Extended data



Extended Data Fig. 1 Location of the 27 urban greenspaces selected for shotgun sequencing analyses.

Location of the 27 urban greenspaces selected for shotgun sequencing analyses and covering the entire biogeographical range in Fig. 1.



Extended Data Fig. 2 Ordinary least squares linear regression between plant diversity and the multiple dimensions of ecosystem functions.

Ordinary least squares linear regression between plant diversity and the multiple dimensions of ecosystem functions, n = 56 study sites.



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#	Associations	Rationale
1	Spatial \rightarrow Others	Spatial location (distance equator) on earth determine multiple environmental variables, such as climate, soil physicochemical properties and soil biota, plant attributes, and ecological functioning.
2 3 4 5	$Climate \rightarrow Others$	Climate regulates soil properties, ecosystem multifunctionality, soil biodiversity, plant attributes. For instance, aridity and MAT are expected to be positively associated with plant cover and richness, soil bacteria diversity; while aridity are known to be negatively associated with ecosystem multifunctionality. Aridity is also expected to increase soil pH and alter the texture.
6	Soil ↔ Plant attributes	Plant and soil attributes are known to be largely associated with each other via multiple soil/plant processes. For example, soil fertility is known to promote plant cover. Soil texture and pH can also by factors controlling plant cover, but can also be affected by plants via weathering and shifting soil aggregates.
7	$\textbf{Soil} \rightarrow \textbf{EMF}$	Soil attributes control soil functioning. Soil texture is expected to influence ecosystem functioning by regulating water availability and soil aggregates; and pH can largely influence the rates of ecosystem processes, such as enzymes and metabolic activity.
8	$Management \rightarrow Soil$	Management in this model includes irrigation, fertilization, mowing. For example, fertilization could increase soil fertility, but long-term chemical fertilizations could result in soil degradation, decreasing soil pH, texture.
9	$\mathbf{Plant} \to \mathbf{EMF}$	Plant richness and cover are known to have positive effects on ecosystem multifunctionality. Plant richness is expected to fuel ecosystem functioning by promoting resource heterogeneity and allowing the co-existence of multiple soil organisms.
10	Soil \rightarrow Soil Biodiversity	Soil attributes are among the most important drivers of soil biodiversity. For example, soil pH is the major regulator of bacterial diversity. Soil Texture is also critical for soil biodiversity as its control soil aggregates and water availability.
1	Management → Soil Biodiversity	Management such as fertilization affect soil biodiversity, for example, long-term chemical fertilization significantly decrease the soil biodiversity, while the long-term addition of organic matter could keep soil biodiversity.
12	Plant → Soil Biodiversity	Plant attributes are key controllers of soil biodiversity. Plant cover, for example, provide resources and habitats to soil organisms. Moreover, plant richness increases the heterogeneity of resources (e.g., litter heterogeneity) than can increase the number of niches available for soil organisms.
13	$Management \rightarrow EMF$	Management measures such as fertilization, irrigation, mowing could directly and indirectly affect ecosystem functioning by regulating soil properties, plant attributes, soil organisms.
(14)	Soil Biodiversity → EMF	Belowground organisms comprise a large fraction of global terrestrial diversity, and are responsible for essential ecosystem functions and services which are valued at trillions of dollars annually, including plant productivity, nutrient cycling, organic matter (OM) decomposition, pollutant degradation, and pathogen control. We hypothesized that soil biodiversity is positively correlated with multiple dimensions of ecosystem functioning.

Extended Data Fig. 3 Conceptual model investigating the direct and indirect linkages between soil biodiversity and ecosystem function.

Conceptual model investigating the direct and indirect linkages between soil biodiversity and ecosystem function. (a) A priori structural equation modeling (SEM) metamodel aimed to evaluate the link between soil biodiversity and ecosystem multifunctionality after controlling for key ecological predictors such as space, climate, and soil and plant attributes. (b) Explanations for each association link priori structural equation modeling metamodel.



Extended Data Fig. 4 Random forest model detects soil biota that are accurately predictive of ecosystem multifunctionality in urban greenspaces across the globe.

Random forest model detects soil biota that are accurately predictive of ecosystem multifunctionality in urban greenspaces across the globe. The result of predicting ecosystem multifunctionality in urban greenspaces across the globe using the random forest (RF) models for the soil biota of the selected groups (bacteria, fungi, protists, and invertebrates). Heat maps of the relative abundance of the 77 indicative soil biota and ecosystem multifunctionality. Statistical analysis was performed using two-sided spearman correlations; *P* values were adjusted by Benjamini Hochberg false discovery correction, and indicated by asterisks, '*' represents Benjamini Hochberg-adjusted $0.01 < P \le 0.05$; '**' represents Benjamini Hochberg-adjusted States.



Extended Data Fig. 5 Random forest model detects soil genes that are accurately predictive of ecosystem multifunctionality in urban greenspaces across the globe.

Random forest model detects soil genes that are accurately predictive of ecosystem multifunctionality in urban greenspaces across the globe. (a) Random forest model detects 159 genes in contributing to the ecosystem multifunctionality in urban greenspaces across the globe. (b) Ordinary least squares linear regression between multifunctionality and the proportion of the selected nutrient cycling associated genes: methane monooxygenase subunit A encoding (*pmoA*) gene, ferredoxin-nitrate reductase encoding (*narB*) gene, alkaline phosphatase D encoding (*phoD*) gene, and sulfate adenylyltransferase subunit 2 encoding (*cysD*) gene; n = 27 study sites.