Water Research 289 (2026) 124922

Contents lists available at ScienceDirect

Water Research

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

# Global biogeographic patterns and assembly processes of landfill leachate microbiomes

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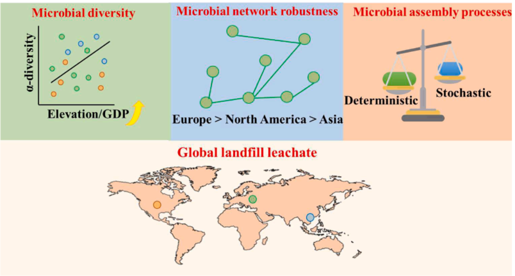
## HIGHLIGHTS

- Regional differences exist in landfill leachate microbial community composition.
- Deterministic factors primarily shaped landfill leachate microbial communities.
- Regional microorganisms have the potential to degrade emerging pollutants.

## GRAPHICAL ABSTRACT



## ARTICLE INFO

*Keywords:*
Landfill leachate treatments
Microbial composition
Cooccurrence network
Assembly mechanism
Global pattern

## ABSTRACT

Approximately 95 % of municipal solid waste is disposed of in landfill globally, generating leachate that is known as a complex mixture of biodegradable and persistent toxic compounds. Microbes are main forces for tackling the toxic leachate but the patterns of microbial assembly in such treatments are largely unknown, limiting the proper optimization of leachate treatment efficiency. This study, for the first time, presents a global-scale analysis involving 151 landfill leachate treatment samples for uncovering mechanisms of microbial assembly from an ecological perspective. The information of microbiome from 97 treatments in Asia, 41 treatments in Europe, and 13 treatments in North America were collected. The results revealed pronounced biogeographic divergence, with Asian samples (particularly those from India) exhibiting lower microbial diversity and richness compared to Europe and North America counterparts. Geographical-climatic and socio-economic factors significantly influenced microbial composition, with elevation and per capita GDP being primary drivers. Further, the community assembly was predominantly governed by deterministic processes. Co-occurrence network analyses demonstrated distinct microbial interaction patterns across continents, with Asian networks being more vulnerable to collapse under external disturbances. This study provides critical insights into the global microbial ecology of landfill leachate treatment, offering a foundation for developing targeted bioremediation strategies.

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https://doi.org/10.1016/j.watres.2025.124922
Received 1 September 2025; Received in revised form 29 October 2025; Accepted 6 November 2025

## 1. Introduction

Landfill has long served as the primary method for managing municipal solid waste (MSW). Over 95 % effectively managed MSW was disposed of via landfilling, exerting immense pressure on surrounding land and the following leachate treatment systems (National Bureau of Statistics Data, 2024 https://www.stats.gov.cn; United Nations Environment Programme, 2024; Emenike et al., 2024). Landfill leachate is a high-strength waste liquid composed mainly of organic and inorganic compounds including heavy metals, and trace-level emerging pollutants (Jayawardhana et al., 2016; Gong et al., 2024). Over time, increasing toxic contaminants from MSWs are mobilized into the leachate, causing excessive levels of emerging contaminants being widely detected (Jia et al., 2024; Laiju et al., 2023). These include per- and polyfluoroalkyl substances (PFAS), pharmaceuticals and personal care products (PPCPs), endocrine-disrupting compounds (EDCs), and related emerging contaminants (Qian et al., 2024). Owing to their persistence, bioaccumulative nature, and toxicity, these pollutants pose significant threats to the environment, ecosystems, and human health (Hu et al., 2024).

Microorganisms play a pivotal role in landfill leachate treatment by breaking down complicated toxic pollutants into smaller and less harmful compounds, thereby facilitating the pollutant removal (Miao et al., 2019). Their structural composition, functional redundancy, and ecological interactions enable the community to adapt to the fluctuating and chemically complex nature of landfill leachate. However, the microbial communities in the leachate treatment plants are “black boxes” characterized by high complexity and diversity of interspecific and intraspecific connections, transcending simple definitions of competition or collaboration. In addition, the physicochemical properties of leachate are far from uniform and are profoundly influenced by the compositions of the landfill waste, the landfill age, and the engineering practices. In particular, variations in regional climate conditions (e.g., temperature and precipitation) and lifestyle factors (e.g., dietary habits and consumption patterns) lead to differences in municipal solid waste composition, resulting in significant heterogeneity of landfill leachate across different geographic regions (Mor and Ravindra, 2023; Wu et al., 2017). This heterogeneity not only affects the concentrations and compositions of pollutants, but also directly influences the structure and function of microbial communities within landfill leachate treatments. In this regard, a mechanistic understanding on assembly of microbial communities, that is a key to deciphering the black box, remains limited.

In recent years, culture-independent techniques, such as high-throughput sequencing, have complemented the traditional culture-dependent methods (e.g., isolation and cultivation) for exploring and deeply understanding microbial communities in landfill leachate facilities (Abiriga et al., 2021; Qian et al., 2024; Yang et al., 2022). Despite these methodological advances, some studies focused on microbial community composition of leachate treatment from different regions have shown significant inconsistencies within the microbiota. For instance, one study identified *Thiomonas* as the dominant genus in landfill leachate in Shaanxi, China (Liu et al., 2022), whereas another research collectively demonstrated landfill leachate from eleven Chinese cities indicated that *Defluviitoga, Sphaerochaeta, Arcobacter, Syntrophomonas*, and *Petrimonas* were the predominant taxa (Zhao et al., 2021). These discrepancies might stem from variations in landfill design, waste composition, treatment strategies, and geographic factors. However, most existing studies are restricted to individual leachate treatment plants or localized areas, leaving a comprehensive investigation from a global level remain unexplored (Lepcha et al., 2025; Zhang et al., 2024a).

This study presents a global meta-analysis of microbial communities in landfill leachate treatments, investigating their composition, biogeographic patterns, and assembly mechanisms. We synthesized published datasets and analyzed raw 16S rRNA gene sequences from public databases to characterize: (i) worldwide microbial diversity patterns, (ii) co-occurrence network structures, and (iii) deterministic vs. stochastic assembly processes. Furthermore, through comparative genomics and functional prediction, we identified regionally distinctive taxa with putative capacities for degrading emerging contaminants. These findings provide a framework for optimizing leachate treatment strategies and advancing global pollutant mitigation efforts.

## 2. Materials and methods

### 2.1. Collection of microbial sequencing data and anthropogenic parameters

Bacterial 16S rRNA gene sequences were obtained from the NCBI Sequence Read Archive (SRA) using the SRA Toolkit (data accessed by September 2024). Raw sequencing reads were identified through database queries using the search terms “landfill leachate” or “landfill leachate microbial community”. Only paired-end Illumina datasets derived from landfill leachate or leachate-associated treatment systems were included. Datasets with incomplete metadata, unclear sample origin were excluded. A total of 270 microbial community datasets from samples of landfill leachate treatments in Asia (China, India, and Japan), North America (Canada), and Europe (Italy, Norway and Poland) were collected from publicly available sources. Detailed information on each sample is provided in the *Supplementary Material.*

The anthropogenic parameters like elevation, human footprint, and per capita GDP etc. surrounding locations of landfill treatments were mainly collected and calculated from publicly released dataset. The detailed anthropogenic parameters and climate information are included in Table S1.

### 2.2. Bioinformatic analysis

The raw sequencing reads were merged (fastq_mergepairs, VSEARCH), followed by primer trimming and quality filtering. The quality-filtered reads were dereplicated and low abundance sequences (minimum size: 13) were removed. An operational taxonomic unit (OTUs) was generated after clustering OTUs at a 97 % similarity threshold using USEARCH. Chimeric sequences were identified and removed using VSEARCH with the SILVA 138 database, and the resulting data were used for feature table construction and taxonomic assignment. The reads with no taxonomic match were discarded. Non-bacterial OTUs, as well as those assigned to mitochondria and chloroplast were removed in R platform (version 4.2). A re-sampling depth of $5.496 \times 10^3$ reads per sample was applied to ensure the data availability for bacterial analysis (R package *vegan*). Least squares linear regression was performed in SPSS to evaluate the relationships between anthropogenic parameters and α-diversity indices. Distance-based redundancy analysis (db-RDA) was conducted in R platform (version 4.2) using forward selection and VIF filtering to identify key anthropogenic drivers shaping microbial community composition. The community’s functional profiles were predicted using the Phylogenetic Investigation of Communities by Reconstruction of Unobserved States (PICRUSt), and PICRUSt2 was used to predict functions (Chen et al., 2024a). The detailed procedures for sequence quality control, OTU clustering, and functional prediction are provided in *Supplementary Material.*

To evaluate compositional differences in microbial communities between countries and continents, principal coordinates analysis (PCoA) based on Bray-Curtis dissimilarities was performed (Chen et al., 2024b). The significance comparisons were tested using a permutational multivariate analysis of variance (PERMANOVA) with the adonis function in the R package *vegan* (Chen et al., 2023). The significance of alpha diversity across countries and continents was determined using Kruskal-Wallis tests in R platform (version 4.2).

### 2.3. Co-occurrence network and robustness analysis

To reduce dataset complexity, low-abundance OTUs ($<$0.01 %) and those with low occurrence frequency (present in $<$10 % of samples at the continental level and $<$25 % at the national level) were removed prior to network construction. The *P*-values of the *t*-test were corrected using the "FDR" method (Zhang and Ren, 2023). Spearman correlation (*P*-value $< 0.01$ and $|r| > 0.7$) were used to generate sub-networks using the R *igraph* package) and exported as a GML format network file for visualization in Gephi software (Zhang et al., 2024b). Topological features of each network were calculated using Gephi, including node count, positive/negative edges, average degree, average path length (APL), network diameter, network density, clustering coefficient (CC), and modularity. The network robustness and vulnerability were estimated using igraph and WGCNA package in R for predicting the structural stability of microbial networks.

### 2.4. Identification of key microorganisms in landfill leachate

The linear discriminant analysis effect size (LEfSe) was used to identify significantly different bacterial taxa as potential biomarkers across different continents or countries (Li et al., 2025). In order to achieve a larger linear discriminant analysis (LDA) value, the standardized scaling factor was set to $1 \times 10^6$. In addition, based on the network analysis in Section 2.3, the nodes in the network were categorized into four groups based on their within-module connectivity (Zi) and among-module connectivity (Pi). Specifically, the nodes with Zi $\geq$ 2.5 and Pi $<$ 0.62 were classified as module hubs, while those with Zi $<$ 2.5 and Pi $\geq$ 0.62 were defined as connectors and the nodes with Zi $\geq$ 2.5 and Pi $\geq$ 0.62 were recognized as the network hubs. Lastly, the nodes with Zi $<$ 2.5 and Pi $<$ 0.62 were categorized the peripheral nodes. Among these, the module hubs, connectors, and network hubs are widely recognized as keystone taxa in the structuring of networks (Kajihara and Hynson, 2024). These biomarkers and keystone taxa are regarded as key microorganisms in landfill leachate.

### 2.5. Quantification of the community assembly process

A null model approach was used to disentangle community assembly mechanisms for quantification of variations in phylogenetic and taxonomic diversity (Gao et al., 2024). The β-nearest taxon index (βNTI) was calculated for indication of phylogenetic β-diversity while the "Bray--Curtis"-based Raup-Crick (RC bray) was employed for quantification of taxonomic β-diversity. A $|\beta\mathrm{NTI}| > 2$ indicates a deterministic process with $\beta\mathrm{NTI} > 2$ representing heterogeneous selection and $\beta\mathrm{NTI} \langle -2$ representing homogeneous selection. In contrast, $|\beta\mathrm{NTI}| < 2$ indicates stochastic processes, further differentiated by RC_bray values: $< -0.95$ for homogenizing dispersal, $\rangle$ 0.95 for dispersal limitation, and intermediate values indicating undominated processes.

## 3. Results and discussion

### 3.1. Diversity of bacterial communities from various leachate biotreatments

After quality control filtering and resampling, 151 high-quality samples out of 270 global samples were retained, with geographic distribution as follows: 97 samples from Asia (China: 75, India: 19, Japan: 3), 41 samples from Europe (Poland: 15, Italy: 26), and 13 samples from North America (Canada) (Fig. 1, *Supplementary Information*). The alpha-diversity results indicated that landfill leachate treatments in Asia exhibited the lowest microbial diversity and richness compared to those

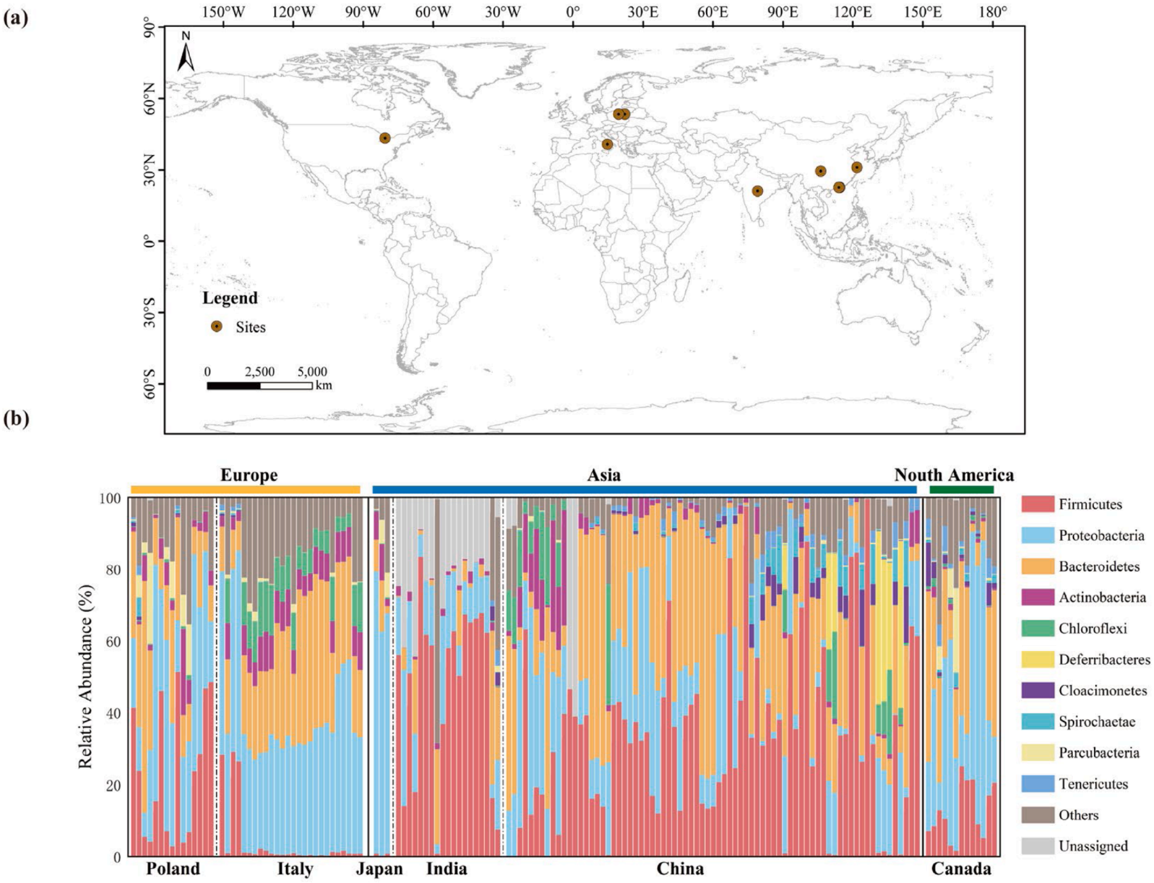

**Fig. 1.** Sample distribution of microbial communities in landfill leachate. (a) collection location, (b) horizontal stack of phylum level.

in Europe and North America, with India showing significantly lower diversity than China and Japan ($P < 0.05$, Kruskal-Wallis test, Fig. S1). Across all samples, a total of 59 bacterial phyla were identified. Though most leachate samples were dominated by members of phyla *Proteobacteria, Firmicutes*, and *Bacteroidetes*, significant differences in microbial composition across continents were observed (Fig. 2 and Table S2). Compared with the continental level, the composition of microbial communities shows greater differences at the national level (Kruskal-Wallis test, Fig. 2c, Table S3).

Among the dominant phyla, *Firmicutes* and *Bacteroidetes* are recognized as the key hydrolytic bacteria, playing critical roles in initial stages of organic matter degradation through hydrolyzing macromolecules such as proteins, polysaccharides, lipids, and nucleic acids. These macromolecules are then fermented into small molecules, including amino acids, sugars, and volatile fatty acids, accompanied by the production of metabolic end-products such as hydrogen, $CO_2$, ethanol, acetate, and other organic acids (Kim et al., 2019; Kvesić et al., 2022; Mayer et al., 2016; Shi et al., 2021). In Asia, the relative abundance of *Firmicutes* was significantly higher than those in the other two continents, while *Bacteroidetes* were significantly more abundant in Europe than in Asia ($P < 0.05$, Kruskal-Wallis test). This variation may be closely related to differences in organic pollution levels in landfill leachate across regions. In particular, landfill leachate in China is characterized by high chemical oxygen demand (COD) levels, ranging from 0.5 to 75.9 g $L^{-1}$ (Qian et al., 2024). Members of *Firmicutes* were particularly efficient in cellulose degradation (Jin et al., 2023; Wei et al., 2021), and some of its genera could withstand extreme environments (Jun et al., 2025; Ziels et al., 2018). In addition, *Bacteroidetes* possess diverse extracellular enzymes and polysaccharide utilization loci that enable them to degrade complex polysaccharides and proteins, contributing to nutrient cycling and breakdown of organic matters under anaerobic conditions (Hao et al., 2021; Hu et al., 2016).

The Venn diagram analysis revealed 46 phyla were shared among microbiomes from global landfill leachate treatments (Fig. 2), while only few unique phyla were identified in specific regions. The Asia and North America shared four phyla (*Hyd24–12, Miscellaneous_Crenarchaeotic, Aenigmarchaeota*, and *Acetothermia*), whereas only one unique phylum was found between Asia and Europe (*Candidate_division_WS6*). Notably, *Dictyoglomi* and *Nanohaloarchaeota* were found exclusively in China and India, respectively, whereas Canada displayed a higher phylum-level uniqueness with five distinct phyla: *Parvarchaeota, SM1K20, SBYG-2791, PAUC34f*, and *LCP-89* (Fig. 2b). The variation in types and concentrations of pollutants in landfill leachates across countries might explain the region-specific distribution of certain non-dominant phyla, such as *Dictyoglomus, Nanohaloarchaeota*, and P*arvarchaeota. Dictyoglomus* generally produces a variety of hydrolytic enzymes, including amylase, mannanase, and xylanase, which degrade polysaccharides (Hamm et al., 2019; Nishida et al., 2011). These enzymes enable *Dictyoglomus* to efficiently break down cellulosic substances commonly detected in landfill leachate, facilitating metabolic interactions among microbial communities and improving the overall removing efficiency of organic matters (Nishida et al., 2011). *Nanohaloarchaeota* and *Parvarchaeota* are typical archaeal taxa adapting to hypersaline environments. Their presence in landfill leachate treatment systems may reflect elevated salinity levels and specific local physicochemical conditions, leading to the selective enrichment of halotolerant species (Nishida et al., 2011). In particular, landfill leachates from Asian regions often contain high concentrations of recalcitrant organic compounds, as well as relatively high salinity, which may contribute to the observed differences in these non-dominant

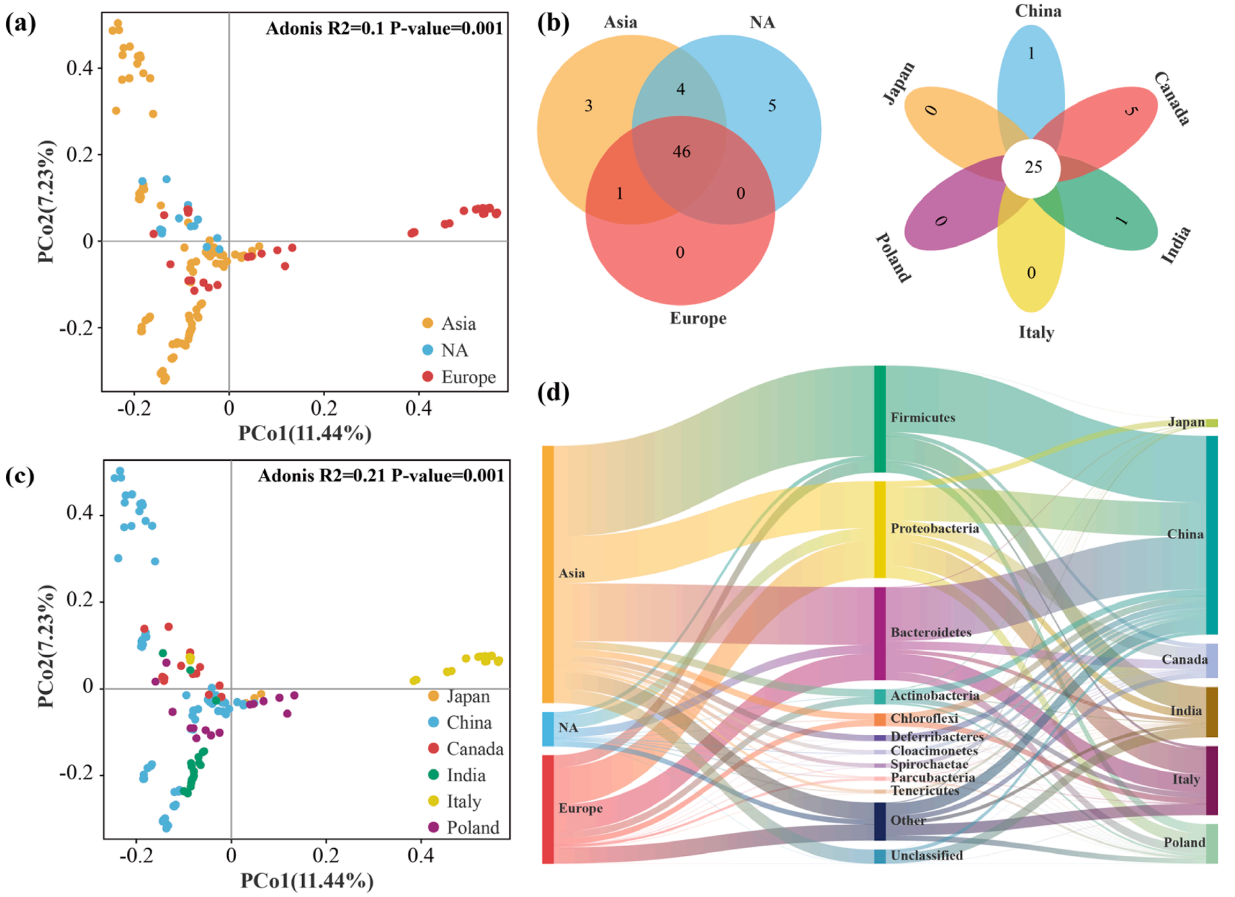

**Fig. 2.** Differences in microbial community composition of landfillleachate across continents and countries. (a) and (c) PCoA based on Bray-Curtis distances;(b) Venn diagram of phylum-level taxa across continents or countries; (d)Phylum-Level taxa composition across different continents or countries.

microbial phyla (Qian et al., 2024).

### 3.2. *Effects of geographical-climatic and socio-economic factors on the diversity of leachate biotreatments*

Regional variations in climate (e.g., precipitation) and lifestyle factors (e.g., dietary habits and consumption patterns) shape the composition of municipal solid waste, thereby contributing to pronounced heterogeneity in landfill leachate across different geographic regions, which in turn alters the diversity of microbial communities. (Mor and Ravindra, 2023; Wu et al., 2017). Accordingly, the correlations between these factors and microbial community diversity were analyzed. The bulk density (oven dry) of surface soil at a depth of 0–5 cm (BDOD 0–5 cm), was identified as one of the most critical factors of leachate microbial α diversity and community composition ($P < 0.05$) (Fig. S2–3). Higher BDOD 0–5 cm values, indicating a higher level of soil compaction and decreasing porosity that significantly resulted in poor aeration and permeability, was unfavored regarding the release of organic matter from MSW. Ultimately, microbial diversity was reduced during biological leachate treatment (Wang et al., 2025a). On the contrary, total precipitation was positively associated with microbial diversity and richness (Shannon and Chao1 indices). This might be due to the enhanced leaching effect on landfilled waste under higher rainfall (Linh et al., 2020), which created moist conditions that accelerated the hydrolysis and fermentation of organic matter (Cossu et al., 2016), thereby increasing microbial diversity in leachate treatment processes.

Among the socio-economic variables, only per capita GDP significantly increased the Shannon and Chao1 indices (Fig. S2–3). Economic development often leads to a higher proportion of kitchen and food waste in municipal solid waste streams (Gu et al., 2017). Such changes in waste composition provide a broader range of substrates and niches for microbial colonization, thereby enhancing community diversity. By contrast, Population Count, Population Density, and Road Density were significantly negatively correlated with microbial α diversity (Fig. 2). Higher values of these factors typically indicate stronger anthropogenic disturbances, such as land-use change, industrial and domestic wastewater discharge, increased waste generation, and traffic-related pollution (Valderrama et al., 2024). These disturbances may increase the

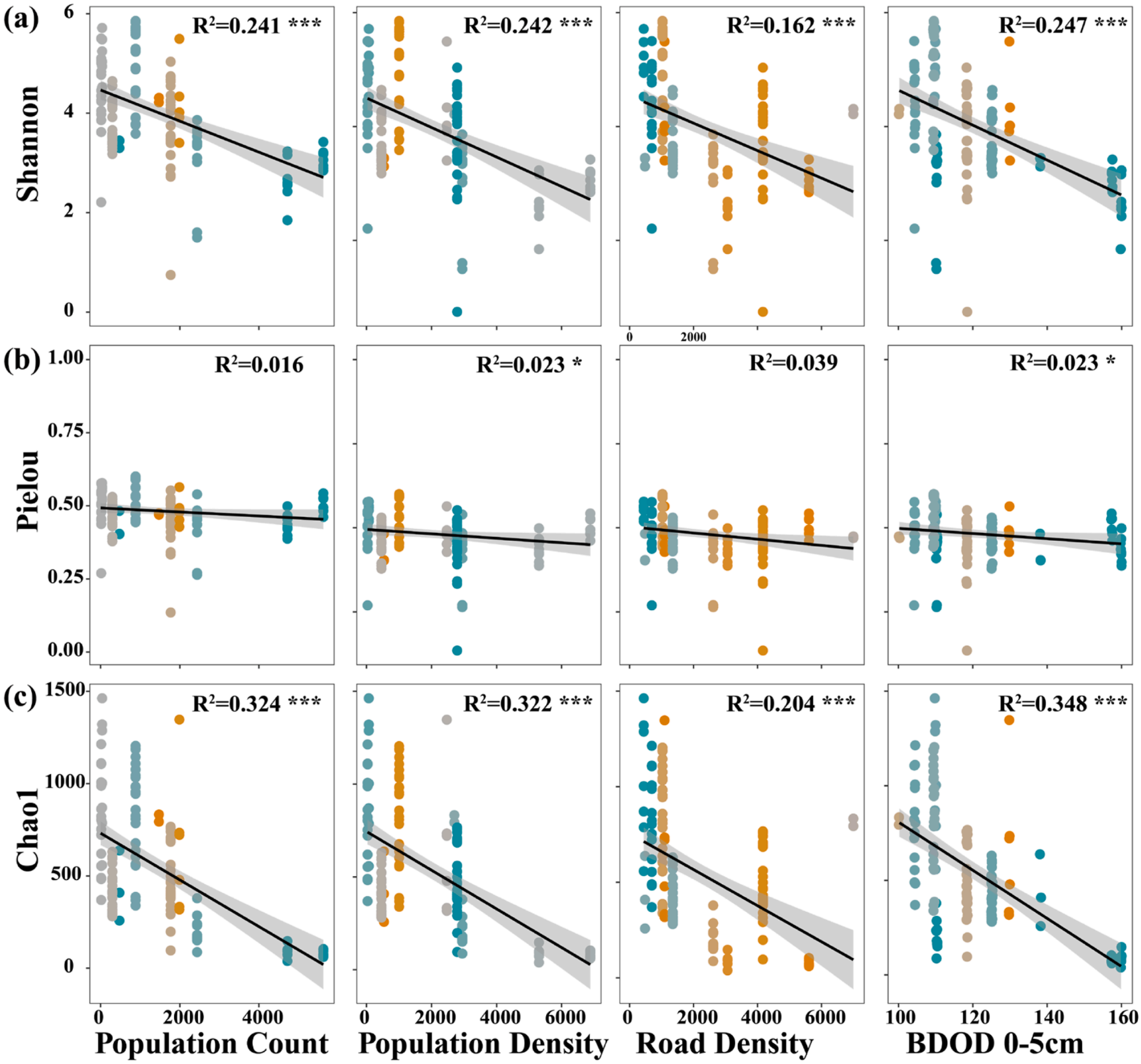

**Fig. 3.** Effects of geographical–climatic and socio-economic factors on the α-diversity of leachate microbial communities. Adjusted $R^2$ and P-values are shown in the figure. Note: BDOD 0–5 cm represents the bulk density (oven dry) of surface soil at a depth of 0–5 cm.

concentrations of emerging contaminants in leachate, including EDCs, PPCPs, heavy metals, and microplastics (Qian et al., 2024), which impose selective pressures on microbial communities and exert complex, mixed effects on α diversity (Gamboa et al., 2025).

Overall, these results demonstrate that the composition of landfill leachate microbial communities is governed by an interplay of geographic–climatic and socio-economic factors, with significant synergistic effects between these drivers determining community composition.

### 3.3. Patterns of co-occurrence complexity

Beyond the taxonomic structures, potential biological interactions identified from co-occurrence networks could complement new insights into complex communities (Zhang and Ren, 2023). The co-occurrence network for Asia consisted of 531 nodes and 8014 edges, whereas the networks for Europe and North America comprised 858 nodes with 36, 000 edges and 851 nodes with 20,545 edges, respectively (Table S4). The bacterial communities in European and North American treatment plants exhibited higher α-diversity, indicated more complex networks compared to those observed in Asian (Fig. 3, S1). Theoretically, complex interactions are often associated with greater robustness and higher stability of the entire community, making it more resilient to environmental disturbances such as hydrologic shock of unfavored contaminants and fluctuation of substrates bioavailability (Liu et al., 2025; Steele et al., 2011). Similarly, a larger network diameter and higher modularity coefficient generally reflect increased resistance to disturbance, as modularity buffers the impacts of taxa loss by localizing disruption effects within individual modules (Table S4) (Hernandez et al., 2021). However interestingly, though communities in Asian treatment plants exhibited the highest network diameter (Asia: 22, Europe: 10 and North America: 18) and modularity coefficient (Asia: 0.561, Europe: 0.36 and North America: 0.35) among the three continents, its network was the most fragile likely due to its significantly lower number of keystone taxa (Asia: 2, Europe: 7 and North America: 33) (Fig.S4). It was also concluded from network architecture in European and North American leachate treatment plants as they harbored more key nodes, contributing to enhanced robustness by mitigating the cascading effects of node loss. Additionally, the results of co-occurrence network suggest that the microbial communities predominantly exhibit cooperative, rather than antagonistic interactions. While cooperative interactions can enhance functional complementarity, they may also generate positive feedback loops, rendering the community more vulnerable to collapse if key taxa decline (Hernandez et al., 2021).

At the national level, notable differences in network composition were observed. (Fig. 4). For examples, the network of Italian treatments show the interactions (62.70 %) between nodes are primarily dominated by *Planctomycetes* and *Proteobacteria*, which were reported widespread in the environment and mainly involved in global carbon and nitrogen cycles (Jeske et al., 2015; Spain et al., 2009; Wiegand et al., 2018). Additionally, the association of Proteobacteria with the degradation of organic contaminants, including pharmaceuticals, has been well documented in constructed wetlands (Li et al., 2024). In these systems, *Planctomycetes* have been associated with the biodegradation of emerging organic contaminants (e.g., sulfamethoxazole) and even proposed as potential bioindicator for pollutant removal (Peng et al., 2025). These two phyla may exhibit higher community adaptability, which enhances the complexity of co-occurrence networks and contributes to greater microbial community stability (Fig. 4).

ZiPi analysis was performed to identify the keystone taxa (i.e., nodes) in the co-occurrence networks by classifying them into network hubs,

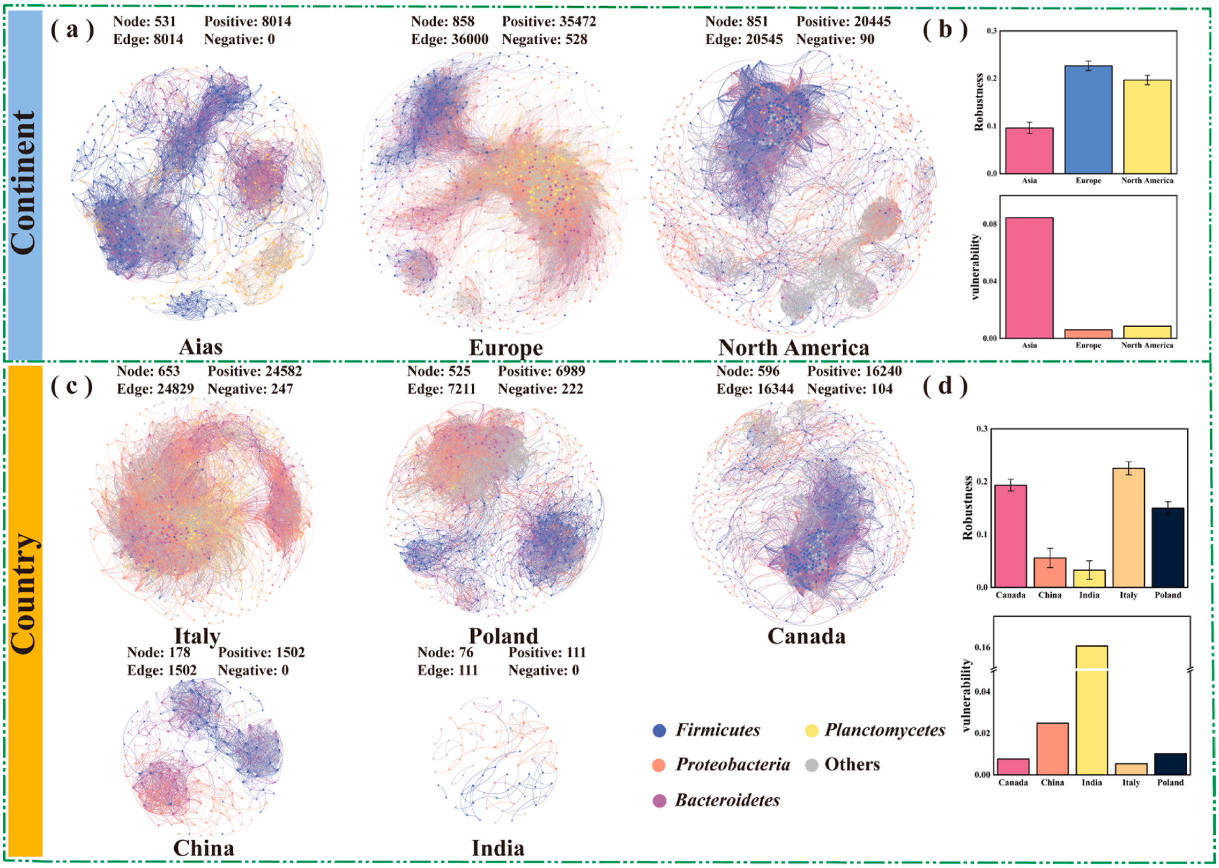

**Fig. 4.** (a) and (c) Co-occurrence network of Continent and Country. The sizes of the nodes (OTUs) are proportional to the degree. The taxonomy of each node is shown in different colors in the phylum level. (b) and (d) Network robustness and vulnerability. Robustness measured as the proportion of taxa remained with 50 % of the taxa randomly removed from the network. Each error bar corresponds to the standard deviation of 100 repetitions of the simulation.

module hubs, and connectors (Fig. S4) (Zhou et al., 2024). It turned out that the network of microbial community in North American leachate treatments exhibited the highest number of key nodes (with 3 connectors and 30- module hubs) compared to those in Asian (2 module hubs) and Europe (2 connectors, 3 module hubs, and 2 network hubs) leachate treatments. These key nodes were predominantly affiliated with *Bacteroidetes* (47.62 %) and *Firmicutes* (26.20 %), along with representatives from eight other phyla. At the national level, the network derived from Italian leachate treatments contained the highest number of key nodes (23 connectors, 8 module hubs, and 6 network hubs). The taxonomic composition of these nodes indicated a significant diversity in microbial communities spanning 12 phyla. Notably, among the six network hub nodes identified in Italian samples, five were affiliated with *Saccharibacteria*, which are widely distributed across various natural environments and have been recognized as active participants in hydrocarbon-degrading microbial consortia (Dong et al., 2024; Figueroa-Gonzalez et al., 2020). Their presence in contaminated habitats suggests a key ecological role in degrading complex organic pollutants and maintaining microbial community stability under stress conditions.

### 3.4. Deterministic processes dominate microbial community assembly

Microbial community assembly is generally influenced by deterministic and stochastic processes (Zhou and Ning, 2017). Understanding the assembly of microbial community in landfill leachate, specifically the balance between deterministic or stochastic processes, is crucial for predicting ecological stability and treatment performance. Deterministic processes, driven by environmental filtering, shape microbial composition and can lead to adaptive evolution, which is reflected in the structure of interaction networks. Consequently, the deterministic assembly pattern provides valuable insights into the long-term performance and stability of the microbial communities underpinning leachate treatment. Linking these assembly processes to microbial adaptation strategies not only clarifies the ecological mechanisms at play but also informs strategies for enhancing treatment efficiency and controlling environmental risk (Wu et al., 2025). To further elucidate their relative contributions in shaping landfill leachate microbiomes, βNTI and RCbray were used to assess the microbial assembly mechanisms. The results indicated that both deterministic and stochastic processes significantly influenced microbial assembly in landfill leachate treatments (Fig. 5). Neutral model analysis reveals that deterministic processes dominated bacterial community assembly in most countries (except China), indicating that microbial β-diversity is shaped by both abiotic and biotic factors (Wang et al., 2013). Stochastic processes contribute to the construction of a more comprehensive organic matter metabolic network and enhance the functional potential of microbial communities involved in landfill leachate treatment (Wu et al., 2025). The deterministic processes affecting community assembly were mainly composed of homogeneous selection, which played a crucial role in the assembly of prokaryotic communities and might promote the similarity of communities (Wang et al., 2022; Zhou and Ning, 2017).

### 3.5. Regional divergence of potential functions

In recent years, growing quantities and diversity of emerging contaminants have been detected in landfill leachate (Jayawardhana et al., 2016; Qian et al., 2024). Enhancing microbial tolerance and degradation capabilities for these contaminants has thus become critical in leachate biotreatment systems. This study conducted functional predictions of key microorganisms (Table S5–6) to further elucidate their potential roles in the degradation of emerging contaminants. KEGG annotation was employed to characterize pollutant-degradation genes among differentially abundant microbes (Fig. S5). Several species within *Bacteroidetes* contained a significant number of genes associated with the

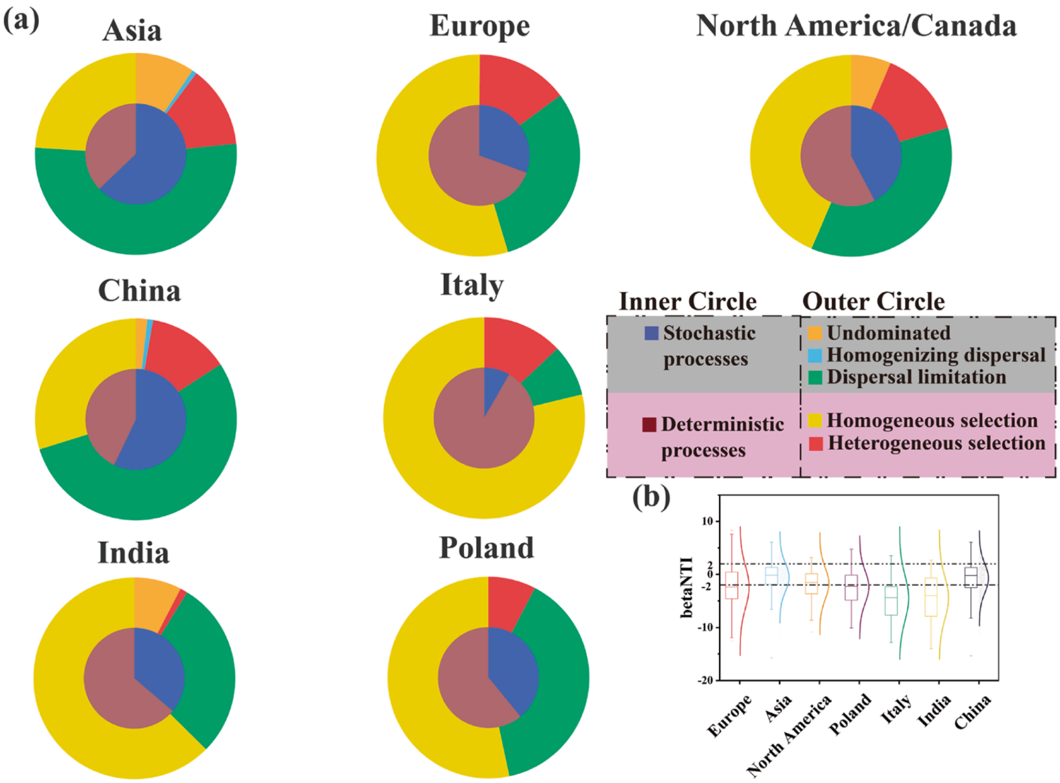

**Fig. 5.** Neutral models and null models assessed random/deterministic assembly processes of the community. (a) Assembly of bacterial communities based on the null-model-based framework. The inner circle represents the contribution of stochastic and deterministic processes to community assembly. The outer circle represents the percentage of detailed ecological processes statistically assigned to stochastic or deterministic processes. (b) Beta-nearest taxonomic index of communities.

degradation of plastics (Lv et al., 2024; L. Wang et al., 2025), PFAS (Lu et al., 2024), and ibuprofen (Rutere et al., 2020) with their abundance being significantly higher in Asian leachate treatments, particularly the ones in China and Japan ($P < 0.05$). Notably, *Pseudomonas*, a *Proteobacteria* genus, exhibited significantly greater abundance in leachate treatment systems from North America, Poland, and Italy relative to other geographical regions. This genus is known for its capacity to degrade various emerging contaminants, such as endocrine disruptors (Liao et al., 2010), bisphenol A (Vijayalakshmi et al., 2018), plastics (Wilkes and Aristilde, 2017), and PFAS (Bygd et al., 2021). Collectively, these microbial taxa demonstrate dual significance: as functional candidates for contaminant bioremediation and as ecological indicators of pollutant dynamics in diverse environments.

## 4. Conclusion

This study, for the first time, provides comprehensive characterization of landfill leachate microbiomes on a global scale, analyzing 151 samples collected from 10 cities across 6 countries spanning three continents. Altitude and per capita GDP are recognized as the key factors determining the structure of the community. Moreover, the deterministic processes were found to the dominant microbial community assembly in landfill leachate. At the co-occurrence network level, *Proteobacteria, Actinobacteriota*, and *Bacteroidota* exhibited significant continental differences in their relative abundances, which in turn contributed to distinct variations in network structures across continents. By establishing the global framework for landfill leachate microbiomes, this work provides a critical basis for future research to identify the environmental drivers of community assembly and experimentally validate the ecological functions of keystone taxa, thereby paving the way for tailorable biotechnologies for regional leachate treatments and development of contaminant removal strategies.

## CRediT authorship contribution statement

**Xinqiang Chen:** Writing – review & editing, Writing – original draft, Investigation, Data curation. **Yunqi Huang:** Writing – original draft. **Xiangrong Zhu:** Writing – review & editing, Supervision, Conceptualization. **Cuifen Gan:** Validation, Software, Formal analysis. **Wenwen An:** Visualization, Software, Formal analysis. **Yongqin Liu:** Writing – review & editing. **Shaofeng Zhou:** Writing – review & editing, Project administration, Funding acquisition, Conceptualization. **Meiying Xu:** Writing – review & editing, Project administration, Funding acquisition, Conceptualization.

## Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

## Acknowledgments

This work is jointly supported by the National Key Research and Development Program of China (2021YFA0910300), National Natural Science Foundation of China (42377132), Young Talent Project of GDAS (2024GDASQNRC-0201), GDAS' Special Project of Science and Technology Development (2024GDASZH-2024010102), the Science and Technology Project of Guangzhou (2024A04J3593), the Guangdong Special Support Plan for Outstanding Talents (No. 2023JC07L096) and the High-end Foreign Experts Project of China (No. S20240268).

## Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.watres.2025.124922.

## Data availability

All data supporting the findings of this study, including sequence accession numbers and associated metadata, are provided in the Supplementary Information.

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