

<https://doi.org/10.1038/s43247-025-02619-0>

Plastisphere provides a unique ecological niche for microorganisms in *Zostera marina* seagrass meadows



Xin Hou^{1,2}, Xiaoran Li², Yunan Lin², Changjun Li¹✉, Ruijia Jing², Lei Zhang³, Jiamin Li³, Ziming Jiang³, Sen Wang³, Qiangqiang Jiao², Xiaotong Wang⁴, Di Zhang¹, Wenchang Liang¹, Lixin Zhu⁵, Xiaohui Wang⁵, Daoji Li⁵ & Xianhua Liu²

Seagrass meadows are renowned for their associated ecosystem services and carbon sequestration capacity, with microorganisms playing a crucial role. However, the invasion of microplastics may disrupt these processes. Here, we conducted a one-month in-situ incubation of three prevalent types of microplastics in the seagrass meadow of Swan Lake, China. The results showed significant differences in microbial communities between the plastisphere and natural matrices. Cyanobacteria exhibited a strong preference for polyethylene terephthalate, and microplastic shape and their contact area with water may be key factors in shaping microbial communities. Meanwhile, microplastic invasion can shift carbon- and nitrogen-fixing microbes and related genes, thereby changing seagrass meadows' carbon and nitrogen cycles. This may impact the carbon sequestration capacity of seagrass meadows and pose potential risks of water blooms. Additionally, the potential ecological risks posed by the large number of resistance genes adsorbed by microplastics in the ecosystem are also worthy of attention.

Seagrass meadows provide critical ecological services, including habitat provision, substrate stabilization, water purification, and biodiversity maintenance^{1,2}. Notably, these ecosystems have emerged as pivotal players in climate change mitigation, exhibiting exceptional capacity for long-term blue carbon sequestration^{3,4}. They store approximately twice as much carbon per hectare as terrestrial ecosystems, with an estimated global soil organic carbon of 19.9 billion tons, representing a carbon stock of equivalent magnitude to the tidal marshes and mangroves^{4,5}. However, seagrass meadows are currently degrading at an alarming rate, with an annual loss rate of about 1.5%, which greatly impairs their carbon storage capacity⁶. Human activities, littering, habitat destruction, typhoons, climate change, and the invasion of alien species are all contributing to the rapid degradation of seagrass meadows^{7–9}. Among these, human activities have the most significant impact on the degradation of seagrass meadows, including water pollution, overdevelopment, and habitat destruction¹⁰. In recent years, microplastics (MPs) pollution has emerged as a pressing issue in marine environmental contamination, increasingly infiltrating coastal vegetation ecosystems. A critical review by Li et al.¹¹ reveals that MPs are widely distributed in global seagrass beds, including within seagrass tissues, sediments, and organisms inhabiting these ecosystems, with pollution levels

likely to intensify in the future. MPs contamination can impair seagrass photosynthesis, alter water and sediment conditions, and consequently disrupt ecological functions such as carbon sequestration^{12–14}. However, these potential adverse effects and their underlying mechanisms have not yet been comprehensively assessed. Therefore, paying attention to and protecting the health of seagrass meadows is crucial for maintaining their capacity to provide ecosystem services.

Seagrass meadows predominantly sequester organic carbon through autochthonous and allochthonous sources, with the majority stored in soils^{15,16}. Autochthonous carbon originates primarily from seagrass biomass and associated epibionts via photosynthesis and chemosynthesis, subsequently buried in sediments through detrital deposition and mortality¹⁷. Allochthonous carbon consists of exogenous organic matter intercepted and sedimented by seagrass canopies, derived from terrestrial inputs, marine detritus, and other aquatic vegetation¹⁸. Additionally, the relative contribution of these carbon sources in soil organic carbon pools is strongly influenced by meadow properties, habitat geomorphology and bioregion^{19,20}. The storage capacity of autochthonous carbon in seagrass meadows primarily relies on two mechanisms: the Biological Pump (BP)²¹ and the Microbial Carbon Pump (MCP)²². Seagrasses assimilate dissolved

¹School of Ocean, Yantai University, Yantai, China. ²School of Environmental Science and Engineering, Tianjin University, Tianjin, China. ³Xinanhe Wastewater Treatment Plant, Yantai City Drainage Service Center, Yantai, China. ⁴School of Fisheries, Ludong University, Yantai, China. ⁵State Key Laboratory of Estuarine and Coastal Research, East China Normal University, Shanghai, China. ✉e-mail: lichangjunv587@ytu.edu.cn

CO₂ of water column into organic carbon via high photosynthetic rates, resulting in substantial primary productivity and biomass accumulation²³. Seagrass tissues exhibit high concentrations of recalcitrant structural compounds (cellulose and lignin), which confer strong resistance to microbial mineralization under anaerobic sedimentary conditions. When coupled with rapid burial dynamics, this biochemical persistence enables multi-millennial carbon sequestration in coastal sediments²⁴.

The microbial-driven MCP utilizes organic carbon in the water column to produce refractory dissolved organic carbon (RDOC), which resists degradation and accumulates in ecosystems over the long term²⁵. This process is a crucial pathway for enhancing oceanic carbon storage, due to its exceptional carbon sequestration capacity, it has been described by Science magazine as the invisible hand behind a vast carbon reservoir²⁶. Compared to the BP, the influence of the MCP on the carbon sequestration capacity of the entire seagrass meadows ecosystem may be more significant. Furthermore, microorganisms play an equally critical role in the functioning of BP. In nitrogen-depleted waters, the ability to fix nitrogen is key to the successful continuation of seagrass meadows²⁷. Nitrogen-fixing microorganisms attached to seagrass leaves and present in the rhizosphere can alleviate ammonia limitation in seagrass ecosystems through microbial nitrogen fixation (MNF), thereby enhancing ecosystem productivity²⁸. Some studies have shown that up to 50% of the ammonia required in seagrass meadows is supplied by MNF²⁹. Additionally, research by Patriquin and Knowles has demonstrated that, in oligotrophic environments, MNF in seagrass meadows can provide 1–1.5 times the ammonia necessary for plant growth (6.9–23 mg N per g)³⁰. Bacteria are the main components of microorganisms in the environment³¹, and nitrogen-fixing microorganisms are also primarily composed of bacteria, such as cyanobacteria, photosynthetic bacteria, and some symbiotic bacteria, etc³². For example, Wiebke et al.³³ reported a symbiotic relationship between seagrass meadows and nitrogen-fixing rhizobia (*Candidatus Celerinatantimonas neptuna*), suggesting that seagrasses have independently evolved a mechanism to cope with nitrogen limitation. Similar to many terrestrial plants, the ancestors of *Ca. C. neptuna* and its relatives likely enabled marine flowering plants to invade and thrive in nitrogen-poor marine habitats, their descendants form the foundation of highly efficient blue carbon ecosystems³³. Thus, ammonia-fixing bacteria and their symbionts play an important role in the sustainability of nitrogen supply and productivity in seagrass meadows, and are the main contributors to new productivity in nutrient-poor seas.

Admittedly, the essential functions of seagrass meadows and their associated microbial communities are increasingly being recognized. However, the extensive intrusion of MPs may be disrupting these functions. Acting as the first barrier to land-based MPs entering marine environments, seagrass meadows, with their high biomass and strong hydrodynamic buffering capacity, have effectively become sinks for MPs^{34,35}. Similar to carbon sequestration capacity, this enrichment effect can also vary due to differences in meadow type, tides, and geographical location^{34–36}. In addition to the MPs themselves, the land-based pollutants they carry, such as heavy metals, antibiotics, and resistance genes, may also adversely affect seagrass meadows and their microbial communities^{37–39}. Additionally, emerging research also demonstrates that novel pollutants, such as sunscreens, can disrupt photosynthetic systems and induce microbiome shifts of seagrasses (*Cymodocea nodosa*), leading to profound perturbations in carbon metabolism pathways⁴⁰. Our team has previously reviewed the mechanisms by which MPs may affect carbon sequestration in seagrass meadows, focusing primarily on how MPs influence the MCP and indirectly impact the BP¹². Through our review, we found that studies on the effects of MPs on seagrass meadows are highly limited, particularly concerning their impact on microbial communities. To address this gap, we designed a one-month in situ experimental study focusing on three prevalent MP polymers found in seagrass ecosystems—polypropylene (PP), polyethylene (PE), and polyethylene terephthalate (PET)¹¹. Although numerous studies have investigated the impacts of MPs on aquatic ecosystems, most have remained focused on a single dimension (e.g., microbial communities or functional genes). In this study, we conducted a comprehensive multidimensional

analysis comparing MPs with their native substrates (water and sediment) using multiple indicators and analyzed their interactions. These indicators include: (1) Material variation (structure, hydrophobicity, functional groups, biofilms); (2) Microbial community diversity and stability (e.g., Shannon, Chao1, network topology features, robustness, community variability, vulnerability, etc.); (3) Community composition (e.g., relative abundance, absolute abundance, Metagenomic gene sets (MGS), differential taxa, LEfSe analysis, specificity, and occupancy); (4) Carbon and nitrogen cycling genes (e.g., gene composition, structure, pathways, and contributions); (5) Antibiotics resistance genes (ARGs), metal resistance genes (MRGs) and biocide resistance genes (BRGs) (composition, structure, and contributions). This multidimensional analysis aims to comprehensively and accurately evaluate the impact of massive MPs intrusion on microbial communities and functional genes in seagrass meadow ecosystems. The findings will provide insights for accurate evaluation of the ecological functions and carbon - sink capacity of seagrass meadows.

Results and discussion

Material changes and biofilm enrichment

By integrating the results of scanning electron microscopy (SEM) and biofilm optical density (OD) measurements, we found that the biofilm content adhered to PET was significantly higher than that on PP (approximately 3-fold higher, $p < 0.05$), while that on PP was in turn significantly higher than that on PE surfaces (approximately 2-fold higher, $p < 0.05$) (Fig. 1). This may be due to their different shapes, resulting in different specific surface areas, which affects the biofilm content^{41,42}. As seen from Fig. 1a2–c2 and a3–c3, PET predominantly exhibits a grid-like structure, which provides a large specific surface area, a characteristic that stems from the mask's need for effective barrier properties. In contrast, the structural complexity and specific surface area of PP films are moderate, whereas PE ropes exhibit the lowest structural complexity and provide fewer attachment points for microorganisms, leading to lower biofilm adhesion. The hydrophilicity results demonstrated that all three MPs were highly hydrophobic prior to in situ incubation, with hydrophobicity ranked as PET (104°) > PP (98°) > PE (95°), but the differences were statistically insignificant. After in situ incubation, the hydrophobicity of PET was greater than that of PE, which was greater than that of PP (Details on the hydrophobicity test and criteria are in Fig. S1 and its note). This change in hydrophobicity is likely the result of the combined effects of wave impact, chemical corrosion, UV aging, and biofilm attachment^{43–46}.

Fourier-transform infrared (FTIR) analysis revealed that after in situ incubation, the three types of MPs shared some similar features. For instance, their characteristic peaks at about 466 cm⁻¹ and 1020 cm⁻¹ were all enhanced. These peaks are associated with molecular skeletal deformation vibrations and C–H rocking vibrations, respectively^{47,48}. The intensity changes indicate alterations in the plastic surface structure, which may be due to wave impact, light aging, or partial microbial degradation⁴⁸. Unlike PET, PE and PP MPs exhibited new characteristic peaks at about 1640 cm⁻¹ and 3300–3500 cm⁻¹. These peaks are likely related to oxidative or biological degradation^{49,50}. Ultraviolet radiation or certain enzymes and other metabolites secreted by microorganisms might lead to the oxidative degradation of PE and PP^{51,52}. During the degradation process, the polymer chains may break, resulting in the formation of structures containing carbonyl, hydroxyl, or other oxidative products⁵³. As the hydrological and other environmental conditions of the placement sites are basically the same, the differences are mainly in the samples themselves. It is probably the behavioral differences of the microbe communities attached to the samples that have resulted in the differences in those characteristic peaks⁵⁴.

Differences in microbial diversity and community composition among samples

Bacteria are the main part of the sample's microbes. In water, they account for 88.88%–91.28% of microbial community copies per unit sample. On sediments and MPs, their proportion is significantly higher ($p < 0.05$), exceeding 95.87% (Fig. S2). This is mainly because biofilms readily form on

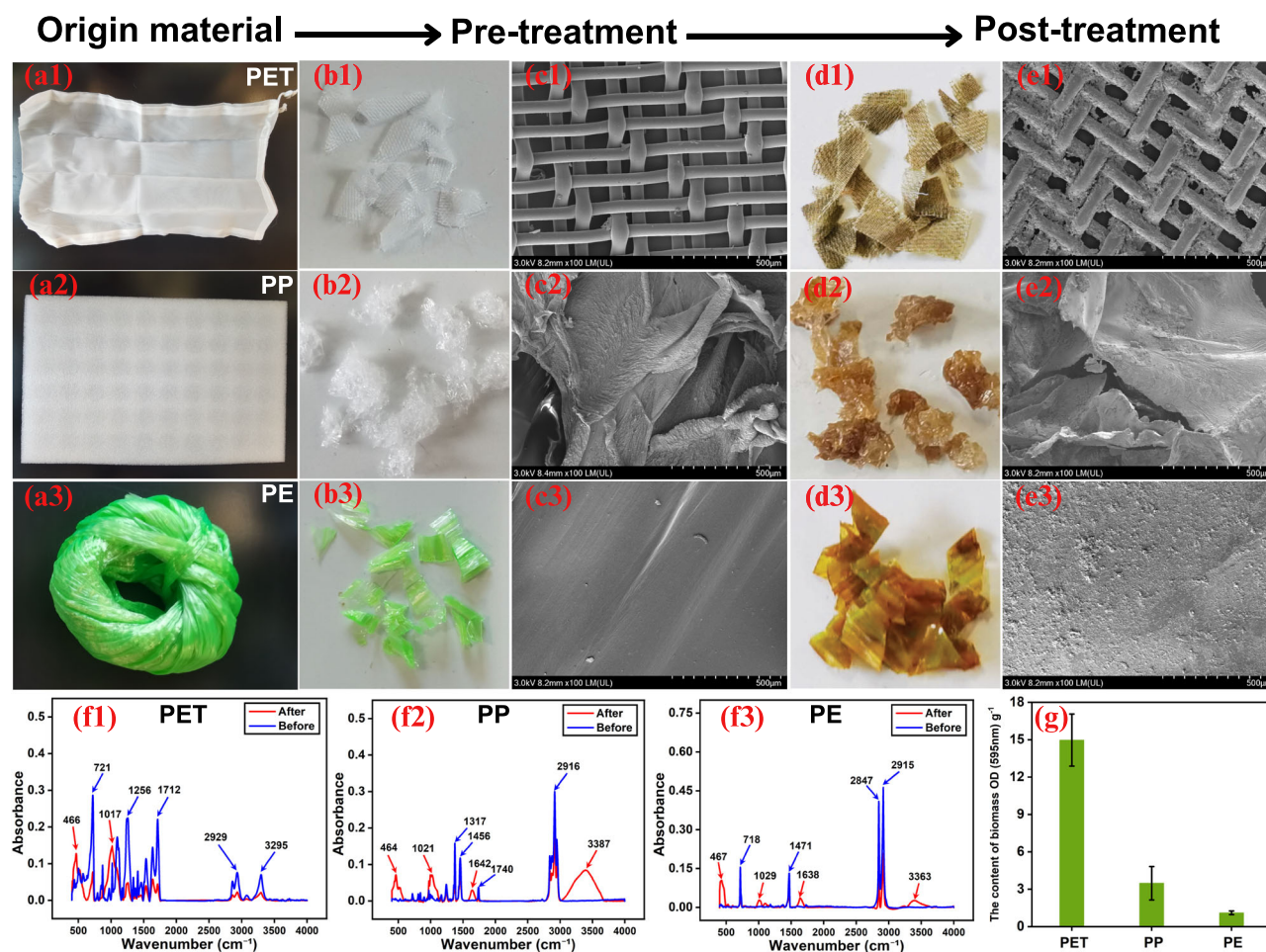


Fig. 1 | Plastic processing workflow and changes in material properties and biofilm accumulation before and after in situ incubation. a1–a3 PET mask, PP film, PE rope; **b1–b3** Trimmed; **c1–c3** SEM images before incubation; **d1–d3** After

incubation; **e1–e3** SEM images after incubation; **f1–f3** FTIR before and after incubation; **g** Biofilm content (OD values). The error bars in the bar charts represent the standard deviation.

and between solid particles, favoring bacterial enrichment⁵⁵. The bacterial diversity and stability in different samples also show significant differences (Fig. 2). Firstly, regarding diversity, we analyzed the differences in bacterial diversity among the samples from multiple dimensions, including unique amplicon sequence variants (ASVs), richness, diversity, and community distance (Fig. 2a–f). From the perspective of unique ASVs, the MPs had fewer unique ASVs (500–907) compared to water (1231) and sediment (1334), with PET (907) exhibiting more unique ASVs than PE (768), and PE having more than PP (500). Regarding alpha diversity, the richness (Chao1) of PE and PP was similar to that of sediment, while PET was more similar to water and significantly lower than PP, PE, and sediment. The diversity indices (Shannon and Simpson) showed that water had significantly lower diversity than the other samples, followed by PET and sediment, while PE and PP exhibited slightly higher diversity than sediment. The rank-abundance curve further confirms the above findings. β -diversity analysis (Fig. 2f) shows that the bacterial community compositions of the samples are significantly different (ADONIS, $R = 0.956$, $p < 0.001$). The microbial communities of PE and PP are similar to each other, while those of the other samples differ greatly in species composition.

Overall, these different indicators reflect similar characteristics, namely, there are significant differences in microbial diversity among different samples. Among them, the diversity features of water and PET MPs are more unique, while sediment, PP and PE MPs exhibit more similar diversity. These differences may be caused by various factors, such as additives, surface charge, functional groups, shape, roughness, hydrophobicity, and biological affinity of MPs^{56–59}. For example, regarding unique

ASVs, water and sediment, as natural samples, tend to have higher microbial affinity compared to MPs, and their surface may have a relatively higher number of unique ASVs⁶⁰. PET MPs, due to their complex surface structure and higher specific surface area, have a larger contact area with water, making their microbial community characteristics more similar to those of water. The hydrophobicity, surface functional groups, and roughness of PE and PP are similar, while PET surfaces exhibit greater differences in functional groups, hydrophobicity, and surface roughness (Fig. 1 and Fig. S2). These factors may be the primary reasons for the differences in microbial diversity on the surfaces of different MPs. For instance, research by Sun et al.⁵⁶, indicates that the higher hydrophobicity of MPs is a key factor in their ability to carry a variety of microorganisms and differing hydrophobicities may result in the transport of different microbial communities. Different functional groups also affect the microbial adsorption characteristics⁶¹. For instance, the study by Zettler et al.⁶² indicated that microorganisms of the phylum Proteobacteria and Bacteroidetes are more inclined to attach to the surface of MPs rich in polar groups, such as PET. In contrast, microorganisms of the phylum Actinobacteria and Firmicutes show a higher preference for non-polar MPs, such as PP and PE.

We analyzed the stability of bacterial communities from multiple perspectives, including average variation degree (AVD), network characteristics, robustness, and vulnerability (Fig. 2g–j). From the network diagram, PET and sediments show more node clustering (Fig. 2i). In terms of AVD, water has the highest value, followed by PET, with sediments, PE, and PP being relatively lower (Fig. 2g). Regarding network vulnerability, PET is the most fragile (0.00186), while other samples are quite similar

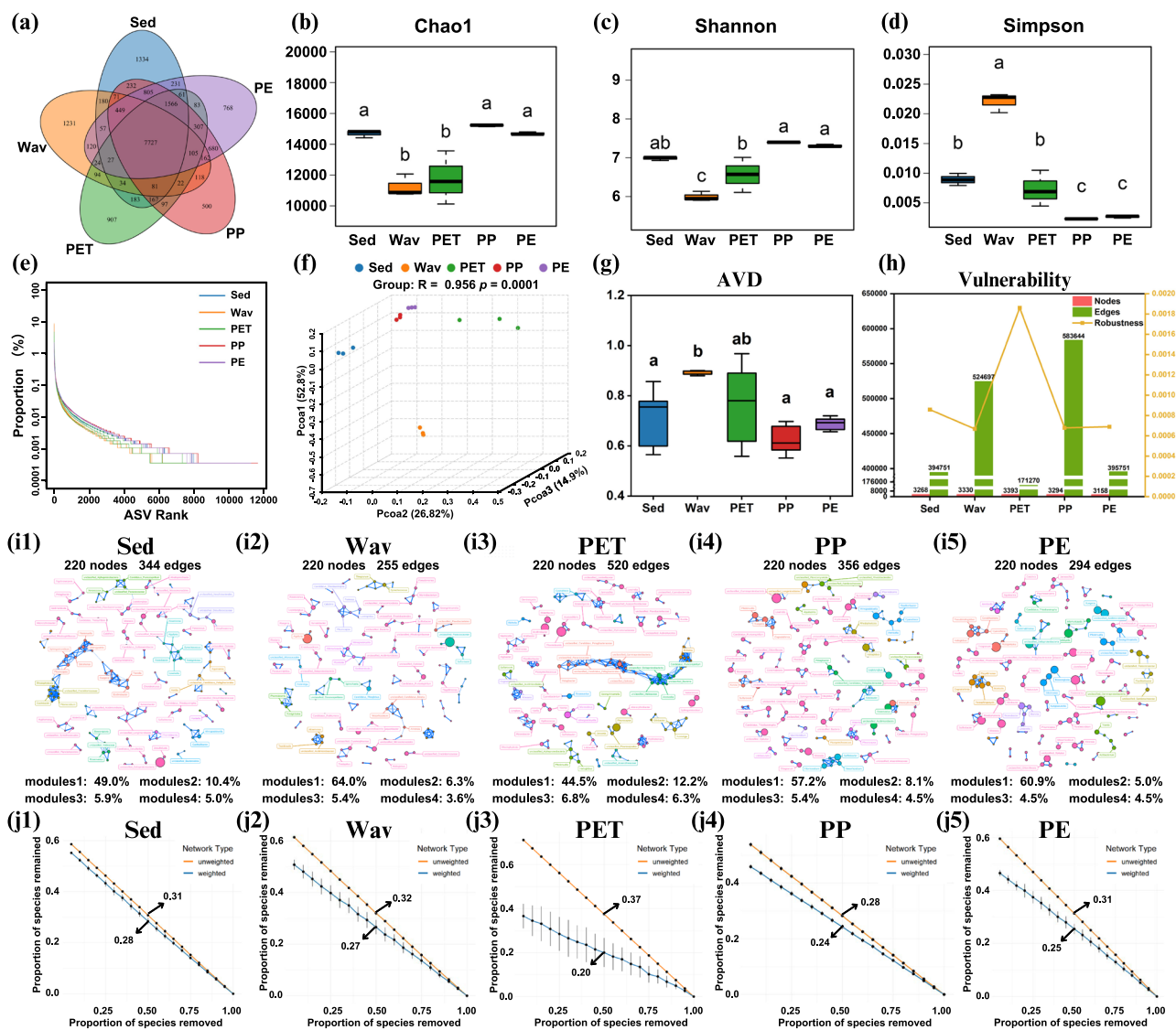


Fig. 2 | Differences in bacterial community diversity and stability based on ASV-level analysis. **a–f** Diversity, **g–j** Stability. **a** Venn diagram of differential species; **b–e** Alpha diversity. **b** Chao1, **c** Shannon, **d** Simpson, **e** Rank-abundance curve; **f** Beta diversity, PCoA analysis based on Bray–Curtis distances; **g** Average variation degree (AVD); **h** Vulnerability (5000 ASVs with the highest relative abundance were screened); **i1–i5** Correlation networks; **j1–j5** Robustness. The upper edge of the box

represents the 75th percentile (third quartile), the lower edge indicates the 25th percentile (first quartile), and the central line denotes the median. The upper whisker extends to the maximum non-outlier value, while the lower whisker shows the minimum non-outlier value. Statistical significance ($p < 0.05$) was determined using one-way ANOVA.

(Fig. 2f). The robustness of the networks was evaluated by randomly removing ASVs from the samples. Under different analysis methods (weighted/unweighted), except for PET, the robustness of other samples was relatively similar (weighted: 0.24–0.28, unweighted: 0.28–0.32), and the difference between the two methods did not exceed 0.06. PET's robustness shows a unique pattern, with significant differences between weighted and unweighted methods. Under the weighted method, PET's robustness (0.20) drops sharply. Overall, PET has the weakest stability, with other samples being similar.

The analysis of community stability is even more interesting because it takes into account more factors (such as ASV count, diversity, species abundance, etc.) and considers the relationships between them. Overall, water's fluidity makes its microbial community composition relatively even, giving it a larger AVD⁶³. PET's porous structure allows extensive water contact, increasing its community AVD. PET's microbial network shows serious clustering, higher modularity, and greater fragility, possibly due to multiple factors. Under similar conditions, different substrates, their physical/chemical properties, and nutrient availability can cause varying

network modularities, impacting AVD, robustness, and vulnerability^{64–67}. PET's unique fence-like structure and surface functional groups may lead to significant heterogeneity in microbial community distribution^{42,61}. This reduces richness and diversity but increases the abundance of certain signature microbial communities, creating unique network features. This was confirmed by our subsequent community composition analysis, which found that PET enrichment of high-abundance cyanobacteria. These highly interconnected, dominant species are crucial for network stability. If they're removed or fail, network function collapses quickly, reducing robustness⁶⁸. The significant differences in robustness between the two analysis methods also support this.

At the same time, we used a neutral model to quantify the impact of random processes. Meanwhile, neutral-model results show (Fig. S3) that, as before, PET exhibited characteristics similar to water ($0 < R^2 < 0.4$), and its community assembly process was less influenced by random factors⁶⁹. In contrast, sediment, PP, and PE showed negative R^2 values, indicating that random processes are not essential in driving the community assembly ecological process, and their community assembly is likely primarily driven

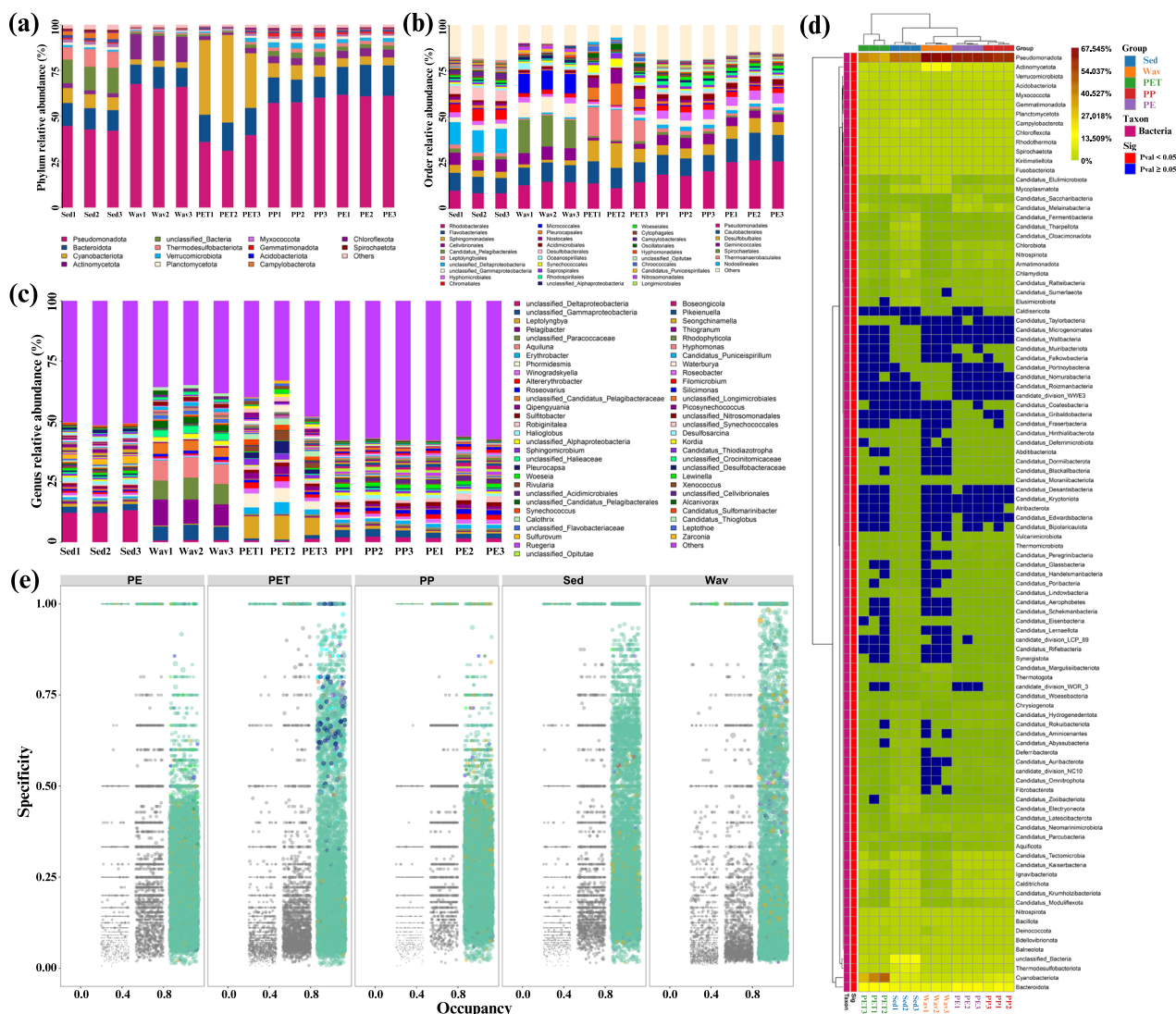


Fig. 3 | Composition and differences of bacterial communities among different samples. a–c Relative abundance of community composition at different taxonomic levels. **a** phylum level, **b** order level, **c** genus level; **d** ANOVA analysis at the phylum level ($p < 0.05$); **e** specificity-occupancy analysis at the genus level (specialized genera

by deterministic processes⁷⁰. Overall, microbial communities on MPs are driven by deterministic processes, yet PET's good water contact partly dilutes this result.

The community composition of the three types of MPs differs significantly from that of water and sediment at various taxonomic levels, unlike their diversity patterns (Fig. 3a-c). At the phylum level (Fig. 3a), Cyanobacteriota dominates on PET, while Pseudomonadota dominates on PP and PE, with their proportions being similar to those in water but much higher than in sediment. This is similar to the previous study, where Pseudomonadota dominate seagrass phyllosphere microbes⁷¹. Moreover, the nitrogen—fixing partner in seagrass rhizosphere, *Candidatus Celerinatantimonas neptuna*, also belongs to the Pseudomonadota³³. At the order level (Fig. 3b), the characteristic taxa on PET primarily include Sphingomonadales, Leptospirales and Pleurocapsales, etc., while the characteristic taxa on PP and PE are mainly Rhodobacterales, Sphingomonadales and Hyphomicrobiales, etc. At the genus level (Fig. 3c), the characteristic taxa on PET primarily include *Leptolyngbya*, *Erythrobacter*, *Phormidesmis* and *Winogradskyella*, etc. The characteristic taxa on PP and PE include *Winogradskyella*, *Altererythrobacter*, *Roseovarius* and *Woeseia*, etc. These differential taxa are commonly dominant in the respective samples. On PET,

are marked in blue, while genera related to nitrogen and carbon fixation within the specialized genera are marked in other colors, information on these genera is detailed in Fig. S5).

Cyanobacteriota is mainly related to photosynthesis⁷². The genera under Pseudomonadota on PP and PE are widely involved in the carbon and nitrogen cycles of the entire ecosystem⁷³.

The differential taxa analysis results for various samples are similar to the descriptions of relative abundance composition. At the phylum level, overall (Fig. 3d), the relative abundance distribution patterns of PET are more similar to water, while PE and PP are more alike. Specifically (Fig. S4a-i), the relative abundance of Cyanobacteriota on PET is significantly higher than in other samples, while Pseudomonadota is significantly higher on PP. PE and Wav than in other samples. The analysis of specialized genera in different samples (Fig. 3e) shows that the number of specialized genera ranks as follows: Wav (419) > Sed (333) > PET (166) > PP (62) > PE (61). The proportion of specialized genera related to carbon and nitrogen cycling was highest on PET and lowest in sediment. LEfSe analysis (Fig. S4j, k) also confirms the above conclusion. The differential taxa in PE and PP mainly belong to Pseudomonadota, while those in PET mainly belong to Cyanobacteriota.

To verify the above conclusion, we carried out differential MGS and absolute quantification analyses (Fig. S5–S8). Cluster analysis assembled 37 MGS (Fig. S6). Consistent with previous results, orders such as

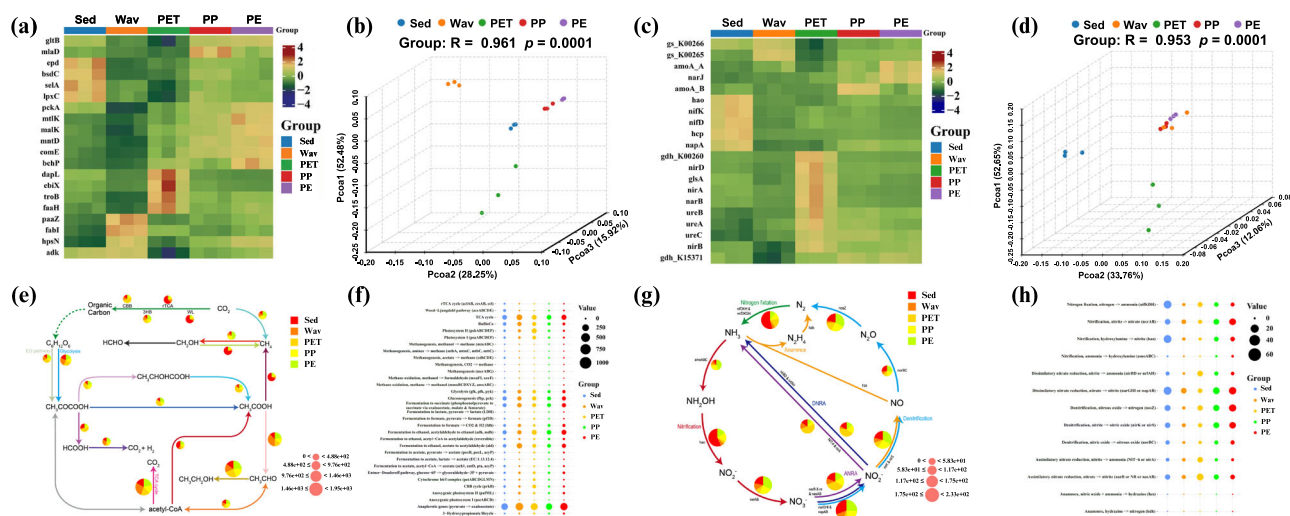


Fig. 4 | Analysis of carbon and nitrogen cycling pathway genes. a ANOVA analysis of carbon cycling genes; **b** PCoA analysis of carbon cycling genes; **c** ANOVA analysis of nitrogen cycling genes; **d** PCoA analysis of nitrogen cycling genes; **e** Carbon

cycling pathways; **f** Relative abundance of carbon cycling pathway genes; **g** Nitrogen cycling pathways; **h** Relative abundance of nitrogen cycling pathway genes.

Rhodobacterales, Flavobacteriales, and Leptolyngbyales exhibited the highest relative abundances on PET, and strong interactions were observed among these MGS. Based on the absolute quantification results (Fig. S7), the top 30 families in terms of absolute abundance largely belonged to the class Pseudomonadota (Fig. S7a). The class with the strongest interaction relationships was Cyanophyceae (Fig. S7b). There were two genera with absolute abundances exceeding 2×10^{12} copies g^{-1} , namely *unclassified_Deltaproteobacteria* and *Leptolyngbya* (Fig. S7c). The copy number per sample was highest in sediment, $\sim 1.18 \times 10^{13}$ copies g^{-1} , followed by PET at $\sim 6.53 \times 10^{12}$ copies g^{-1} (Fig. S8a). Although the copy number per sample was higher in sediments than in PET, the absolute abundance of Cyanobacteriota was higher on PET than in sediments (Fig. S8b), indicating the absolute dominance of Cyanobacteriota on PET.

Overall, analyses across multiple levels—including bacterial relative abundance, specialized genera, differential taxa, LEfSe, LDA, absolute quantification, and MGS—consistently conclude that MPs host distinct bacterial communities compared to water and sediments. These distinct communities are predominantly associated with carbon and nitrogen cycling within seagrass meadow ecosystems. Specificity-occupancy analysis further reveals that MPs harbor more active taxa related to carbon and nitrogen cycling, such as cyanobacteria and rhizobia. For instance, PET MPs are enriched with cyanobacteria, which are typical primary producers playing a crucial role in seagrass meadow ecosystems. Cyanobacteria can establish a degree of symbiosis with seagrasses and eukaryotic organisms, enabling strong photosynthetic and nitrogen-fixing capabilities. These activities contribute extensively to the carbon and nitrogen cycles in seagrass meadows while also facilitating the adsorption of environmental pollutants, such as heavy metals^{28,33,74,75}. In addition, the adsorption of heavy metals by MPs themselves, as well as their extensive adsorption of cyanobacteria, may further intensify the impact of heavy metal pollution in the habitat⁷⁶. The complex structure of PET masks enhances water flow and sunlight exposure on their surfaces, providing favorable conditions for cyanobacterial growth by ensuring ample light, CO_2 , and essential nutrients such as nitrogen and phosphorus^{77,78}. In contrast, PE and PP MPs are characterized by dominant taxa from the class Pseudomonadota, including genera such as *Winoogradskyella*, *Altererythrobacter*, and *Roseovarius*. These genera are commonly involved in microbial processes of the carbon and nitrogen cycles within seagrass meadow ecosystems^{79–81}. Compared to sediments, the lower density of MPs allows them to float with water currents, making their surfaces more accessible to sunlight, CO_2 , and nutrients. Furthermore, compared to free-floating microbes in water, MPs provide a stable habitat, leading to more distinct microbial community compositions^{62,82,83}. The

unique surface dynamics of MPs—including surface charge, hydrophobicity, and the presence of polar functional groups—are also significant factors driving biofilm formation and community differentiation^{84–86}. Absolute quantification results further support this, showing that PET masks with more complex structures have higher microbial copy numbers and biofilm content per unit sample.

Differences in carbon-nitrogen cycling genes and resistance genes among samples

Microbial carbon and nitrogen metabolism exhibit significant differences across different samples (Fig. 4). From the perspective of the carbon cycle, genes associated with fatty acid synthesis and metabolism, such as *dapL*, *cbiX*, *troB*, and *fahH*, showed significantly higher expression levels on PET compared to water and sediment samples, potentially linked to surface biosynthetic activities. On PP, the expression of the *mldA* gene was relatively higher, while on PE, genes related to carbohydrate and heavy metal ion metabolism and transport, including *pckA*, *mtlK*, *malK*, *mntD*, *comE*, and *bchP*, displayed elevated expression levels (Fig. 4a). Regarding the composition of genes involved in carbon cycle pathways, significant differences were observed between samples (ADONIS, $R = 0.961$, $p < 0.001$), with PET being most distinct from other samples, while PP and PE also showed gene compositions distinct from water and sediment samples (Fig. 4b). Further clarification of these differences at the pathway level revealed that genes involved in the CBB cycle and glycolysis exhibited higher expression levels on PET, whereas genes involved in CO_2 conversion to CH_4 and subsequently to CH_3OH were more prominently expressed on PP and PE (Fig. 4e, f).

In the nitrogen cycle, genes related to N_2O and nitrate reduction, such as *nirD*, *glsA*, *nirA*, *narB*, and *ureB*, were more highly expressed on PET, while genes such as *amoA_A*, *narJ*, and *amoA_B*, associated with ammonia oxidation and nitrite reduction, exhibited higher expression on PP and PE (Fig. 4c). Differences in gene composition among samples were also highly significant (ADONIS, $R = 0.953$, $p < 0.001$), with PET remaining the most distinct sample, although sediment, PP, and PE displayed highly similar compositions. Across the entire nitrogen cycle pathway, genes involved in the full denitrification process (e.g., *narB*, *nr*, *nasAB*, *nirK*, *nirS*, *norBC*, and *nosZ*) exhibited higher expression levels on MPs. Additionally, PET demonstrated significantly higher expression levels of genes involved in nitrogen reduction (e.g., *NIT-6*, *nirA*, *nirBD*, and *nrfAH*) compared to other samples (Fig. 4g, h). These findings collectively suggest that microorganisms on MPs possess unique carbon and nitrogen metabolic characteristics compared to those in water and sediment. Through influencing microbial

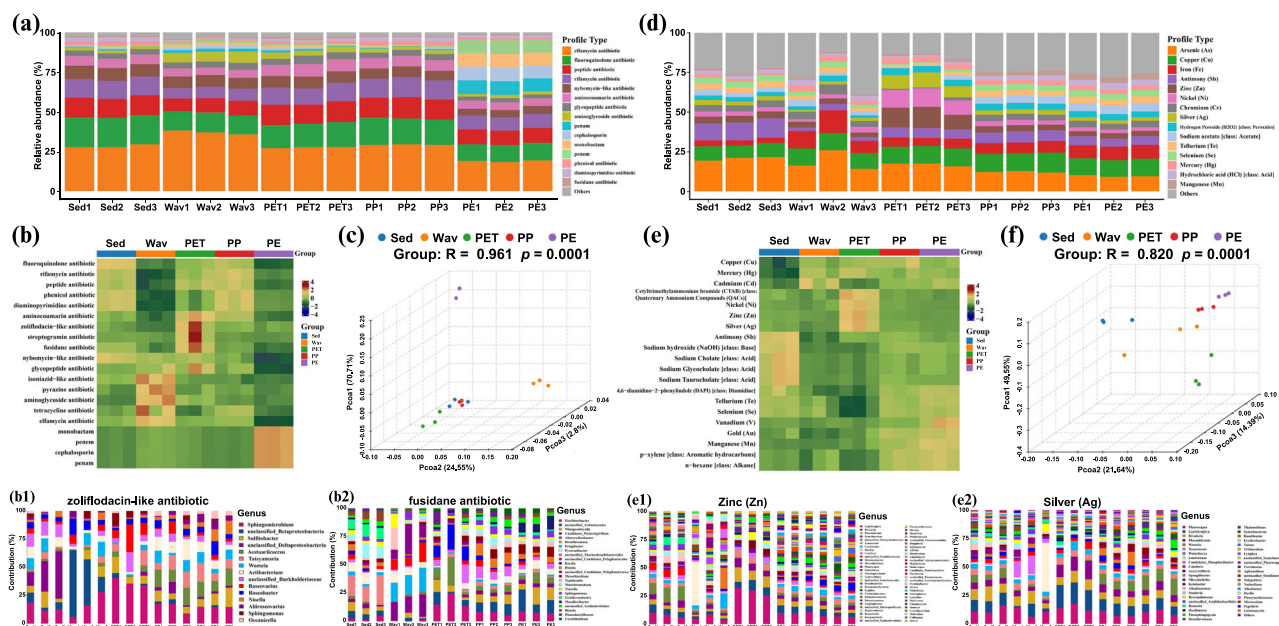


Fig. 5 | Analysis of ARGs, MRGs, and BRGs across different samples. a–c ARGs. **a** Relative abundance. **b** ANOVA analysis. **b1, b2** Significant gene contribution analysis. **b1** Zoliflodacin-like antibiotic, **b2** Fusidane antibiotic. **c** PCoA analysis. **d–f**

MRGs and BRGs. **d** Relative abundance. **e** ANOVA analysis. **e1, e2** Significant gene contribution analysis. **e1** Zinc (Zn), **e2** Silver (Ag). **f** PCoA analysis.

community composition and the expression of genes related to carbon and nitrogen cycles, MPs could impact the carbon sequestration potential of seagrass meadows and the emission of greenhouse gases.

We analyzed the functional differences and contributions of carbon and nitrogen cycling at different levels. For the carbon cycle, the analysis focused on two main aspects: carbon fixation and transport. Functional genes related to carbon fixation exhibited the highest expression levels on PET, with key representatives including Carbon Fixation, Photosynthesis, and the Cytochrome b6f complex (Fig. S10a–c). The primary taxa contributing to these differences were predominantly Cyanobacteria, including genera such as *Leptolyngbya*, *Phormidium*, *Synechococcus*, and *Pleurocapsa* (Fig. S10a1, b1). In contrast, functional genes associated with transport showed the highest expression levels on PE, primarily including Transport and ABC Transport (Fig. S10a–c). The main taxa contributing to these differences were genera such as *Roseovarius*, *Ruegeria*, *Roseobacter*, and *Rhodophycicola* (Fig. S10a3), many of which are known to form close symbiotic relationships with plants^{87–89}. Additionally, functional genes associated with organic transformation and xenobiotic metabolism also exhibited the highest expression levels on PE. For the nitrogen cycle, nitrogen fixation and assimilatory nitrate reduction were more pronounced on PET (Fig. S10d), enabling a greater transfer of nitrogen into organisms. The primary taxa contributing to these differences included *Leptolyngbya*, *Phormidium*, *Waterburya*, *Erythrobacter*, *Rivularia* and *Calothrix* (Fig. S10d1, d2). Most of them belong to Cyanobacteria and exhibit strong symbiotic relationships with plants, collaborating with them to facilitate nitrogen fixation^{89–91}.

Overall, compared to water and sediment, the plastisphere harbors microorganisms with distinctive carbon and nitrogen metabolic characteristics. Specifically, carbon and nitrogen fixation processes are more active on PET, while denitrification is more pronounced on PE and PP. These processes are closely linked to the carbon and nitrogen cycles within the seagrass meadow ecosystem. Contribution analysis indicates that the differences in functional genes related to carbon and nitrogen cycling are predominantly driven by cyanobacteria, whose relative abundance on the three types of MPs is generally higher than in water and sediment (Fig. S6). This suggests that differences in species composition across samples drive variations in microbial community functions⁹². From the absolute quantification results, although the per-sample gene copy number in sediments is

significantly higher than in MPs, the absolute abundance of certain genera and genes related to carbon and nitrogen cycling in PET samples is comparable to that in sediments (Fig. S5, S9). All evidence points to more intense microbial activity related to carbon and nitrogen cycling on MPs. As previously reviewed, substantial MPs inputs may impact the carbon sequestration capacity of seagrass meadows¹². On the one hand, plastisphere, as unique carriers of these blue carbon microorganisms, could weaken the cooperative relationships between nitrogen-fixing microbes and plants, reducing the nitrogen-fixing capacity of plant root systems and thereby affecting the primary productivity of the entire seagrass meadow⁹³. On the other hand, the intense carbon and nitrogen metabolic activities of microorganisms on these unique carbon spheres may enhance their role as microbial carbon pumps (MCP), facilitating the fixation of more refractory dissolved organic carbon (DOC) on the seabed⁹⁴.

The distribution of ARGs, MRGs, and BRGs across different samples exhibited significant differences (all $R > 0.8$, $p < 0.001$) (Fig. 5a–f). Most ARGs showed higher relative abundances on MPs. Specifically, ARGs related to Zoliflodacin-like antibiotics, Aminocoumarin antibiotics, Streptogramin antibiotics, and Fusidane antibiotics were relatively more abundant on PET, with the primary contributing genera being *Sphingomicrobium*, *unclassified_Burkholderiaceae*, *Roseovarius*, and *Sphingomonas* (Fig. 5b1, b2). In contrast, ARGs associated with Monobactam, Penem, Cephalosporin, and Penam antibiotics were most abundant on PE, with key contributing genera including *Dankookia*, *Salmonella*, *Hoeflea*, and *Alcanivorax* (Table S2). The taxa driving ARG variations on PET were predominantly Cyanobacteria, which are well-known for their strong interactions with ARGs⁹⁵. In contrast, the taxa driving ARG variations on PE were mostly pathogenic bacteria. Among them, *Dankookia*, *Alcanivorax*, and *Hoeflea* are associated with various diseases and infections. These bacterial groups frequently encounter penicillin and cephalosporin antibiotics and carry a large number of resistance genes⁹⁶. The unique capacity of bacterial taxa to carry ARGs, combined with their preference for specific MPs, contributes to the observed differences among samples.

For MRGs and BRGs, most BRGs exhibited relatively higher expression levels in sediments, while MRGs were more abundant on MPs. Representative examples include Ni, Zn, and Ag resistance genes on PET, Cu resistance genes on PP, and V resistance genes on PE. The primary genera driving these differences were Cyanobacteria, including

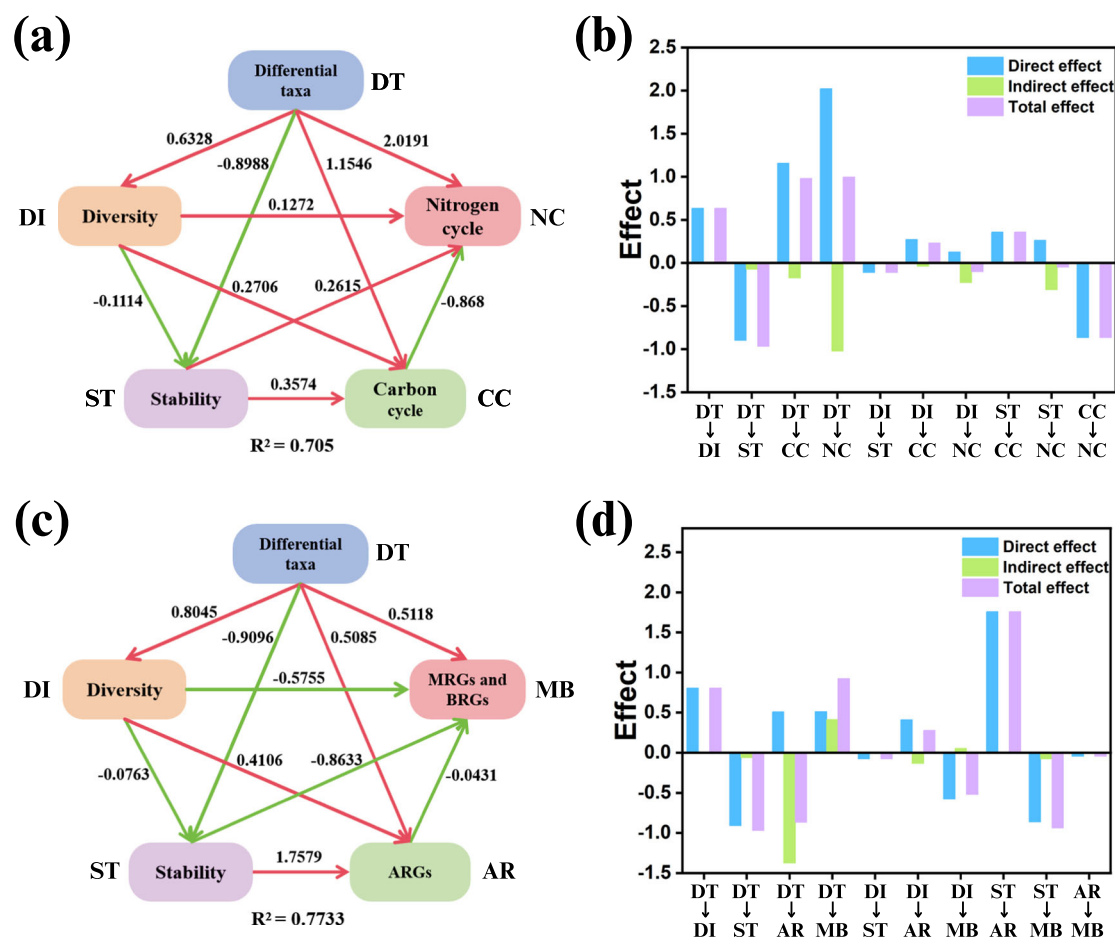


Fig. 6 | Analysis of the driving factors behind the distribution of carbon-nitrogen cycle-related genes and resistance genes. a Carbon-nitrogen cycle-related genes; **b** Influence between latent variables; **c** ARGs, MRGs, and BRGs; **d** Influence between

latent variables. Red represents positive correlation, and green represents negative correlation.

Leptolyngbya, *Rivularia*, *Xenococcus*, and *Waterburya* (Figs. 5d, e, e1, e2). Previous studies have demonstrated that Cyanobacteria can adsorb heavy metals through multiple mechanisms⁹⁷. Their cell walls are rich in polysaccharides, proteins, and lipids, which contain functional groups such as hydroxyl, carboxyl, and amino groups that form coordination bonds with metal ions, facilitating heavy metal adsorption. Additionally, the secretion of extracellular polymeric substances (EPS) significantly enhances metal-binding capacity, further strengthening the adsorption of heavy metals⁹⁸. These factors likely contribute to the higher abundance of heavy metal-related genes on PET MPs.

Drivers and implications of plastisphere as a unique ecological niche for microorganisms in seagrass meadows

Through path analysis using partial least squares path model (PLS-PM), we comprehensively considered the relationships among diversity, stability, differential taxa, carbon-nitrogen cycle-related genes, and resistance genes (Fig. 6; Table S3, S4). The results showed that microbial community differences between samples were the primary driving factor for both carbon-nitrogen cycle-related genes and resistance genes, with inconsistent impacts from diversity and stability. Specifically, diversity and stability were positively correlated with carbon-nitrogen cycle-related genes, while negatively correlated with resistance genes. This may be because microbial activity in the carbon-nitrogen cycle typically requires a more stable and suitable environment, during which microbial diversity and stability are relatively high⁹⁹. In contrast, a large accumulation of resistance genes usually indicates that the community is under stress from certain pollutants, leading to lower microbial diversity and stability^{100,101}. Overall, compared to water and

sediment, the plastisphere exhibits distinctive characteristics in terms of microbial community diversity (alpha and beta), stability (network topological features, robustness, vulnerability, and AVD), community composition (relative abundance, absolute abundance, MGS, differential taxa, specificity, and occupancy), as well as functional genes related to carbon and nitrogen cycling and resistance genes (composition, structure, pathways, and contributions). These differences were primarily driven by microbial community differences across samples, and such differences in microbial communities depend on a series of conditions, including matrix structure, hydrophobicity, charge, functional groups, and other characteristics. These features of MPs are markedly different from those of water and sediment, especially their unique structure and higher hydrophobicity⁵⁶. At the same time, the structure and hydrophobicity of PET fragments differ significantly from those of PE and PP (Fig. 1 and S1), which may be the main reason for the microbial community differences between different MPs. Additionally, plastic additives, such as functional additives, colorants, fillers and reinforcements, are incorporated into plastics during manufacturing to enhance their durability, flexibility, and other functional properties¹⁰². Over time, these additives can leach into the surrounding environment due to weathering, UV radiation, and microbial degradation¹⁰³. The gradual release of plastic additives is also a factor that cannot be ignored, as it may affect the assembly process of microbial communities over a longer period of time¹⁰⁴. Taken together, these findings underscore that plastisphere represent a unique ecological niche for microbes in seagrass meadows.

However, with the continuous influx of MPs, this unique ecological niche may have negative impacts on the entire seagrass meadow

ecosystem. On one hand, MPs alter the original microbial community structure in the ecosystem, affecting normal metabolic activities of microorganisms and exacerbating greenhouse gas emissions^{105,106}. Additionally, the impact on microbial carbon pumps (MCPs) may impair the carbon sequestration capacity of coastal blue carbon ecosystems, which is particularly concerning¹⁰⁷. On the other hand, the impact of MPs on microorganisms may affect various aspects of the entire seagrass meadow ecosystem. Firstly, MPs may disrupt the synergistic carbon and nitrogen fixation between microorganisms and plants, potentially threatening both carbon sequestration capacity and the survival of seagrass communities^{108,109}. Secondly, microorganisms within the plastisphere harbor a high abundance of heavy metals, metal resistance genes (MRGs), and antibiotic resistance genes (ARGs), which could pose ecological risks when ingested by marine organisms. These risks may extend through the food chain, potentially impacting human health^{110,111}. Thirdly, the large quantities of cyanobacteria adsorbed on MPs surfaces may release harmful algal toxins^{112,113}. These toxins not only impair the physiological development and viability of fish, shellfish, and other aquatic species, but also present a cross-boundary contamination through buoyant MPs that facilitate long-distance transport via ocean currents^{114,115}. This could exacerbate the proliferation and spread of harmful algal blooms (HABs), further destabilizing aquatic ecosystems and impairing their long-term functionality¹¹⁶. Moreover, the accumulation of these microorganism-rich plastispheres in sediments may also have unknown impacts on the structure and function of the sediments. Therefore, while our study provides new insights and research opportunities regarding the impacts of the plastisphere on marine microbial ecology and ecotoxicology, the associated negative effects on environmental health and ecosystem services require further investigation. Furthermore, effective management measures must be implemented to mitigate these potential risks.

Conclusions

Through this study, we identified the plastisphere as a unique ecological niche within seagrass meadows, exhibiting distinctive characteristics in microbial community diversity, stability, species composition, as well as functional genes related to carbon and nitrogen cycling and resistance genes. Specifically, regarding diversity, bacterial alpha diversity on PET was lower and more similar to that of water, while PP and PE exhibited higher diversity, resembling sediment more closely. In terms of stability, microbial correlation networks on PET were more complex, with higher AVD and greater vulnerability. Consequently, these networks are more prone to functional collapse and a rapid decline in robustness under external disturbances. Conversely, microbial networks on PP and PE demonstrated greater stability, characterized by lower AVD and vulnerability. In terms of community composition, the characteristic taxa on PET were predominantly cyanobacteria, whereas PP and PE supported denitrifying bacteria and pathogenic bacteria. These unique microbial community structures drive the active carbon and nitrogen cycling processes observed on MPs and the elevated enrichment of resistance genes. These differences are collectively attributed to a range of factors, including the hydrophobicity, structure, surface charge, and functional groups of MPs. However, structural characteristics and hydrophobicity likely play a pivotal role in determining these variations. Additionally, it is important to note that, although *Zostera marina* is widely recognized as the most extensive marine plant in the world¹¹⁷, its growth characteristics and microbial community composition may still vary from other seagrass species. Consequently, evaluating the impact of MPs intrusion on microbial communities in a wider variety of seagrass beds could be the subsequent objective. These studies enable us to accurately assess the impact of MPs intrusion on seagrass meadow ecosystems, particularly concerning their carbon sequestration capacity. At the same time, the potential risks associated with heavy metals and resistance genes carried by MPs should not be underestimated, as these risks have yet to receive sufficient attention.

Materials and methods

Sample placement and collection

In September 2024, a 30-day in situ incubation experiment was carried out in the *Zostera marina* seagrass meadow at Swan Lake (Fig. S11) in Rongcheng City, Shandong Province, China (37°21'38"N, 122°33'30"E). After extensive preliminary research and literature review, we selected the three most common types of plastics found in seagrass meadows for in situ simulation studies¹¹. When procuring the plastics, we considered the common forms found in seagrass meadows, such as masks (PET), films (PP), and ropes (PE). These plastics were procured from Alibaba Group (Hangzhou, China). The polymer types were determined by a micro-Fourier transformed infrared spectrometer (μ -FTIR, Thermo Nicolet iN10) in a transmission mode. The plastics were cut into small fragments ~1 mm in size (Fig. 1), sterilized with 70% ethanol for 30 min, and sterilized by autoclaving, followed by thorough rinsing with sterile water. To minimize the impact of metal containers on MRG results, 3 g of MPs samples were wrapped in double-layered cotton cloth, which was also sterilized. The samples were secured with ropes and rocks near the sediment at the base of the seagrass meadow, and the connection points between the ropes and the samples were further secured with stones (Fig. S12). Each representative sample was placed in three adjacent seagrass beds (approximately 20 meters apart), forming three parallel sample groups. Based on the studies by Yang et al.¹¹⁸ and Li et al.¹¹⁹, the incubation period was set to one month. After incubation, the MPs samples were collected. Near each MPs sample site, 100 g of surface sediment and 1 L of water were collected. These served as natural matrix controls that had directly contacted the MPs samples. All samples were stored in sterile glass containers, transported on dry ice, and stored at -20°C for further analysis. Environmental parameters (e.g., temperature, salinity) were recorded during sampling using a portable YSI meter and summarized in Table S1.

Biofilm content and material characterization

According to previous studies, the OD is proportional to the biofilm content on the surface of MPs^{120–122}. The detailed protocol for OD measurement is provided in Text S1. Biofilm formation was observed through the SEM and FTIR spectroscopy was used to analyze changes in functional groups on the MPs before and after incubation. The changes in the hydrophobicity of the MPs before and after in situ incubation were calculated using contact angle measurements (measured at the moment when the liquid was completely separated from the needle).

DNA sequencing, quality control, and annotation analysis

The metagenomic sequencing and quality control part of this study is essentially consistent with Feng et al.¹²³, the specific methods are detailed in Text S2. In addition, we also performed absolute quantification of pairs of metagenomic data by using the internal standard method (the specific method is detailed in Text S3).

Data analysis and visualization

The AVD analysis was conducted following the method of Chen et al.¹²⁴ and Xun et al.⁶³, while network vulnerability and robustness analysis were conducted following the method of Cornell et al.¹²⁵. Specificity-occupancy analysis was conducted following the method of Gweon et al.¹²⁶. PLS-PM was used to analyze the interactions among bacterial community differential taxa, diversity, stability, carbon-nitrogen cycle-related genes, and resistance genes. The network diagram and neutral models were drawn using an online platform (clouduutu.com.cn). To quantify variation, standard deviations (SD) were calculated for parametric data.

In addition to the analyses mentioned above, Rank-Abundance, PCoA, Venn diagrams, relative abundance bar plots (threshold > 0.01), LEfSe (threshold > 2), LDA, box plots, heatmaps, bubble charts, cycle pathway plots and circos plots, were all generated using R (v4.4.3, 2024), based on the ASV table (phylum, family, and genus levels). Except for the pairwise comparisons of MGS that used the Wilcoxon test, all significant differences were determined based on ANOVA variance analysis ($p < 0.05$), and the 20

most significant differences were selected when screening for differential genes. Maps were created using Ocean Data Viewer (ODV, v5.1.7). Graphical Abstract figure was drawn using Adobe Illustrator (v2025) and the Canva platform. FTIR plots were generated with Origin (v2021).

Reporting summary

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

Data availability

All data needed to evaluate the conclusions in the paper are present in the paper and the Supplementary Materials and available at <https://doi.org/10.5281/zenodo.15272707>.

Code availability

No custom code was developed for the results in this manuscript.

Received: 12 April 2025; Accepted: 23 July 2025;

Published online: 06 August 2025

References

- Nordlund, L. M. et al. Seagrass ecosystem services—what's next? *Mar. Pollut. Bull.* **134**, 145–151 (2018).
- Raven, J. A. Seagrasses: Biology, ecology and conservation. *Phycologia* **45**, 602–603 (2006).
- Duarte, C. M., Losada, I. J., Hendriks, I. E., Mazarrasa, I. & Marbà, N. The role of coastal plant communities for climate change mitigation and adaptation. *Nat. Clim. Change* **3**, 961–968 (2013).
- Fourqurean, J. W. et al. Seagrass ecosystems as a globally significant carbon stock. *Nat. Geosci.* **5**, 505–509 (2012).
- Chmura, G. L., Anisfeld, S. C., Cahoon, D. R. & Lynch, J. C. Global carbon sequestration in tidal, saline wetland soils. *Glob. Biogeochem. Cycles* **17**, 1111 (2003).
- Waycott, M. et al. Accelerating loss of seagrasses across the globe threatens coastal ecosystems. *Proc. Natl. Acad. Sci. USA* **106**, 12377–12381 (2009).
- Arias-Ortiz, A. et al. A marine heatwave drives massive losses from the world's largest seagrass carbon stocks. *Nat. Clim. Change* **8**, 338–344 (2018).
- Egea, L. G., Infantes, E. & Jimenez-Ramos, R. Loss of POC and DOC on seagrass sediments by hydrodynamics. *Sci. Total Environ.* **901**, 165976 (2023).
- Jiménez-Ramos, R. et al. Carbon metabolism and bioavailability of dissolved organic carbon (DOC) fluxes in seagrass communities are altered under the presence of the tropical invasive alga *Halimeda incrassata*. *Sci. Total Environ.* **839**, 156325 (2022).
- Orth, R. J. et al. A global crisis for seagrass ecosystems. *BioScience* **56**, 987–996 (2006).
- Li, C. J., Zhu, L. X., Li, W. T. & Li, D. J. Microplastics in the seagrass ecosystems: a critical review. *Sci. Total Environ.* **902**, 166152 (2023).
- Hou, X. et al. Distinct impacts of microplastics on the carbon sequestration capacity of coastal blue carbon ecosystems: a case of seagrass beds. *Mar. Environ. Res.* **202**, 106793 (2024).
- Menicagli, V. et al. Early evidence of the impacts of microplastic and nanoplastic pollution on the growth and physiology of the seagrass *Cymodocea nodosa*. *Sci. Total Environ.* **838**, 156514 (2022).
- Litchfield, S. G., Tan, M. L. S., Schulz, K. G. & Kelaher, B. P. Disposable surgical masks affect the decomposition of *Zostera muelleri*. *Mar. Pollut. Bull.* **188**, 114695 (2023).
- Serrano, O. et al. Australian vegetated coastal ecosystems as global hotspots for climate change mitigation. *Nat. Commun.* **10**, 4313 (2019).
- Kennedy, H. et al. Seagrass sediments as a global carbon sink: Isotopic constraints. *Glob. Biogeochem. Cycles* **24**, BG4026 (2010).
- Duarte, C. M. & Krause-Jensen, D. Export from seagrass meadows contributes to marine carbon sequestration. *Front. Mar. Sci.* **4**, 13 (2017).
- Sanchez-Vidal, A., Canals, M., de Haan, W. P., Romero, J. & Veny, M. Seagrasses provide a novel ecosystem service by trapping marine plastics. *Sci. Rep.* **11**, 254 (2021).
- Mazarrasa, I. et al. Factors determining seagrass blue carbon across bioregions and geomorphologies. *Glob. Biogeochem. Cycles* **35**, e2021GB006935 (2021).
- Mazarrasa, I. et al. Habitat characteristics provide insights of carbon storage in seagrass meadows. *Mar. Pollut. Bull.* **134**, 106–117 (2018).
- Falkowski, P. G., Barber, R. T. & Smetacek, V. Biogeochemical controls and feedbacks on ocean primary production. *Science* **281**, 200–206 (1998).
- Liang, C., Schimel, J. P. & Jastrow, J. D. The importance of anabolism in microbial control over soil carbon storage. *Nat. Microbiol.* **2**, 17105 (2017).
- Duarte, C. M. & Chiscano, C. L. Seagrass biomass and production: a reassessment. *Aquat. Bot.* **65**, 159–174 (1999).
- Gacia, E., Duarte, C. M. & Middelburg, J. J. Carbon and nutrient deposition in a Mediterranean seagrass (*Posidonia oceanica*) meadow. *Limnol. Oceanogr.* **47**, 23–32 (2002).
- Jiao, N. et al. Microbial production of recalcitrant dissolved organic matter: long-term carbon storage in the global ocean. *Nat. Rev. Microbiol.* **8**, 593–599 (2010).
- Stone, R. The invisible hand behind a vast carbon reservoir. *Science* **328**, 1476–1477 (2010).
- Den Hartog, C. *The Sea-Grasses of the World* (North-Holland, 1970).
- Welsh, D. T. Nitrogen fixation in seagrass meadows: regulation, plant–bacteria interactions and significance to primary productivity. *Ecol. Lett.* **3**, 58–71 (2000).
- Patriquin, D. The origin of nitrogen and phosphorus for growth of the marine angiosperm *Thalassia testudinum*. *Mar. Biol.* **15**, 35–46 (1972).
- Patriquin, D. & Knowles, R. Nitrogen fixation in the rhizosphere of marine angiosperms. *Mar. Biol.* **16**, 49–58 (1972).
- Thompson, L. R. et al. A communal catalogue reveals Earth's multiscale microbial diversity. *Nature* **551**, 457–463 (2017).
- Tschitschko, B. et al. Rhizobia-diatom symbiosis fixes missing nitrogen in the ocean. *Nature* **630**, 899–904 (2024).
- Mohr, W. et al. Terrestrial-type nitrogen-fixing symbiosis between seagrass and a marine bacterium. *Nature* **600**, 105–109 (2021).
- Dahl, M. et al. A temporal record of microplastic pollution in Mediterranean seagrass soils. *Environ. Pollut.* **273**, 116451 (2021).
- Egea, L. G. et al. Comparison of macroplastics dynamic across a tidal-dominated coastal habitat seascape including seagrasses, salt marshes, rocky bottoms and soft sediments. *Mar. Pollut. Bull.* **196**, 115590 (2023).
- Ouyang, X. G. et al. Fate and effects of macro- and microplastics in coastal wetlands. *Environ. Sci. Technol.* **56**, 2386–2397 (2022).
- Stapleton, M. J., Ansari, A. J. & Hai, F. I. Antibiotic sorption onto microplastics in water: a critical review of the factors, mechanisms and implications. *Water Res.* **233**, 119790 (2023).
- Khan, A. R. et al. Micro/nanoplastics: critical review of their impacts on plants, interactions with other contaminants (antibiotics, heavy metals, and polycyclic aromatic hydrocarbons), and management strategies. *Sci. Total Environ.* **912**, 169420 (2024).
- Dong, H. et al. Interactions of microplastics and antibiotic resistance genes and their effects on the aquaculture environments. *J. Hazard. Mater.* **403**, 123961 (2021).
- Vilaplana, M. I. et al. The temperate seagrass species *Cymodocea nodosa* and the associated bacteria co-response to sunscreen pollution. *Mar. Environ. Res.* **208**, 107115 (2025).

41. Qin, P. et al. Early stage of biofilm assembly on microplastics is structured by substrate size and bacterial motility. *iMeta* **2**, e121 (2023).
42. Postek, W., Staskiewicz, K., Lilja, E. & Waclawa, B. Substrate geometry affects population dynamics in a bacterial biofilm. *Proc. Natl. Acad. Sci. USA* **121**, e2315361121 (2024).
43. Mincer, T. J., Zettler, E. R. & Amaral-Zettler, L. A. Biofilms on plastic debris and their influence on marine nutrient cycling, productivity, and hazardous chemical mobility. *Handb. Environ. Chem.* **78**, 221–233 (2016).
44. Zhai, X. Y., Zhang, X. H. & Yu, M. Microbial colonization and degradation of marine microplastics in the plastisphere: a review. *Front. Microbiol.* **14**, 1127308 (2023).
45. Wright, S. L., Thompson, R. C. & Galloway, T. S. The physical impacts of microplastics on marine organisms: a review. *Environ. Pollut.* **178**, 483–492 (2013).
46. Gewert, B., Plassmann, M. M. & MacLeod, M. Pathways for degradation of plastic polymers floating in the marine environment. *Environ. Sci. Process. Impacts* **17**, 1513–1521 (2015).
47. Dukek, P., Schleheck, D. & Kovermann, M. High-resolution NMR spectroscopic approaches to quantify PET microplastics pollution in environmental freshwater samples. *Chemosphere* **367**, 143657 (2024).
48. Dimassi, S. N. et al. Insights into the degradation mechanism of PET and PP under marine conditions using FTIR. *J. Hazard. Mater.* **447**, 130796 (2023).
49. Shah, A. A., Hasan, F., Hameed, A. & Ahmed, S. Biological degradation of plastics: a comprehensive review. *Biotechnol. Adv.* **26**, 246–265 (2008).
50. Su, X. et al. Comprehensive understanding on the aging process and mechanism of microplastics in the sediment-water interface: Untangling the role of photoaging and biodegradation. *Environ. Sci. Technol.* **58**, 16164–16174 (2024).
51. Andrad, A. L. et al. Oxidation and fragmentation of plastics in a changing environment; from UV-radiation to biological degradation. *Sci. Total Environ.* **851**, 158022 (2022).
52. Basak, N. & Meena, S. S. Microbial biodegradation of plastics: challenges, opportunities, and a critical perspective. *Front. Environ. Sci. Eng.* **16**, 161 (2022). Shilpa.
53. Su, X. et al. Novel insight into the aging process of microplastics: an in-situ study in coastal wetlands. *Water Res.* **248**, 120871 (2024).
54. Chen, Y. M. et al. Distribution characteristics and microbial synergistic degradation potential of polyethylene and polypropylene in freshwater estuarine sediments. *J. Hazard. Mater.* **471**, 134328 (2024).
55. Jia, J. et al. Biofilm formation on microplastics and interactions with antibiotics, antibiotic resistance genes and pathogens in aquatic environment. *Eco Environ Health* **3**, 516–528 (2024).
56. Sun, Y. Z. et al. Plastisphere microbiome: methodology, diversity, and functionality. *iMeta* **2**, e101 (2023).
57. Yi, M. L., Zhou, S. H., Zhang, L. L. & Ding, S. Y. The effects of three different microplastics on enzyme activities and microbial communities in soil. *Water Environ. Res.* **93**, 24–32 (2021).
58. Wang, Q. et al. Colonization characteristics and dynamic transition of archaea communities on polyethylene and polypropylene microplastics in the sediments of mangrove ecosystems. *J. Hazard. Mater.* **471**, 134343 (2024).
59. Focardi, A. et al. Plastic leachates impair picophytoplankton and dramatically reshape the marine microbiome. *Microbiome* **10**, 179 (2022).
60. Wu, X. et al. Environmental Health and Safety Implications of the Interplay Between Microplastics and the Residing Biofilm. *Environ. Health* **3**, 118–132 (2024).
61. Oberbeckmann, S., Löder, M. G. J. & Labrenz, M. Marine microplastic-associated biofilms - a review. *Environ. Chem.* **12**, 551–562 (2015).
62. Zettler, E. R., Mincer, T. J. & Amaral-Zettler, L. A. Life in the “Plastisphere”: Microbial communities on plastic marine debris. *Environ. Sci. Technol.* **47**, 7137–7146 (2013).
63. Xun, W. B. et al. Specialized metabolic functions of keystone taxa sustain soil microbiome stability. *Microbiome* **9**, 35 (2021).
64. Shade, A., Caporaso, J. G., Handelsman, J., Knight, R. & Fierer, N. A meta-analysis of changes in bacterial and archaeal communities with time. *ISME J* **7**, 1493–1506 (2013).
65. Van der Gucht, K. et al. The power of species sorting: local factors drive bacterial community composition over a wide range of spatial scales. *Proc. Natl. Acad. Sci. USA* **104**, 20404–20409 (2007).
66. Wagner, M. R. et al. Host genotype and age shape the leaf and root microbiomes of a wild perennial plant. *Nat. Commun.* **7**, 12151 (2016).
67. Goldford, J. E. et al. Emergent simplicity in microbial community assembly. *Science* **361**, 469–474 (2018).
68. Bellingier, M. & Cassi, D. Robustness of weighted networks. *Phys. A Stat. Mech. its Appl.* **489**, 47–55 (2018).
69. Chen, W. D. et al. Stochastic processes shape microeukaryotic community assembly in a subtropical river across wet and dry seasons. *Microbiome* **7**, 138 (2019).
70. Zhu, M. J. et al. Unraveling antibiotic resistomes associated with bacterial and viral communities in intertidal mudflat aquaculture area. *J. Hazard. Mater.* **459**, 132087 (2023).
71. Li, X. Q. et al. Exploring the structure and assembly of seagrass microbial communities in rhizosphere and phyllosphere. *Appl. Environ. Microbiol.* **91**, e02437–24 (2025).
72. Domínguez-Martín, M. A. et al. Structures of a phycobilisome in light-harvesting and photoprotected states. *Nature* **609**, 835–845 (2022).
73. Wang, S. S. et al. Chemolithoautotrophic diazotrophs dominate dark nitrogen fixation in mangrove sediments. *ISME J.* **18**, wræ119 (2024).
74. Paerl, H. W. & Huisman, J. Blooms like it hot. *Science* **320**, 57–58 (2008).
75. Falkowski, P. G. & Raven, J. A. *Aquatic Photosynthesis* (Princeton Univ. Press, 2013).
76. Wang, Q. J. et al. Effects of biofilm on metal adsorption behavior and microbial community of microplastics. *J. Hazard. Mater.* **424**, 127340 (2022).
77. Wright, R. J., Erni-Cassola, G., Zadjelovic, V., Latva, M. & Christie-Oleza, J. A. Marine plastic debris: A new surface for microbial colonization. *Environ. Sci. Technol.* **54**, 11657–11672 (2020).
78. Paerl, H. W. & Otten, T. G. Harmful cyanobacterial blooms: causes, consequences, and controls. *Microb. Ecol.* **65**, 995–1010 (2013).
79. Alejandre-Colomo, C. et al. Cultivable *Winogradskyella* species are genomically distinct from the sympatric abundant candidate species. *ISME Commun.* **1**, 51 (2021).
80. Fan, K. Q. et al. The metabolism of pyrene by a novel *Altererythrobacter* sp. with in-situ co-substrates: A mechanistic analysis based on pathway, genomics, and enzyme activity. *Chemosphere* **307**, 135784 (2022).
81. Slobodkina, G. et al. Lithoautotrophic lifestyle of the widespread genus *Roseovarius* revealed by physiological and genomic characterization of *Roseovarius autotrophicus* sp. nov. *FEMS Microbiol. Ecol.* **98**, fiac113 (2022).
82. Zhang, X. Y. et al. Microbial colonization of microplastic (MP) in aquatic environments: MP toxicity, microbial degradation potential and their interactions. *Trends Anal. Chem.* **181**, 118028 (2024).
83. Rummel, C. D., Jahnke, A., Gorokhova, E., Kühnel, D. & Schmitt-Jansen, M. Impacts of biofilm formation on the fate and potential effects of microplastic in the aquatic environment. *Environ. Sci. Technol. Lett.* **4**, 258–267 (2017).
84. Krsmanovic, M. et al. Hydrodynamics and surface properties influence biofilm proliferation. *Adv. Colloid Interface Sci.* **288**, 102336 (2021).

85. Rosenberg, M. & Kjelleberg, S. Hydrophobic interactions in bacterial adhesion. *Adv. Microb. Ecol.* **9**, 353–393 (1986).
86. Palmer, J. S., Flint, S. H., Schmid, J. & Brooks, J. D. The role of surface charge and hydrophobicity in the attachment of *Anoxybacillus flavithermus* isolated from milk powder. *J. Ind. Microbiol. Biotechnol.* **37**, 1111–1119 (2010).
87. Buchan, A., González, J. M. & Moran, M. A. Overview of the marine *Roseobacter* lineage. *Appl. Environ. Microbiol.* **71**, 5665–5677 (2005).
88. Porsby, C. H., Nielsen, K. F. & Gram, L. *Phaeobacter* and *Ruegeria* species of the *Roseobacter* clade colonize separate niches in a Danish turbot (*Scophthalmus maximus*)-rearing farm and antagonize *Vibrio anguillarum* under different growth conditions. *Appl. Environ. Microbiol.* **74**, 7356–7364 (2008).
89. Lee, M. W. et al. *Roseovarius phycicola* sp. nov. and *Roseovarius rhodophyticola* sp. nov., isolated from marine red algae. *Int. J. Syst. Evol. Microbiol.* **74**, 006574 (2024).
90. Díaz, Y. O. et al. Characterization of nitrogen-fixing cyanobacterial consortia isolated from the rhizosphere of *Carica papaya*. *Agronomy* **14**, 2132 (2024).
91. Pi, C. Y., Liu, X., Wang, Z. & Bao, W. K. Bryophyte-cyanobacteria symbioses and their nitrogen fixation capacity—a review. *Chin. J. Plant Ecol.* **42**, 407–418 (2018).
92. Roy, S., Karapurkar, J., Baidya, P., Jose, M. & Bagchi, S. Community composition, and not species richness, of microbes influences decomposer functional diversity in soil. *Soil Biol. Biochem.* **187**, 109225 (2023).
93. Li, C. et al. Ecology and risks of the global plastisphere as a newly expanding microbial habitat. *Innovation* **5**, 100543 (2024).
94. Jiao, N. et al. The microbial carbon pump and climate change. *Nat. Rev. Microbiol.* **22**, 408–419 (2024).
95. Kim, M. J. et al. Interplays between cyanobacterial blooms and antibiotic resistance genes. *Environ. Int.* **181**, 108268 (2023).
96. Zhang, Z. Y. et al. Assessment of global health risk of antibiotic resistance genes. *Nat. Commun.* **13**, 1–11 (2022).
97. Ciani, M. & Adessi, A. Cyanoremediation and phyconanotechnology: cyanobacteria for metal biosorption toward a circular economy. *Front. Microbiol.* **14**, 1166612 (2023).
98. Kalita, N. & Baruah, P. P. Cyanobacteria as a potent platform for heavy metals biosorption: uptake, responses and removal mechanisms. *J. Hazard. Mater. Adv.* **11**, 100349 (2023).
99. Liu, Z. X. et al. Soil pH and carbon quality index regulate the biogeochemical cycle couplings of carbon, nitrogen and phosphorus in the profiles of isohumolsols. *Sci. Total Environ.* **922**, 171269 (2024).
100. Jiang, C. X., Diao, X. P., Wang, H. H. & Ma, S. Y. Diverse and abundant antibiotic resistance genes in mangrove area and their relationship with bacterial communities—a study in Hainan Island, China. *Environ. Pollut.* **276**, 116704 (2021).
101. Martinez, J. L. Environmental pollution by antibiotics and by antibiotic resistance determinants. *Environ. Pollut.* **157**, 2893–2902 (2009).
102. Andrady, A. L. & Rajapakse, N. Additives and chemicals in plastics. *Hazardous chemicals associated with plastics in the marine environment. The Handbook of Environmental Chemistry* (eds Takada, H., Karapanagioti, H. K.) 1–17 (Springer International, 2019).
103. Hahladakis, J. N., Velis, C. A., Weber, R., Iacovidou, E. & Purnell, P. An overview of chemical additives present in plastics: Migration, release, fate and environmental impact during their use, disposal and recycling. *J. Hazard. Mater.* **344**, 179–199 (2018).
104. Wang, L., Wang, X. Y., Wu, H., Fan, S. Q. & Lu, Z. M. Integration of metagenomic analysis and metabolic modeling reveals microbial interactions in activated sludge systems in response to nanoplastics and plasticizers. *Water Res.* **271**, 122863 (2025).
105. Ramanam, R. et al. Gross negligence: impacts of microplastics and plastic leachates on phytoplankton community and ecosystem dynamics. *Environ. Sci. Technol.* **57**, 5–24 (2023).
106. Wang, S. M., Zhou, Q. X., Hu, X. A. & Tao, Z. X. Polyethylene microplastic-induced microbial shifts affected greenhouse gas emissions during litter decomposition in coastal wetland sediments. *Water Res.* **251**, 121167 (2024).
107. Huang, W. & Xia, X. H. Element cycling with micro(nano)plastics. *Science* **385**, 933–935 (2024).
108. Molin, J. M., Groth-Andersen, W. E., Hansen, P. J., Kühl, M. & Brodersen, K. E. Microplastic pollution associated with reduced respiration in seagrass (*Zostera marina* L.) and associated epiphytes. *Front. Mar. Sci.* **10**, 1216299 (2023).
109. Zhu, R. J. et al. A global estimate of multiccosystem photosynthesis losses under microplastic pollution. *Proc. Natl. Acad. Sci. USA.* **122**, e2423957122 (2025).
110. Turner, A., Holmes, L., Thompson, R. C. & Fisher, A. S. Metals and marine microplastics: adsorption from the environment versus addition during manufacture, exemplified with lead. *Water Res.* **173**, 115577 (2020).
111. Liu, Y. et al. Microplastics are a hotspot for antibiotic resistance genes: Progress and perspective. *Sci. Total Environ.* **773**, 145643 (2021).
112. Pestana, C. J. et al. Potentially poisonous plastic particles: Microplastics as a vector for cyanobacterial toxins microcystin-LR and microcystin-LF. *Environ. Sci. Technol.* **55**, 15940–15949 (2021).
113. Kim, J. Y. et al. Effects of micro-sized biodegradable plastics on *Microcystis aeruginosa*. *Sci. Total Environ.* **912**, 169044 (2024).
114. Svendsen, M. B. S., Andersen, N. R., Hansen, P. J. & Steffensen, J. F. Effects of harmful algal blooms on fish: insights from *Prymnesium parvum*. *Fishes* **3**, 11 (2018).
115. Lassudrie, M., Hégaret, H., Wikfors, G. H. & da Silva, P. M. Effects of marine harmful algal blooms on bivalve cellular immunity and infectious diseases: a review. *Dev. Comp. Immunol.* **108**, 103660 (2020).
116. Ren, X. Y. et al. Fate, abundance and ecological risks of microcystins in aquatic environment: the implication of microplastics. *Water Res.* **251**, 121121 (2024).
117. Reusch, T. B. H. & Olsen, J. L. Reconstructing the worldwide colonization history of the world's most widespread marine plant. *Nat. Plants* **9**, 1180–1181 (2023).
118. Yang, K. et al. Temporal dynamics of antibiotic resistome in the plastisphere during microbial colonization. *Environ. Sci. Technol.* **54**, 11322–11332 (2020).
119. Li, R. et al. Viral metagenome reveals microbial hosts and the associated antibiotic resistome on microplastics. *Nat. Water* **2**, 553–565 (2024).
120. De Tender, C. et al. Temporal dynamics of bacterial and fungal colonization on plastic debris in the North Sea. *Environ. Sci. Technol.* **51**, 7350–7360 (2017).
121. Lobelle, D. & Cunliffe, M. Early microbial biofilm formation on marine plastic debris. *Mar. Pollut. Bull.* **62**, 197–200 (2011).
122. Li, W. J. et al. Colonization characteristics of bacterial communities on plastic debris influenced by environmental factors and polymer types in the Haihe Estuary of Bohai Bay, China. *Environ. Sci. Technol.* **53**, 10763–10773 (2019).
123. Feng, P. Y. et al. Human supplementation with *Pediococcus acidilactici* GR-1 decreases heavy metals levels through modifying the gut microbiota and metabolome. *NPJ Biofilms Microbiomes* **8**, 63 (2022).
124. Chen, L. Q. et al. Oxygen influences spatial heterogeneity and microbial succession dynamics during Baijiu stacking process. *Bioresour. Technol.* **403**, 130854 (2024).
125. Cornell, C. R. et al. Land use conversion increases network complexity and stability of soil microbial communities in a temperate grassland. *ISME J.* **17**, 2210–2220 (2023).
126. Gweon, H. S. et al. Contrasting community assembly processes structure lotic bacteria metacommunities along the river continuum. *Environ. Microbiol.* **23**, 484–498 (2021).

Acknowledgements

This work was partially supported by the National Natural Science Foundation of China (42306175, 42076088, 42377380), Natural Science Foundation of Shandong Province, China (ZR2023QD153), Yantai University Start-up Foundation (HX22B116), the Special Funds for the Taishan Scholar Project of Shandong Province (tstp20240518), the Development Plan of Youth Innovation Team in Colleges and Universities of Shandong Province (2023KJF014).

Author contributions

Xin Hou: Conceptualization, Writing - original draft; Xiaoran Li: Data analysis; Yunan Lin: Sample data collection; Changjun Li: Experiment, Funding acquisition, Resources, Writing—review & editing; Ruijia Jing: Sample data collection; Lei Zhang, Jiamin Li, Ziming Jiang, Sen Wang: Resources; Qiangqiang Jiao: Sample data collection; Xiaotong Wang: Funding acquisition, Writing—review & editing; Di Zhang, Wenchan Liang, Lixin Zhu, Xiaohui Wang, Daoji Li: Writing—review & editing; Xianhua Liu: Funding acquisition, Writing—review & editing.

Competing interests

The authors declare no competing interests.

Additional information

Supplementary information The online version contains supplementary material available at <https://doi.org/10.1038/s43247-025-02619-0>.

Correspondence and requests for materials should be addressed to Changjun Li.

Peer review information *Communications Earth and Environment* thanks Virginia Menicagli and the other, anonymous, reviewer(s) for their contribution to the peer review of this work. Primary Handling Editors: Somaparna Ghosh. A peer review file is available.

Reprints and permissions information is available at <http://www.nature.com/reprints>

Publisher's note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>.

© The Author(s) 2025