correlative studies are included, but analytical techniques used are also noted to understand the cause-effect relationship depicted
Time Period	1990-2025
Language	Studies published in the English language.
Functional diversity of microbial community	Studies depicting functional traits such as antibiotic resistance and nitrogen-cycling genes are also considered
Exclusion Criteria	**Rationale**

Urban green spaces	Excluding spaces like urban green roofs, bioswales, agricultural lands, natural forests away from cities, and vertical gardens. The review intends to understand the role of the plant community in shaping the soil microbiome. Hence, spaces like urban green roofs, bioswales, vertical gardens and agricultural lands will include microbial communities generally not found in urban soil or intentionally change the evenness of the communities. Natural forests and grasslands will be extremely protected compared to urban soils.
Heavily industrialized areas, areas that have been left behind (like landfills and so on), inoculated and sealed soils.	Excluding spaces that involved extensive urbanization, because those sites will be far away from urban spaces and consist of heavy metals which may drastically alter the community.
Non-urban	Excluding studies involving green spaces are present in rural areas.

Table 2: The table shows the different inclusion and exclusion criteria that were used to select the studies. The criteria includes synonyms and the rationale behind each criteria.

Pilot data extraction headings were developed based on the knowledge after scoping

prior to full-text extraction. As the process went on, the headings were modified to include headings that seemed relevant to our study. Any point of uncertainty throughout the process was settled after consulting with other authors. Every reasonable attempt was made to access the full-text articles for screening. The data extracted were: Geographical distribution, Study design, Vegetation identified, Microbes identified, Microbial C/N or Biomass, Type of urban green space, and the Publication date, with each category containing subcategories to account for the alternatives observed.

The results were then presented graphically using QGIS and Excel to develop bar graphs and a geographical map. As mentioned above, for the map metadata i.e, in vegetation identified, study design, and so on was extracted and displayed as bar graphs. The location of the studies was displayed on a geographical and climate map. As mentioned above, the categorization of each data point was informed by the degree of variation observed. To accommodate the range of alternatives, each category was further divided into relevant subcategories. The resulting categories for each data point are shown in Table 3.

Data Points	**Subcategories**	**Rationale**
Geographical Distribution of Studies	Countries where studies were conducted	It will help us understand the global research coverage, regional biases and gaps in knowledge
Study Designs	Experimental	It allows us to test the hypotheses in a controlled manner, allowing us to find a causal relationship
	Observational	It provides real-world insights into natural patterns without any manipulation. Here, it was

		collected to understand the trends in the field over time.
	Review	All these were collected to understand the trends in the field over time, and if it has been gaining more traction.
	Systematic Analyses	
	Survey	
Vegetation identified	Composition	These were collected to develop a thorough understanding of the vegetation at the site.
	Diversity	
	Functional Groups	
	Species number	
Microbes identified	Prokaryotes or Eukaryotes	These were collected to understand the microbial community observed in the soil sample.
	Based on Phyla	
Microbial C/N or biomass observed	Microbial C and N biomass	
	Bacterial biomass	
	Fungal biomass	
Types of urban green spaces	Urban forests	These were collected to understand the different sites that studies have observed.
	Urban parks	
	Remnant forests and so on	
Publication date	Published month and year	It was collected to understand the temporal trends in the field.
Journal published		
Electronic Journal		
Funding Agency	Agencies that have funded the research	It was collected to understand if these studies were backed by governmental agencies or

		private agencies.

Table 3: The tables show each data point that was extracted along with subcategories for each. It takes into account the variability observed while scoping.

Results

The study selection process is summarized in the PRISMA flow diagram (Figure 3). A total of 4,697 records were identified from different databases, which includes Web of Science (n=4039) with the highest number of papers, followed by Google Scholar (n=424), and Scopus (n=234). Duplicate records (n=3,872) were removed then based on titles and abstracts 825 records were screened, after which 697 records were excluded. For retrieval 193 reports were taken, out of which 29 reports could not be retrieved. The remaining 164 reports were assessed for eligibility. After which 16 reports were excluded as they were not meeting the inclusion criteria. Therefore in total, 148 studies were included in the final review.

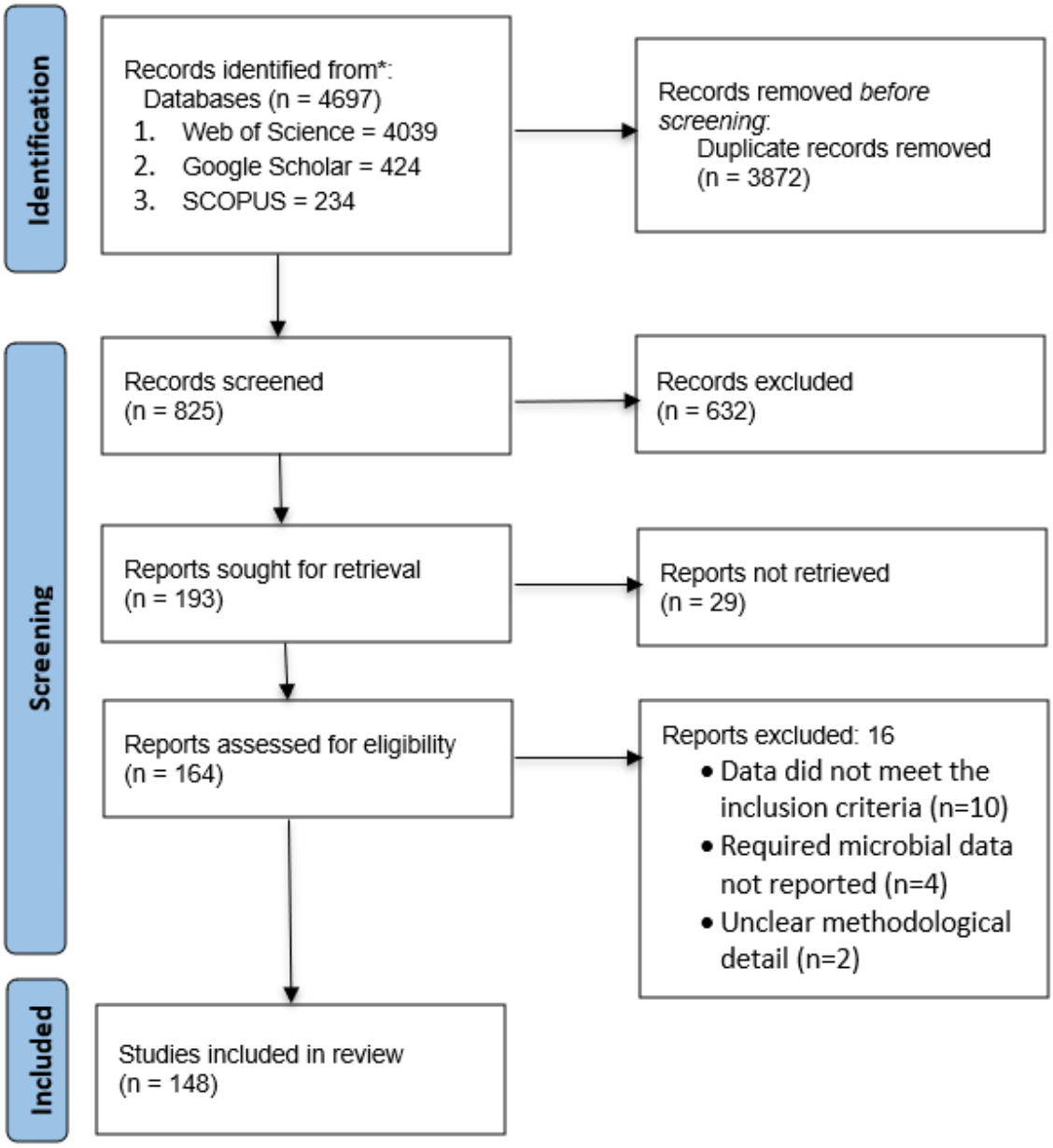
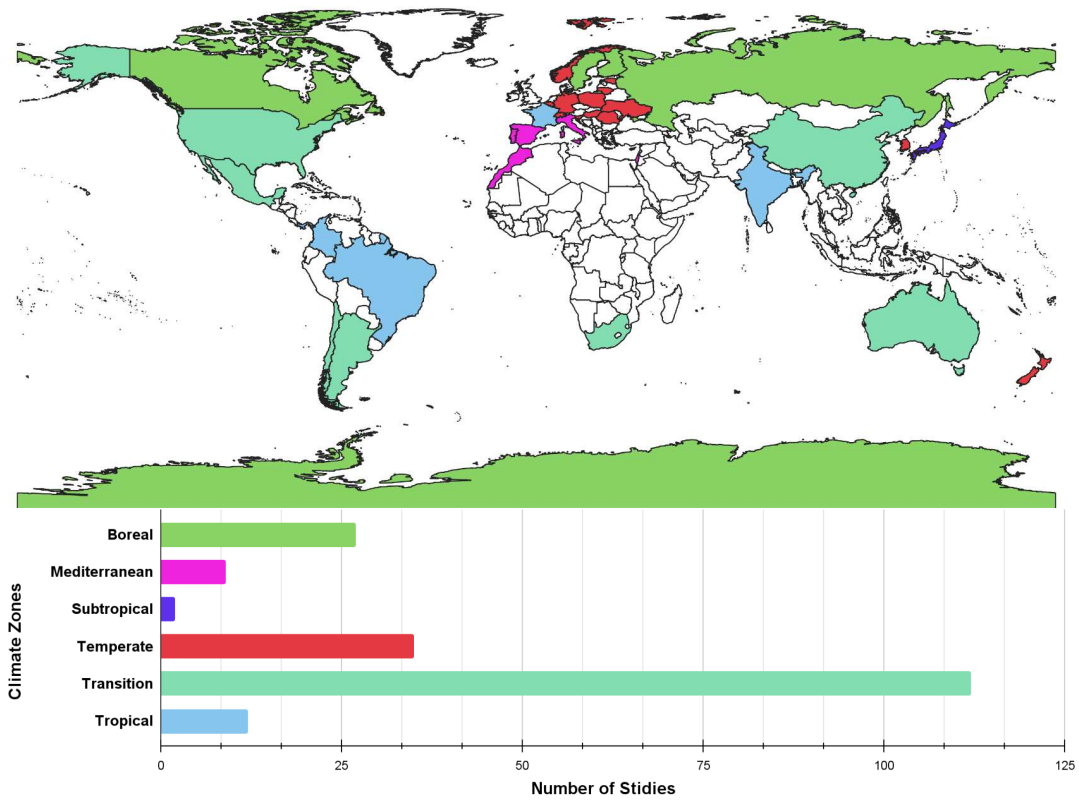


Fig. 3 : PRISMA flow chart illustrating the number of studies identified, screened, removed and included in the systematic review at each step of the selection process. Source: Page MJ, et al. BMJ 2021;372:n71. doi: 10.1136/bmj.n71.

Global Distribution of Selected Studies:

The least represented climatic zones in the selected studies were Mediterranean zone(n=9) and Subtropical zone(n=2). Such a disparity also indicates that our knowledge in this domain is still in its infancy. Tropical and subtropical cities have a different character in terms of their vegetation composition, management practices, decomposition processes, and biogeochemical cycles in soils compared to temperate cities; therefore, it is not safe to generalize our results obtained in temperate cities for tropical/subtropical cities environments.

The geographical distribution of the selected studies shows an uneven spread across countries, the chart highlights the global interest and regional gaps in selected topics like urbanization, vegetation and soil microbiome. The total number of studies ranged from 1 to 54, the country with the highest number of studies was China (n=54) , followed by the United States of America (n = 36). A moderate number of studies were reported from Finland (n=17), Australia (n=14), and Poland (n=9). In contrast, most of the countries contributed only a small number of studies, typically ranging from one to three publications. Overall the results indicate that a small number of countries accounted for a large proportion of the total studies showing a clear uneven representation across the globe. It is visible through the uncoloured area that there are no urban soil microbiomes and vegetation studies from Africa, the Middle East, and Central Asia (Figure 4.b). The absence of data from these regions underscores broader inequities in global urban ecological research.



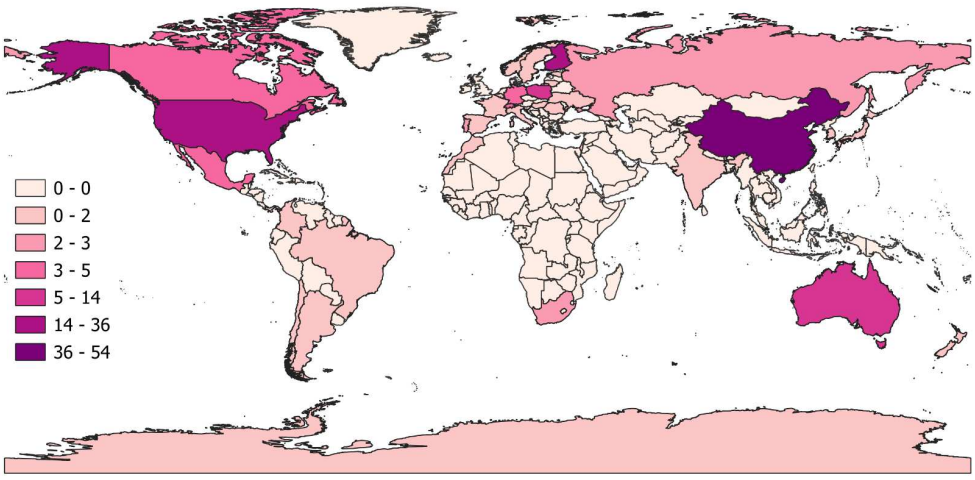


Fig. 4 : Shows Global distribution of the 148 shortlisted studies across climatic change and countries. (a) Illustrates the climatic zones mentioned in the studies, classified into Boreal, Mediterranean, Subtropical, Temperate, Transition, Tropical region. (b) Map displays number of studies carried out per country, which is divided into various frequency classification.

Distribution of Publications over the last 35 years:

To examine how research output has changed over time, the year-wise distribution of

publication included in the review was analyzed (Figure 5). The study reveals a gradual shift from little interest in urban soil ecology in early years to much higher outputs in the last 5 years. During the initial period; 2006(n=1) studies were published, the number steadily increased after 2014(n=5), with a clear rise observed after 2019(n=7) and peaked in the most recent years, around 2023(n=22), with the highest publication counts; recorded in the year 2025(n=23). Overall, the data demonstrate that vegetation–soil microbiome interactions in cities represent an emerging and rapidly expanding field of research. Fig S1 and S2 show a distribution of journals that have published these articles and funding sources respectively.

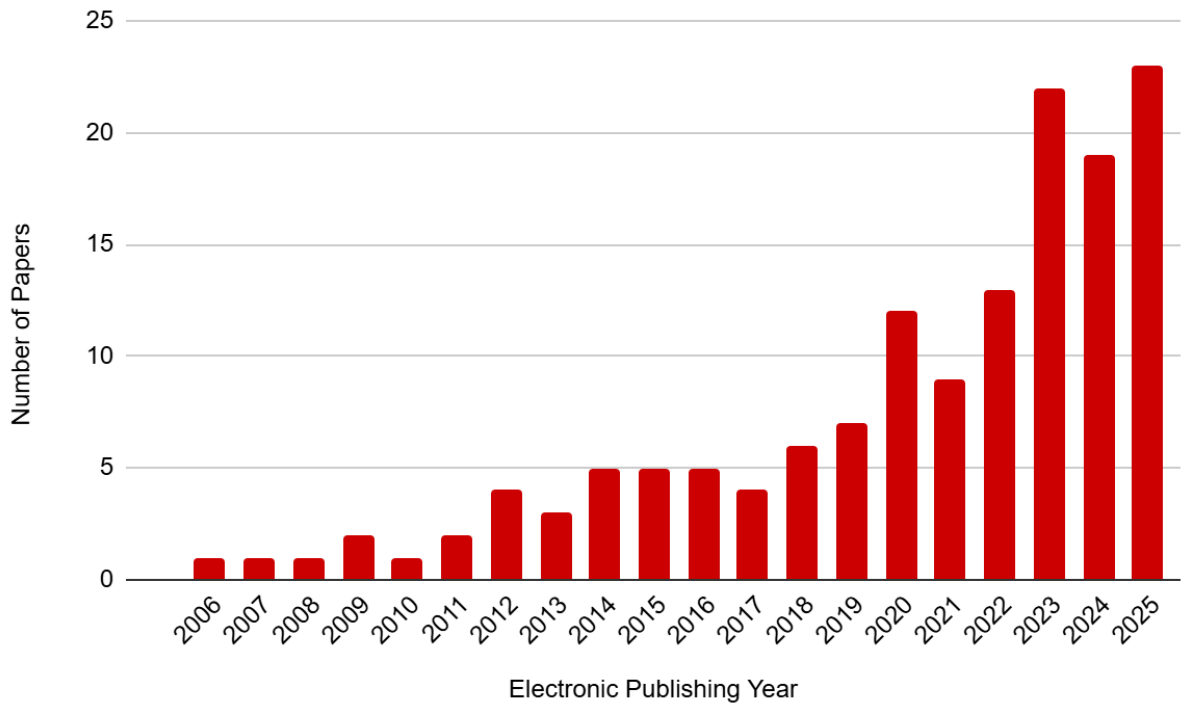


Fig. 5: Year-wise distribution of the number of studies included in the review across the study period.

Distribution of Studies by Site Type:

To understand the type of environment in which microbial studies have been conducted, the selected studies were classified based on site type (Figure.6). A wide range of site

types was reported across different UGS, therefore they were grouped into four main categories for analysis. Parks, Forest, and Lawn/Grassland represented the primary site types. Studies that differ from these main categories were grouped under Mixed/ Others, which consisted of multi-land use urban landscapes, residential and institutional green spaces, post-industrial sites, agricultural sites, and studies conducted along urbanization gradients.

Forest based studies were reported in 54 of the 148 reviewed studies. When disaggregated by country and site, these corresponded to 253 forest site records, the majority of which represented urban forest ecosystems, including mixed urban forests, remnant and fragmented patches, bamboo forests, and afforested urban forest parks. The chart shows that the most commonly studied sites were Parks(n=519), followed by Forests(n=253). Several studies were carried out in Lawn/Grassland(n=156) areas and rest sites which were grouped in Mixed/ Others(n=118) were also in moderate numbers of studies. Overall, the distribution of studies across different site types was uneven, with most research focused on a limited number of commonly studied environments.

No.	%	Pathway	Vegetation Driver	Urban Modifier	Microbial Response	Exp. Support	Evidence	Direction
20	14	Direct	Establishment, diversity, litter & root inputs	Compaction, N deposition, land conversion, restoration	Diversity shifts; enzyme activity; nutrient cycling; multifunctionality	Yes	Strong causal	Complexity & organic inputs ↑ function; compaction ↓ function
2	1	Direct	Vegetation structure & host	Compaction, simplification	↓ AMF richness, infectivity & symbiosis	Yes	Strong causal	Host presence ↑ symbiosis; simplification

			availability					↓ function
41	28	Direct	Tree identity & plant functional traits (litter chemistry, host specificity)	Land conversion, park management, invasion	Shifts in microbial diversity, ECM/AMF composition & networks	No	Moderate mechanistic	Tree identity strongly structures fungi; weaker bacterial response
33	23	Direct	Productivity & organic matter inputs	Fertilization, mowing, irrigation	↑ Biomass, enzyme activity, N mineralization & C cycling	No	Moderate mechanistic	Higher productivity ↑ microbial biomass & activity
28	19	Direct	Vegetation loss & fragmentation	Soil sealing, salinity, metals, impervious surfaces	↓ ECM/AMF colonization; ↑ pathogens; homogenization	No	Moderate mechanistic	Urban stress weakens symbioses; favors tolerant taxa
21	14	Indirect	Vegetation alters soil physicochemical conditions	pH shifts, metals, nutrient pools, compaction	Community restructuring; gene shifts; C stabilization changes	No	Moderate mechanistic	Soil chemistry often overrides vegetation effects

Table 4 Synthesis of vegetation drivers, urban modifiers, microbial responses, and strength of evidence across reviewed studies. The direct vegetation effects are dominant in the literature, but the strongest evidence for causality comes from experimental studies. Compaction and sealing of soils under urban stressors commonly reduce symbiotic associations and increase tolerant microbe groups.

Mechanism	Total studies	Experimental	Observational
Vegetation establishment, diversity, litter, root inputs	20	10	10
Vegetation structure controlling symbiosis	2	1	1
Vegetation identity and functional traits	41	0	41
Vegetation productivity and organic matter inputs	33	0	33
Vegetation loss and fragmentation effects	28	0	28
Indirect soil physicochemical mediation	21	0	21

Table 5 Distribution of mechanistic pathways linking vegetation and soil microbiomes in urban green spaces, study design-based classification. This figure emphasizes the prevalence of observational study designs in the mechanistic pathways of vegetation-microbe interactions, with the exception of vegetation establishment, diversity, and litter/restore manipulations in experimental designs. This distribution points to the need to test the causal links of vegetation identity, productivity, fragmentation, and physicochemical mediation in the soil microbiome.

Table 4 provides an overview of the main vegetation factors and their modifiers, and the microbial responses. Of the total data set (approximately 85%), direct vegetation factors dominated the results, with only 14% falling under the category of indirect factors and changes in soil physicochemical properties.

The strongest evidence for cause and effect (14%) was provided by experimental studies manipulating vegetation establishment, diversity, litter, and restoration. All studies showed enhanced microbial multifunctionality and enzyme activities with increasing

vegetation complexity and organic layer thickness. Compaction and land use had negative impacts.Tree species and functional traits (28%) showed significant associations with changes in fungal communities, especially ECM and AMF communities. However, bacterial communities showed less clear relationships. Productivity-driven factors (23%) showed moderate associations with enhanced microbial biomass and nutrient mineralization.

Vegetation loss and fragmentation (19%) showed significant associations with reduced symbiotic fungi and homogenization due to urban stressors such as soil sealing, salinity, and heavy metals. Indirect factors (14%) showed significant associations with changes in soil pH, nutrient pools, and metal concentrations overriding the direct effects of vegetation.The evidence shows that increasing complexity and organic layer thickness enhance microbial function, and urban stressors reduce symbiotic relationships and increase the proportion of stress-tolerant microorganisms.

Table 5 summarizes the strength of evidence supporting different vegetation-microbiome mechanisms, as a function of the study design used to address these mechanisms. Among the six mechanistic pathways, only vegetation establishment, diversity manipulation, and organic input interventions have substantial experimental testing (10 of 20 studies). In contrast, vegetation structure controlling symbiosis was investigated by only two studies, of which only one was an experimental approach. In contrast, the mechanisms of vegetation identity and functional traits (n = 41), vegetation productivity and organic matter inputs (n = 33), vegetation loss and fragmentation (n = 28), as well as indirect soil physicochemical mediation (n = 21) of the microbiome have

only observational evidence.Only 11 of 148 studies (7.4%) included experimental manipulation of vegetation variables.

This suggests that, whereas the relationship between vegetation traits and the structure of the microbiome has been extensively demonstrated, there has been limited experimental testing of these associations, which has focused mainly on restoration and diversity manipulation, whereas the effect of the other vegetation traits has been inferred from comparisons of different types of vegetation, based on observational studies alone.

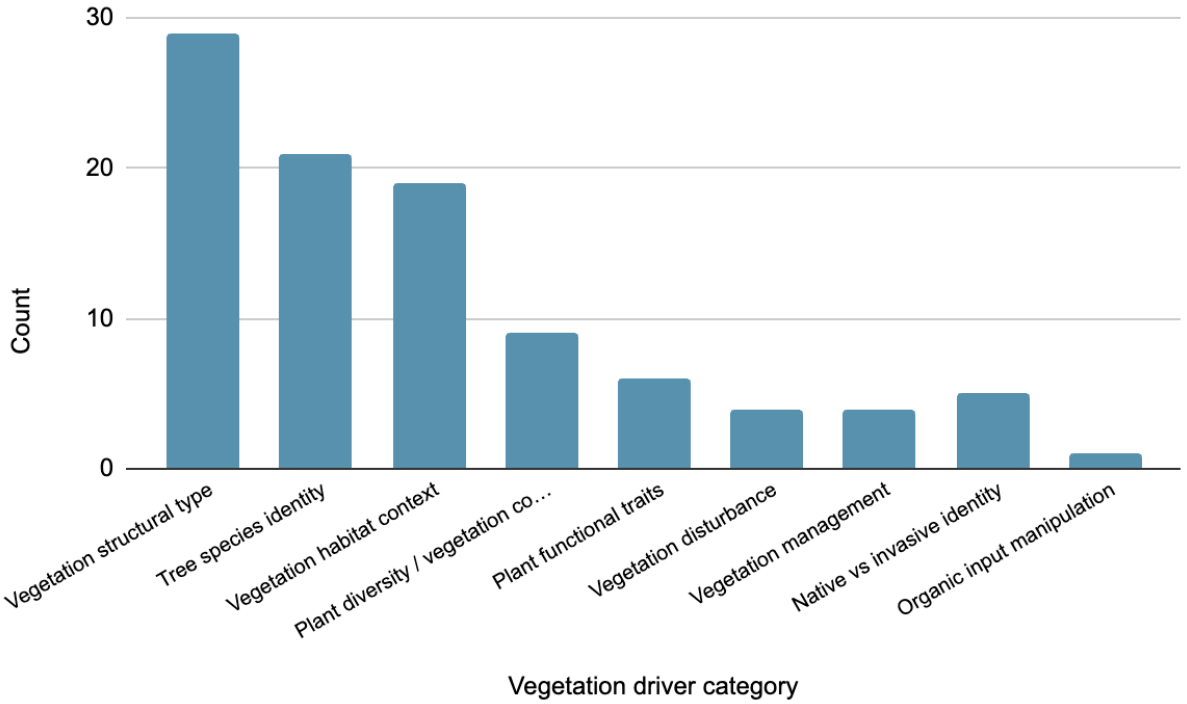
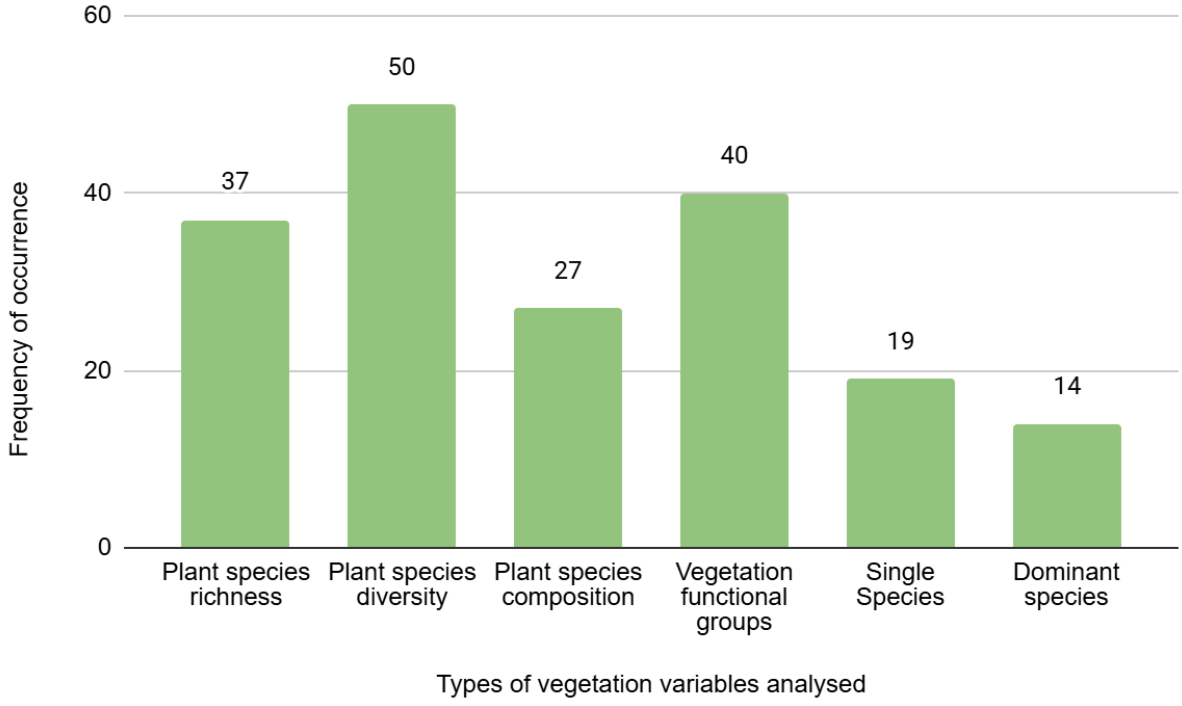


Fig 6 The frequency of vegetation driver categories investigated across the studies. While structural vegetation attributes, such as vegetation type or tree identity, were the most investigated, functional trait-based and disturbance-related vegetation driver analyses were relatively limited, indicating a bias towards more descriptive rather than

mechanistic vegetation microbiome studies.

The proportion of vegetation driver category types (Fig. 6), however, shows that the most studied types of vegetation attributes were the structural types of vegetation. Vegetation structural types were the most common types of vegetation driver, followed by tree species and vegetation habitat context. However vegetation disturbance, and organic manipulation were less common in the literature.The prevalence of vegetation structural and compositional types may suggest that the vast majority of studies focus on the descriptive rather than the experimental approach to understanding the mechanistic pathways of vegetation patterns. Less common types of disturbance and organic manipulation studies suggest that the effects of management on vegetation and, in turn, on microbial dynamics are not well understood.

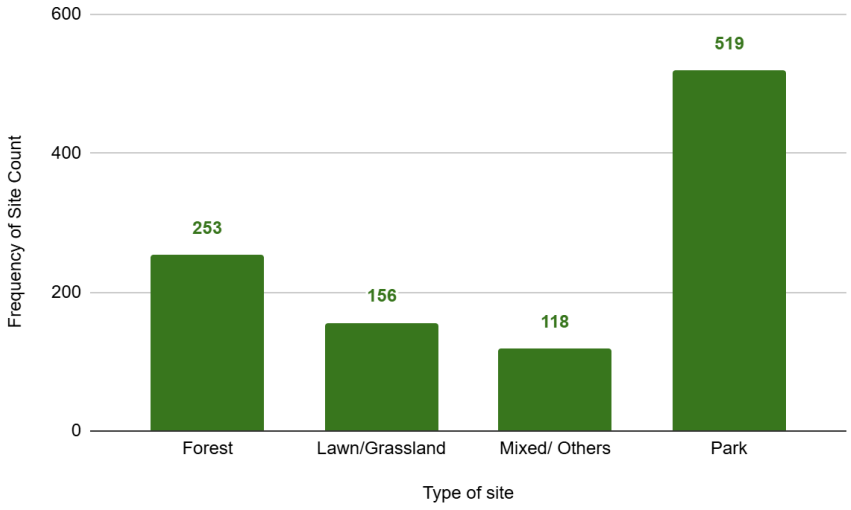
To understand which vegetation-related variables were examined, the selected papers were grouped based on the variables they analysed, represented in (Figure 7).
The results show that plant species diversity(n=50) was the most commonly analysed variable followed by vegetation functional groups(n=40) and plant species richness(n=37). Plant species composition(n=27) was also frequently studied, but comparatively less. Fewer studies focused on single species(n=19) and dominant species(n=14).
The findings indicate that most studies have primarily focused on community-level vegetation metrics, particularly diversity and functional group classifications, rather than species-specific analysis.



401

402 **Fig. 7 :** Frequency of vegetation -related variables examined across the included studies, showing dominance of

403 community-level metrics (diversity, richness, functional groups) over species-specific measures.



404

Fig. 8 : Site type classification of the included studies, showing the frequency of sites categorized as Forest, Lawn/Grassland, Mixed/Others, and Park.

To identify the most frequently studied attributes of the vegetation-related characteristics, the studies were grouped based on the type of vegetation-related characteristic studied (Fig. 7). The results showed that there was a strong dominance of community-level characteristics. Plant species diversity was the most frequently studied characteristic, with 50 studies, followed by vegetation-related functional groups, with 40 studies, and plant species richness, with 37 studies. Plant species composition was also frequently studied, but to a lesser extent than the diversity-related characteristics, with 27 studies. In contrast, fewer studies focused on single species, with 19 studies, and dominant species, with 14 studies.

This suggests that the majority of the research focused on the overall characteristics of the plant community rather than the mechanisms of the single species or dominant species. Even though the overall characteristics of the plant community provide a general idea of the relationship between the microbiome and the vegetation, the lack of studies on single species or dominant species may limit the overall knowledge of the relationship between the microbiome and the single species or dominant species of the host.Figure 8 shows the number of studies per category of major UGS site type. The most studied site type was parks, which comprised 519 site records, followed by Forests with 253 site records. Lawn/Grassland sites comprised 156 records, while the Mixed/Other category, which includes residential campus sites, institutional sites, multi-land-use gradients, and post-industrial sites, comprised 118 records.

The dominance of park and forest sites may indicate that there has been more research interest in these more managed or semi-natural urban landscape types, while the less managed or more altered urban spaces have been less studied. This may create a bias towards the current knowledge of the interaction between vegetation and the soil microbiome towards the more structured or greener sites, possibly missing the more managed or altered sites.

Functional Trait Categories Examined in the Studies:

To understand the functional traits examined in the included studies, microbial functional traits were grouped into major categories (Figure 11). The heat map illustrates the representation of the functional trait category across all studies, with colour intensity reflecting the number studies reporting that function.

The results show that functions related to decomposition (19.3% n=53) and nutrient cycling (18.2%, n=50) were the most frequent traits. A moderate representation was observed for symbiosis (12.8%, n=35) and other functional categories (12.4%, n=34). Traits related resistance (10.6%, n=29) and stress (7.7%, n=21) were comparatively reported less frequently, while the smallest proportion among all categories were represented by biomass-related function(4.7%, n=130).

Additionally, a few studies did not report any information related to functional traits and were therefore grouped under NA, accounting for (14.2%, n=39) of the total studies. The distribution indicates that adaptive and structural microbial traits are still

underrepresented in existing research.

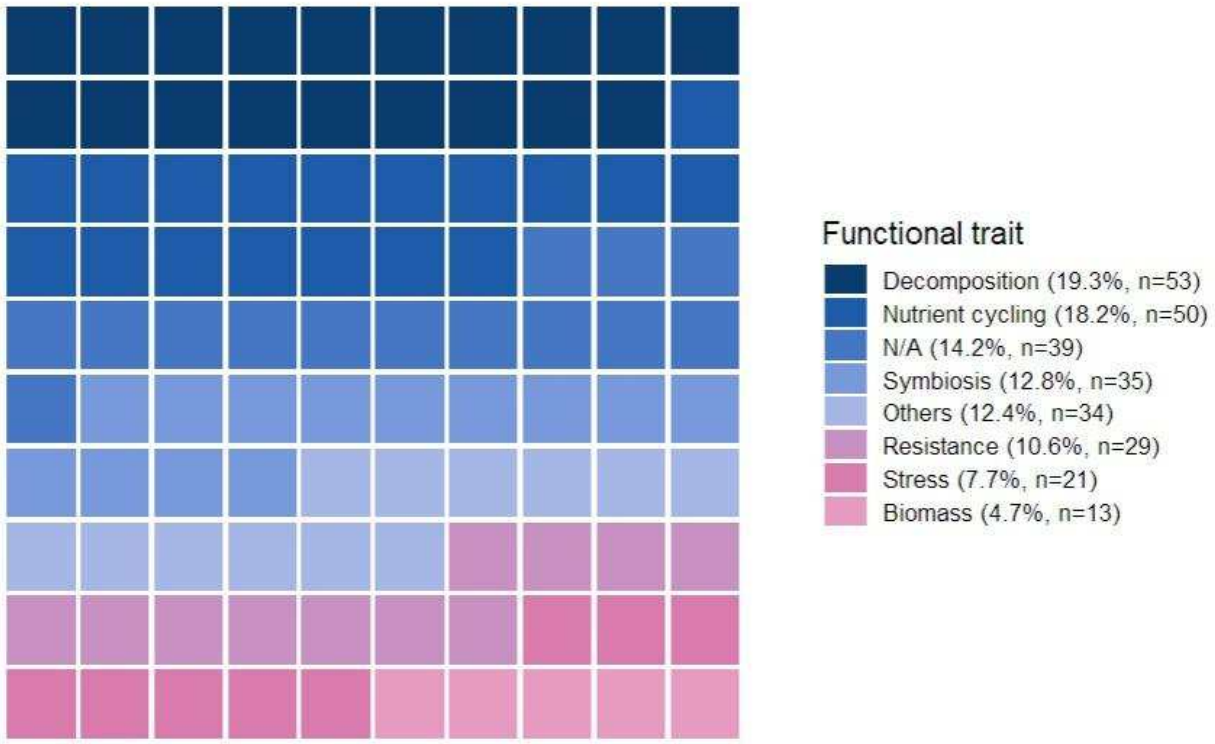


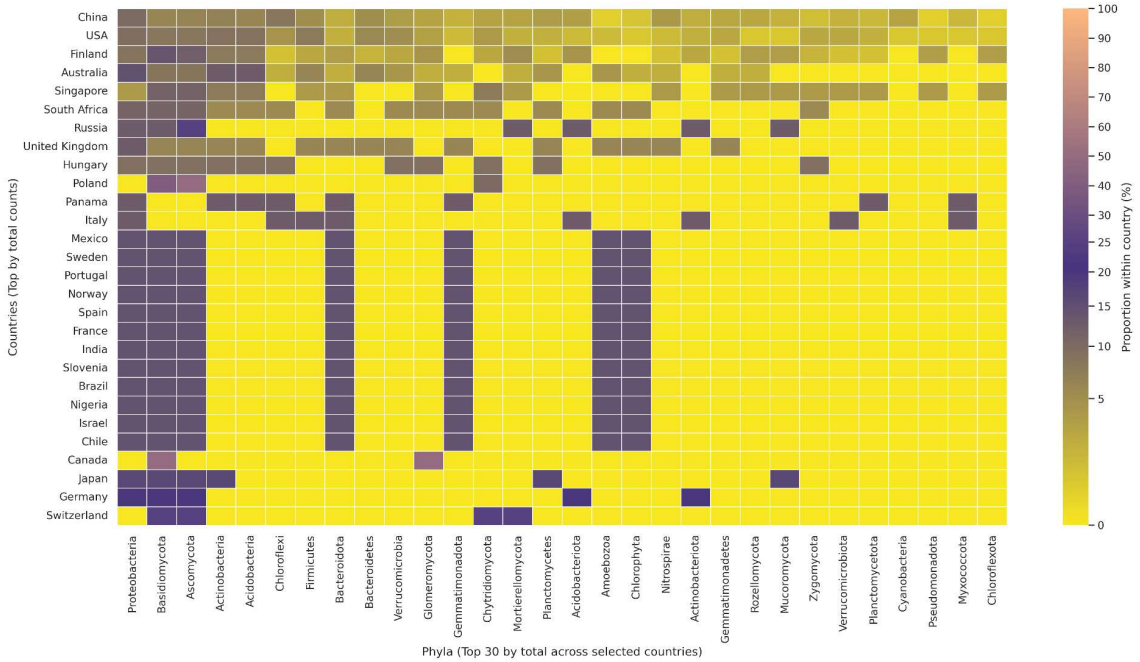
Fig. 10 : Heat map for functional trait categories reported across all studies included in the review. Color intensity reflects the relative representation of each trait category based on a number of studies reporting that function.

Comparative Distribution of Microbial Phyla across Countries

The overall pattern of microbial taxa reported across the included studies were analyzed, and the top 16 most frequently reported taxa were selected for representation (Figure. S1). Different prokaryotic genera were identified across studies, although many simply reported the presence of bacteria without further classification. To identify the geographic distribution patterns of the reported microbial communities, the dominant microbial phyla were compared across different countries (Fig. 12). The heat map and proportional bar charts indicate that the dominant bacterial phyla included Proteobacteria (Pseudomonadota), Actinobacteria (Actinomycetota), and Acidobacteria,

while the dominant fungal phyla included Ascomycota and Basidiomycota. These dominant bacterial and fungal phyla were reported across the globe, especially in China, the United States, Finland, and Australia, which had the maximum number of studies.

In contrast, the less dominant bacterial phyla such as Verrucomicrobia, Gemmatimonadetes, Mortierellomycota, and Planctomycetes had less consistent and scattered distributions. Even though the dominant bacterial and fungal phyla appear to have global distributions, the relative abundance of these dominant microbial communities varied across the countries, which could be due to factors such as climate, vegetation, and methodology. Fig S3 shows



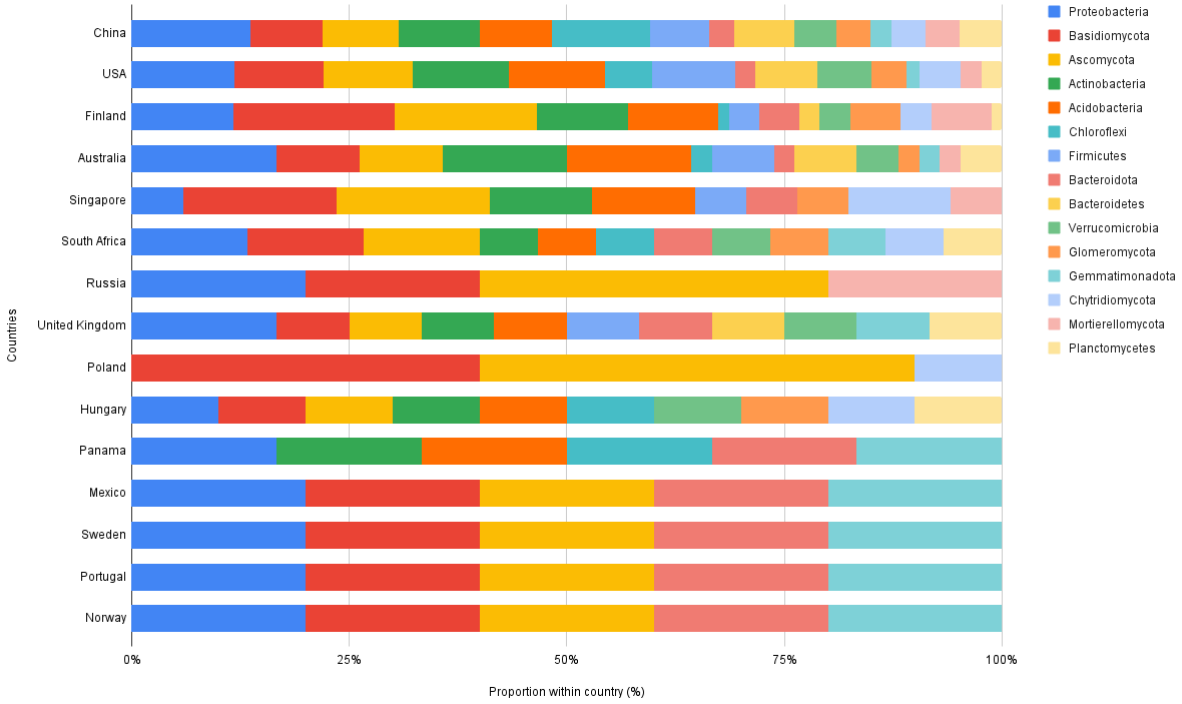


Fig 12. Comparative distribution of dominant microbial phyla in countries included in the review article. (a) Heat map showing the frequency of phyla reported in each country, with the intensity of the color representing the frequency of reporting. (b) Stacked bar charts showing the proportional distribution of major phyla in each country. While dominant phyla such as Proteobacteria, Actinobacteria, and the major fungal phyla Ascomycota and Basidiomycota are reported in most countries, the less abundant phyla vary from country to country.

Functional Category	Studies Reporting (n)	% of Total (147)	General Pattern Observed
Microbial Biomass	18	12%	Mostly MBC/MBN used as activity proxy; often linked to vegetation type or management
Fungal–Bacterial Structure (F:B, Guilds, ECM/AMF)	42	29%	Strong focus on trophic guilds, ECM/AMF dynamics, and symbiotic shifts under urbanization
Functional Genes / Biogeochemical Potential	78	53%	Dominant focus on C and N cycling genes; stress-response and metal tolerance common

Enzyme Activity	24	16%	Mainly C-, N-, P-acquiring enzymes (BG, NAG, phosphatase); respiration indices frequent
Pathogens / ARGs	21	14%	ARG abundance, MGEs, fungal pathotrophs; often linked to anthropogenic inputs

Table 6 Summary of microbial functional categories reported in the included studies (total = 148). Overall, functional gene analysis and biogeochemical potential are the most studied functional categories in the literature, followed by biomass-based functional categories and pathogen-related functional categories.

Table 6 presents a summary of the major microbial functional categories that were investigated in the reviewed research. The most frequently studied category was functional genes and biogeochemical potential, at 53%, which mostly involved carbon and nitrogen cycle processes, as well as stress responses and metal tolerance. Fungal-bacterial community structure, such as ECM/AMF and trophic guild analyses, accounted for the second most frequently studied category at 29%.

Other functional dimensions were less frequently studied in the reviewed research. For example, enzyme activity accounted for 16%, while pathogens/antibiotic resistance accounted for 14%. Microbial biomass accounted for 12%, although it was mostly used as a proxy to study microbial activity instead of diversity.This table suggests that studies have given a lot of attention to the study of nutrient cycles and microbial community structure, while there has been less attention given to the study of biomass and pathogens.

Discussion

This systematic review is a synthesis of current knowledge on the effects of above-ground vegetation on soil microbial communities in urban green spaces. From the total of 148 studies, geographical and thematic biases were identified. Research is highly concentrated in developed countries, including the United States, Europe, and China. Biodiversity-rich countries such as Africa, India, and Southeast Asia are poorly represented which skews our understanding of urban soil microbiomes (Fig. 4). Aside from that, the majority of the studies were conducted in urban parks and forests, while urban wetlands, playgrounds, and highly modified urban spaces are poorly studied.

The synthesis of 148 studies has led to the identification of six major mechanistic pathways by which vegetation and soil microbial communities are interconnected in UGS across a gradient in some studies. The strongest evidence for causality is from studies that experimentally manipulated vegetation establishment, diversity, and input, which have consistently shown positive relationships with microbial multifunctionality, enzyme activities, and nutrient cycling. Conversely, the evidence for the mechanistic pathways of vegetation identity, productivity, and fragmentation is generally reported but based almost entirely on observational studies. This suggests that, while correlations between vegetation characteristics and microbial community structure are common, the experimental evidence for such relationships in urban ecosystems is scarce.

Several consistent patterns were observed in the reviewed studies. For example, higher vegetation diversity and organic matter is generally associated with higher microbial multifunctionality. Urban soil compaction, on the other hand, has been observed to

interfere with symbiotic relationships between fungi and plants, such as ectomycorrhizal (ECM) and arbuscular mycorrhizal (AMF) relationships, which impact the interactions between tree species and microorganisms. Additionally, tree species and functional traits have been observed to impact fungal communities more than bacterial communities, which suggests the significance of the host specificity and litter chemistry. It has already been shown observationally in non urban sites such as meadow steppes by Song et. al, 2025. It will be interesting to understand the same in urban areas which bear the brunt of anthropogenic pressures. Moreover, the urban soil physicochemical characteristics, such as changes in pH, nutrient addition, and heavy metal accumulation, often regulate or modify the effects of vegetation on the microbiome. Overall, the results indicate that the urban vegetation affects the urban microbiome via organic amendments and host specificity, and the urban stressors modify these effects.

Methodological trends also show the rapid advancement of soil microbiome studies. In the past, studies were based on biomass-related methods, such as chloroform fumigation extraction and substrate-induced respiration, which were not very helpful in understanding the diversity of the soil microbiome. From the mid-2010s, the trend has been to use high-throughput sequencing methods, which have been very helpful in understanding the soil microbiome. Studies should focus on classifying microbes into AMR or opportunistic pathogen categories to better understand public health risks in the coming years.

In all studies, the most dominant microbe in the microbial community were bacterial phyla such as Actinomycetota and Pseudomonadota. These are important in the process

of decomposition, nutrient cycling, naturally derived antibiotics and bioactives. However, when it came to eukaryotes, fungi such as Ascomycota and Basidiomycota were the most dominant in the microbial community, also known for their role in soil stability, decomposition and indicate land use efficiency. However, mere phylum level investigation of microbes leaves a lot to our imagination of what we are surrounded by. Genus level characterisation of microbes and non fungal eukaryotes such as algae or protozoa will provide a more complete picture of urban soils. Overall, this review points to major knowledge gaps in the study of vegetation-soil microbiome interactions, which include the need for greater experimental testing of the effects of vegetation, the need to focus more on the diversity and function of vegetation species, and the need for greater global coverage of the regions from which the studies were conducted.

UGS areas have become vital for maintaining ecosystem functions in rapidly urbanizing areas. Incorporating soil microbiome into urban planning will be critical for maintaining urban ecosystems. Soil needs to move from being an overlooked substrate of growth to an ecosystem harboring life continuously and one that is capable of affecting human lives and fauna. Planners can aid this by removing unnecessary soil sealing, creating pockets of biodiversity such as restoring urban forests, prioritising native vegetation over aesthetic value of plants and practicing sustainable urban agriculture.

Conclusions:

This systematic review is based on the comprehensive and systematic screening of available information on the impacts of above-ground vegetation on the soil microbiome community across diverse green spaces within urban areas. The Global South is

572 significantly underrepresented in current research. And so, as a consequence a large
573 section of biodiversity is unexplored. A comprehensive understanding of this
574 biodiversity is crucial to aid in addressing global issues like climate change,
575 deforestation and so on. Since the early 2000s, there has been a steady increase in the
576 number of studies examining the soil microbiome. Moreover, the methodologies used by
577 these studies have also varied, from high-throughput sequencing and experimental
578 approached to surveys and case studies. This suggests a recognition of the ecological
579 relevance of the soil microbiome in the scientific community. Most studies have limited
580 their assessment of the site vegetation of a given site to dominant species. But, it is
581 imperative that all studies thoroughly evaluate vegetation diversity, as it provides a
582 more accurate understanding of the factors that will shape the soil.

583 Researchers should direct their attention toward these variable regions to get a more
584 holistic view of the complex interaction between vegetation and microbiome, which may
585 play a crucial role in urban ecosystems. Since the early 2000s, urban soil microbiome
586 studies have been steadily increasing, with simultaneous advancements in methodology
587 from biomass-based techniques to next-generation sequencing. However, urban green
588 spaces are often evaluated based on dominant species, with little consideration of their
589 diversity. UGS thus may not be receiving the best possible management, as little
590 consideration is being given to their diversity. Microbial understanding also needs to
591 move beyond phylum indication and needs to be put together as a database to better
592 understand soil biodiversity. By collating results from a vast amount of literature, this
593 systematic review aims to provide valuable insights that can aid in managing urban
594 green spaces, thus being beneficial for future research.

Future research priorities

Future studies should emphasize the importance of experimental studies to directly investigate urban vegetation-soil microbiome mechanisms. The current synthesis study revealed that a small proportion of studies use an experimental design to manipulate the vegetation variables. This shows a major gap in the understanding of the causal effects of vegetation on the microbiome. It is essential to extend the current research to the rapidly urbanizing areas of the Global South to get a broader perspective of the range of vegetation and soil ecosystems.One needs to focus on the functional traits of the vegetation, physicochemical properties of the soil, and the functional microbiome with proper classification to understand the effects of vegetation management on the microbiome ecosystem.

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