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鄱阳湖候鸟栖息地微塑料表面细菌群落结构特征与生态风险预测

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摘要: 近年来鄱阳湖的微塑料环境污染日益受到关注. 选取鄱阳湖白沙湖为研究区, 采集白沙湖水体和沉积物以及其中的微塑料样品, 通过傅里叶红外光谱确定微塑料的聚合物类型为聚乙烯(PE)、聚酯纤维(PET)、聚丙烯(PP)和聚苯乙烯(PS). 并利用16S高通量测序技术分析水体、沉积物中和微塑料表面细菌群落结构组成. 微塑料表面细菌的物种丰富度与多样性均低于周围水体和沉积物. NMDS分析结果表明, 微塑料表面与周围沉积物、水体中的细菌群落结构差异较大. 水体和沉积物中的细菌群落组成与微塑料表面存在差异, 门水平上沉积物与沉积物中微塑料表面优势菌门为变形菌门(Proteobacteria)和拟杆菌门(Bacteroidota), 其在微塑料表面相对丰度高于沉积物; 水体中微塑料表面变形菌门相对丰度高于水体, 而拟杆菌门、放线菌门(Actinobacteriota)的相对丰度明显低于水体. 属水平上马赛菌属(*Massilia*)和假单胞菌属(*Pseudomonas*)是微塑料表面的优势菌属, 相对丰度明显高于周围水体和沉积物. 通过BugBase表型预测发现微塑料细菌群落可移动基因元件含量、生物膜形成、潜在致病性及胁迫耐受等表型相对丰度明显高于周围水体和沉积物. 结果发现微塑料可能会促使致病细菌在内的有害菌的传播, 提高细菌群落的潜在致病性, 且微塑料表面细菌群落具有更高的可移动基因元件含量表型. 通过揭示微塑料污染对微观层面湿地生态的潜在危害, 可为维护湿地生态稳定性提供科学参考.

关键词: 鄱阳湖; 细菌; 微塑料(MPs); BugBase; 假单胞菌

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Characterization of Microplastic Surface Bacterial Community Structure and Prediction of Ecological Risk in Poyang Lake, China

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Abstract: In recent years, the environmental pollution of microplastics in Poyang Lake has received increasing attention. Baisha Lake of Poyang Lake was selected as the study area, and samples of water and sediments of Baisha Lake and the microplastics therein were collected, and the polymer types of microplastics were identified as polyethylene (PE), polyester (PET), polypropylene (PP), and polystyrene (PS) using Fourier infrared spectroscopy. We also analyzed the structural composition of bacterial communities in water, in sediments, and on microplastic surfaces using 16S high-throughput sequencing. The species richness and diversity of bacteria on the microplastic surfaces were lower than those in the surrounding water and sediments. The results of NMDS analysis showed that the bacterial community structures on the microplastic surfaces differed greatly from those in the surrounding sediments and water. The bacterial community composition in water and sediment differed from that on the microplastic surfaces, and the dominant bacterial phyla on the microplastic surfaces were Proteobacteria and Bacteroidota, and their relative abundance on the microplastic surfaces was higher than that in sediment. The relative abundance of Proteobacteria was higher than that in water. The relative abundances of Bacteroidota and Actinobacteriota were significantly lower than that of water. *Massilia* and *Pseudomonas* were the dominant genera on the microplastic surfaces, and their relative abundances were significantly higher than those in the surrounding water and sediments. BugBase phenotype prediction revealed that the relative abundance of contains mobile elements, biofilm formation, potential pathogenicity, and stress tolerance phenotypes of microplastic bacterial communities were significantly higher than those of the surrounding water and sediments. The results revealed that microplastics may have contributed to the spread of harmful bacteria, including pathogenic bacteria, and increased the potential pathogenicity of bacterial communities. Additionally, microplastic surface bacterial communities had higher phenotypes of mobile gene element content. Revealing the potential harm of microplastic pollution to wetland ecology at the micro level may provide a scientific reference for maintaining the ecological stability of wetlands.

Key words: Poyang Lake; bacteria; microplastics(MPs); BugBase; *Pseudomonas*

因价格低廉、耐用性高且外观较好, 塑料制品深受市场喜爱^[1]. 2021年全世界塑料生产量超过3.9亿t, 中国塑料生产量在全球的份额持续增长, 已达到全球生产量的32%^[2]. 塑料具有难降解性, 可长期留存于环境中^[3], 受化学、机械和生物作用会降解为细小颗粒^[4], 其中粒径小于5 mm的定义为微塑料

(MPs)^[5]. 此外, 部分工业产品如洗漱用品和化妆品中会增添微塑料^[6], 最终输入环境之中. 微塑料具有

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疏水表面且比表面积大和吸附能力强的特征^[7,8],可为微生物提供稳定的栖息地^[9,10],有利于其定殖形成独特的“微塑料圈”^[11]。微塑料不仅可以支持致病菌和有害水华物种的生长并远距离转移^[12],还可能有助于抗生素耐药性的传播^[13]。此外,通过食物摄取、呼吸作用以及皮肤接触等方式,微塑料会向生物体与人体内转移^[14],危害人体各系统及相关器官的正常功能^[15]。

湿地的生态系统服务功能很强,是最具有价值的生态系统类型^[16],在径流调节、气候改善和环境净化等方面具有不可替代的作用^[17],也是微塑料的重要“汇”^[18]。鄱阳湖是我国第一大淡水湖泊,具有“高水成湖,低水成河”的自然地理特征^[19],是国际重要湿地,具有极为丰富的生物资源与较高的生物多样性^[20],其主导功能总价值达 3.627×10^{10} 元^[21]。近年来,鄱阳湖微塑料污染受到越来越多关注,在鄱阳湖水体、沉积物与生物体内都有微塑料的发现^[22,23]。但关于微塑料对微生物群落组成结构和功能性状改变尚有待进一步探讨。因此,为维护鄱阳湖区域生态环境健康,保障人类食品、卫生安全与可持续发展,深入研究鄱阳湖微生物群落结构和功能性状变化的微塑料驱动机制存在必要性。

本研究选取鄱阳湖候鸟栖息地白沙湖湖区为研究区,采集湖区沉积物和水体及其中各类型微塑料样品,通过16S高通量测序技术鉴定水体和沉积物中以及微塑料表面细菌群落结构,分析细菌群落在湿地环境与微塑料和不同聚合物类型微塑料之间的差异。利用BugBase表型预测分析微塑料表面细菌群落性状变化,深入探讨微塑料输入对湿地细菌性状的影响,明晰微塑料驱动下的生态威胁。本研究进一步揭示了鄱阳湖微塑料污染机制与潜在生态风险,以为鄱阳湖生态安全保护提供科学依据,也为其他地区湿地环境微塑料污染研究提供参考。

1 材料与方法

1.1 研究区设置

鄱阳湖位于长江南岸,江西省北部,地理位置为北纬 $28^{\circ}24' \sim 29^{\circ}46'$,东经 $115^{\circ}49' \sim 116^{\circ}46'$,属亚热带季风气候区,年降雨量在1 400~1 900 mm之间,年平均气温为 17°C ^[20]。鄱阳湖是我国最大的淡水湖泊,上连赣江、修水、饶河、信江和抚河这5条河流,下承黄金水道长江,湖区湿地面积2 700 km²,受气候影响洪、枯季节水面面积和蓄水容积变化大,生物资源丰富^[16]。基于前期鄱阳湖微塑料研究的成果,本研究拟将研究区设置在鄱阳湖湿地候鸟栖息地白沙湖。

1.2 样品采集

水体中微塑料样品使用拖网式的采集方法,将浮游生物网(0.52 m×0.36 m, 333 μm)固定于船尾,匀速行驶,每隔15~20 min采集一次样品。网上采集到的样品用无菌水冲洗到已消毒的白色托盘中,用灭菌镊子将可辨别的微塑料放入2 mL离心管中。同时收集2 L表层(0~10 cm)水体样品,放入用无菌水清洗过的采集瓶带回实验室。在每个采样点设置3个50 cm×50 cm的正方形采样方,每个样方相隔50 m以上,用灭菌不锈钢铲收集表层2 cm的沉积物1 L,放置已消毒的托盘上分离沉积物与微塑料,并用灭菌镊子将其分别放入不同的2 mL离心管中。所有采集的样品放置于冷藏箱带回实验室进行后续分析。

1.3 样品理化性质分析

将所有收集到的样品立即在超净工作台中取出放置于灭菌的培养皿中密封以进行进一步处理,整个过程保证无菌操作以防DNA变质和污染。在实验室利用傅里叶变换红外光谱(FTIR, Nicolet 6700, Perkin Elmer)分析微塑料的聚合物组成成分并对微塑料进行分类。进一步结合扫描电子显微镜(SEM, S-3400N, 日本日立电子)观察微塑料表面形态。将分类后的微塑料样品放置于2 mL离心管中,储存在 -80°C 的冰箱中,以备后续进行DNA测定。

1.4 样品DNA提取

将装有各类型微塑料样品的2 mL离心管取出,使用MoBio Powersoil DNA(Qiagen, 美国)试剂盒提取离心管中沉积物、水体以及微塑料表面的DNA。根据试剂盒的操作步骤说明进行DNA提取,将提取到的DNA储存于 -80°C 的冰箱中以便扩增测序。

1.5 PCR扩增

以上一步提取到的合格DNA作为模板,采用带有Barcode的引物338F(5'-ACTCCTACGGGAGGCA GCA-3')和806R(5'-GGACTACHVGGGTWTCTAA T-3')进行扩增。用1%琼脂糖凝胶电泳检测PCR产物提取质量,接着用DNA凝胶回收试剂盒(Axygen Biosciences, 美国)进行纯化回收。回收产物利用Illumina MiSeq PE300测序平台进行高通量测序。

1.6 序列处理与数据分析

使用QIIME2软件中包含的dada2方法对序列进行去噪获得扩增子序列变异体(amplicon sequence variants, ASVs)。以Silva为参考数据库对特征进行分类学注释,得到物种分类信息,使用R软件计算样品 α 多样性指数(Chao1、Shannon和Simpson指数),进而分析细菌的物种丰富度与多样性。并基于系统发生树的加权算法(Weighted Unifrac)进行 β 多样性分析,利用非度量多维标定法(non-metric multi-

dimensional scaling, NMDS)分析微塑料表面细菌群落与周围水体、沉积物之间组间差异.根据物种注释,选取各样品在门(phylum)和属(gene)分类水平上最大丰度排名前10的物种,利用Origin 2023制作物种相对丰度堆叠图.使用BugBase预测细菌群落的表型特征,分析微塑料对于其表面微生物功能表型的影响.

2 结果与分析

2.1 白沙湖微塑料表面微观特征

本研究采集到的微塑料样品的聚合物组成主要

为聚乙烯(polyethylene, PE),聚酯纤维(polyester, PET),聚丙烯(polypropylene, PP)和聚苯乙烯(polystyrene, PS)(图1).扫描电镜观测结果显示微塑料总体上均受风化作用影响,表面粗糙并带有撕裂. PP边缘相对光滑,表面具有网丝状和团状附着物,带有轻度撕裂,在局部SEM图像中可较清晰观察到丝状撕裂物[图2(a)]; PET表面具有裂纹,并且有轻度破损[图2(b)]; PE风化较为严重,表面凹凸不平,十分粗糙,多有孔隙[图2(c)]; PS微塑料有明显破损,有明显较大孔隙,从局部SEM图像可以看到PS表面有更为明显的细小孔隙与带状附着物[图2(d)].

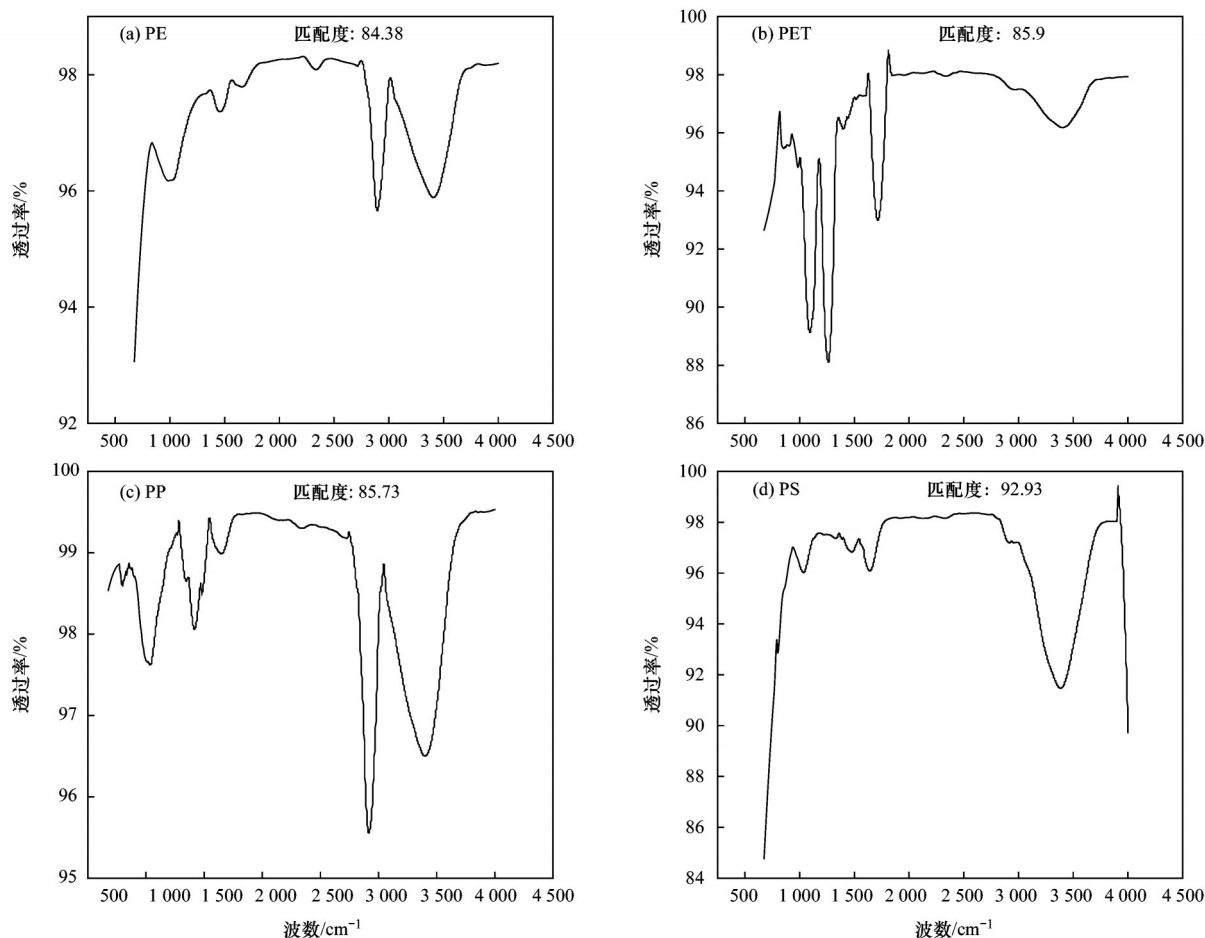


图1 微塑料红外光谱图

Fig. 1 FTIR spectrum of different types of microplastics

2.2 白沙湖微塑料细菌群落生物多样性

通过对水体、沉积物中以及微塑料表面细菌群落进行统计分析,白沙湖水体及其中微塑料共得到874条ASV,沉积物及其中微塑料共得到977条ASV.所有样品处理的测序Coverage指数为100%,样品稀释曲线趋于平缓,表明测序数据量大,样品测序完整.沉积物及其中微塑料表面之间的细菌ASV数量范围为134~480,水体及其微塑料表面的ASV数量范围为112~365.在 α 多样性中,微塑料表面细菌群落的生物丰富度总体上

均低于周围水体和沉积物, PP微塑料表面物种丰富度最低且显著低于周围沉积物和水体($P < 0.05$).在物种多样性上除PET外其余3种微塑料表面物种多样性显著低于周围沉积物($P < 0.05$,表1).

通过非度量多维标定法(NMDS)比较微塑料表面细菌群落与周围环境之间的差异.沉积物与水体NMDS的Stress均小于0.1,结果较好,具有可靠性.图3显示微塑料样品与沉积物、水体距离均较远且多分布在不同区域,说明微塑料表面细菌群落结构

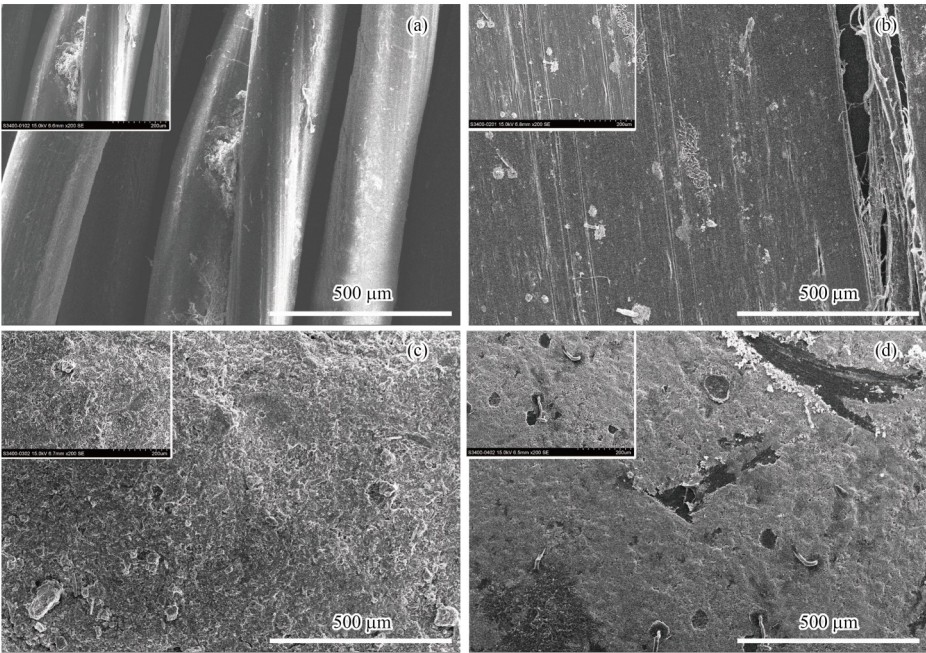


图 2 微塑料表面 SEM 图
Fig. 2 SEM images of the microplastics

表 1 水体、沉积物中和不同类型微塑料表面细菌 α 多样性指数¹⁾

Table 1 The α diversity of bacteria in the water, sediment and on the surface of microplastics

类别	样品	Coverage 指数/%	Chao1 指数	Simpson 指数	Shannon 指数
沉积物	PE	100	273.33 ± 182.56ab	0.94 ± 0.02b	5.39 ± 0.82b
	PET	100	291 ± 113.64ab	0.92 ± 0.09ab	5.46 ± 1.72ab
	PP	100	239.33 ± 33.55b	0.95 ± 0.02b	5.69 ± 0.45b
	PS	100	268.67 ± 84.10ab	0.95 ± 0.01b	5.59 ± 0.52b
	沉积物	100	407 ± 26.46a	0.99 ± 0.01a	7.84 ± 0.34a
水体	PE	100	263 ± 52.72ab	0.94 ± 0.03a	5.46 ± 0.24b
	PET	100	221 ± 77.67ab	0.79 ± 0.19a	4.34 ± 1.84ab
	PP	100	166 ± 69.20b	0.91 ± 0.06a	4.72 ± 1.04b
	水体	100	330 ± 41.61a	0.97 ± 0.01a	6.57 ± 0.19a

1) 数据为平均值 ± 标准偏差; 同列相同小写字母表示差异不显著 ($P > 0.05$)

与周围水体和沉积物均存在较大差异. 沉积物中微塑料样品相距较近[图 3(a)], 而水体中微塑料样品

相对分散[图 3(b)], 可知水体中不同类型微塑料表面细菌群落存在一定差异.

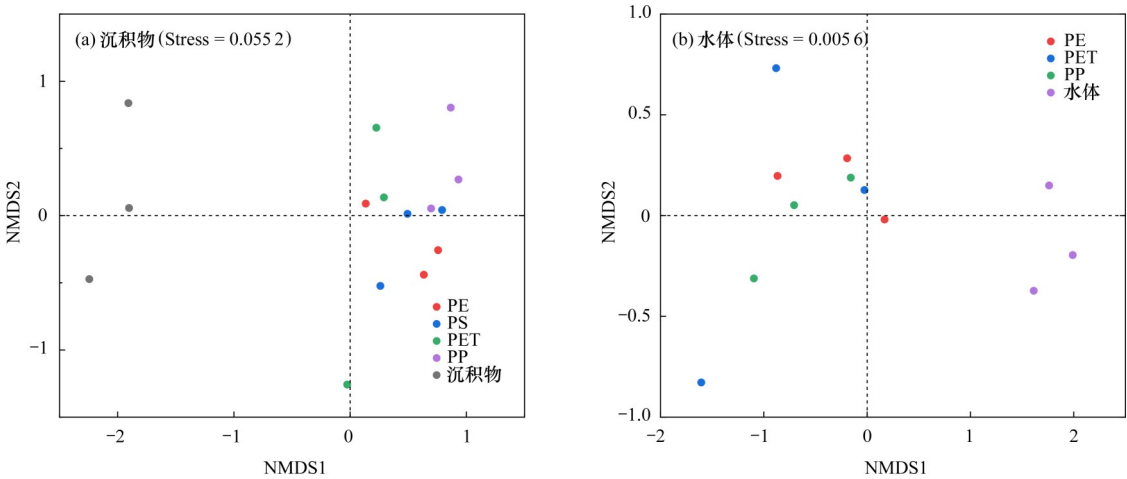


图 3 weighted unifrac 非度量多维度标定法 (NMDS)
Fig. 3 The weighted unifrac non-metric multi-dimensional scaling

2.3 白沙湖微塑料表面细菌群落结构分析

本研究中检测到白沙湖沉积物及其中微塑料表面细菌共有 26 门、49 纲、106 目、183 科、286 属和 323 种. 水体及其中微塑料表面共检测出 26 门、47 纲、100 目、176 科、277 属、和 318 种. 在门水平上, 沉积物、水体中与微塑料表面细菌群落组成分类如图 4 所示, 其中仅展示丰度排名前 10 的物种, 其余物种合并表示为 Others. 沉积物、水体和微塑料表面细菌群落门水平上主要由变形菌门 (Proteobacteria)、拟杆菌门 (Bacteroidota)、放线菌门 (Actinobacteriota)、厚壁菌门 (Firmicutes)、蓝细菌门 (Cyanobacteria)、疣微菌门 (Verrucomicrobiota)、脱硫杆菌门 (Desulfobacterota)、绿弯菌门 (Chloroflexi) 和硝化螺菌门 (Nitrospirota) 等组成, 其中变形菌门和拟杆菌门占有绝对优势 (55.27%~94.32%). 如图 4 (a) 所示, 沉积物中微塑料表面的变形菌门、拟杆菌门、放线菌门以及厚壁菌门的相对丰度较沉积物明显增加. 在图 4(b) 中, 微塑料表面变形菌门物种相

对丰度明显高于周围水体, 而拟杆菌门与放线菌门的相对丰度低于水体.

图 5 是水体、沉积物中与微塑料表面细菌组成在属水平上的分类组成, 其中显示排名前 10 的物种, 其中有 3 个属为未分类 (Unclassified), 其余物种合并显示为 Others. 图 5(a) 中, 马赛菌属 (*Massilia*) 和假单胞菌属 (*Pseudomonas*) 是沉积物中微塑料表面的优势菌属, 相对丰度高于沉积物, 共达 33.18%~45.61%; 黄杆菌属 (*Flavobacterium*)、紫色杆菌属 (*Janthinobacterium*) 和未分类的草酸杆菌属 (Unclassified_Oxalobacteraceae) 在微塑料表面的占比略低, 但仍较周围沉积物有所升高. 水体样品以黄杆菌属和未分类的丛毛单胞菌属 (Unclassified_Comamonadaceae) 为优势菌属; 而水体中的 3 种微塑料以假单胞菌属和马赛菌属的相对丰度占优势, 紫色杆菌属和未分类的草酸杆菌属的占比较水体明显升高, 水体中的优势菌属在其表面相对丰度明显降低 [图 5(b)].

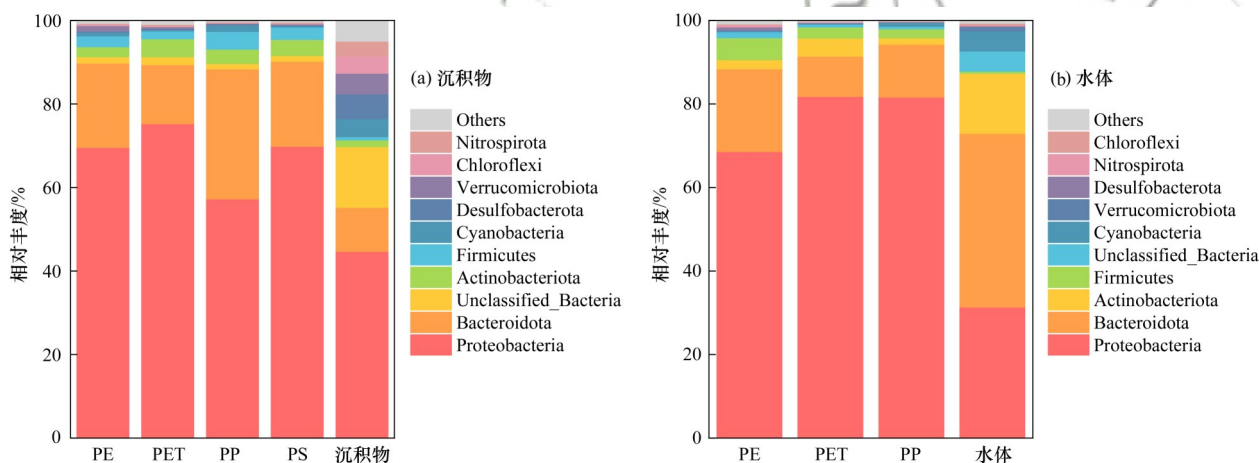


图 4 水体、沉积物和微塑料表面细菌门水平分布

Fig. 4 Distribution of bacteria in water, sediment, and microplastic surfaces at the phylum level

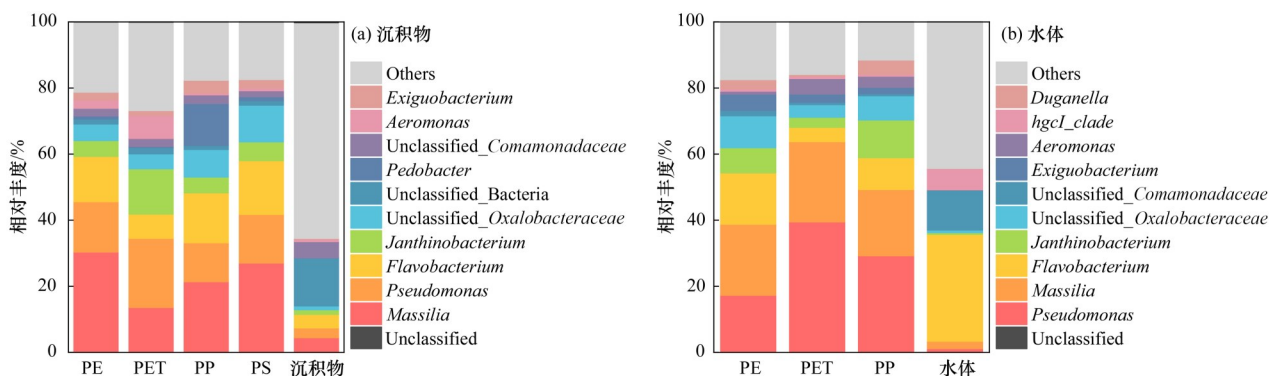


图 5 水体、沉积物和微塑料表面细菌属水平分布

Fig. 5 Distribution of bacteria in water, sediment, and microplastic surfaces at the genus level

2.4 BugBase 表型分析

BugBase 预测了好氧 (aerobic, Aer)、厌氧 (anaerobic, Ana)、可移动基因元件含量 (contains_mobile_elements, CMEs)、兼性厌氧 (facultatively_

anaerobic, FA)、生物膜形成 (forms_biofilms, FBs)、革兰氏阴性 (gram_negative, GN)、革兰氏阳性 (gram_positive, GP)、潜在致病性 (potentially_pathogenic, PP) 及胁迫耐受 (stress_tolerant, ST) 这 9

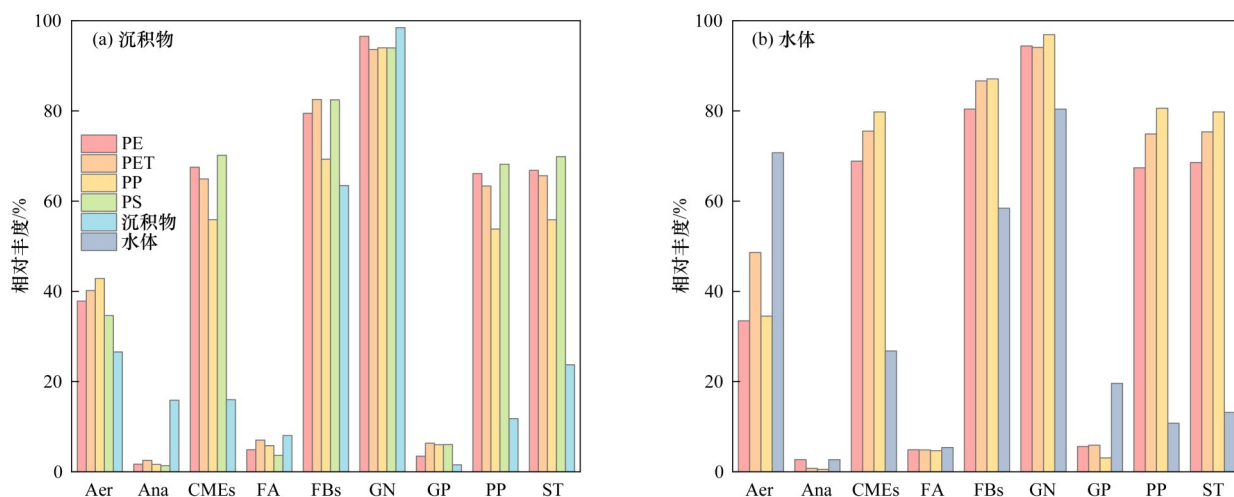


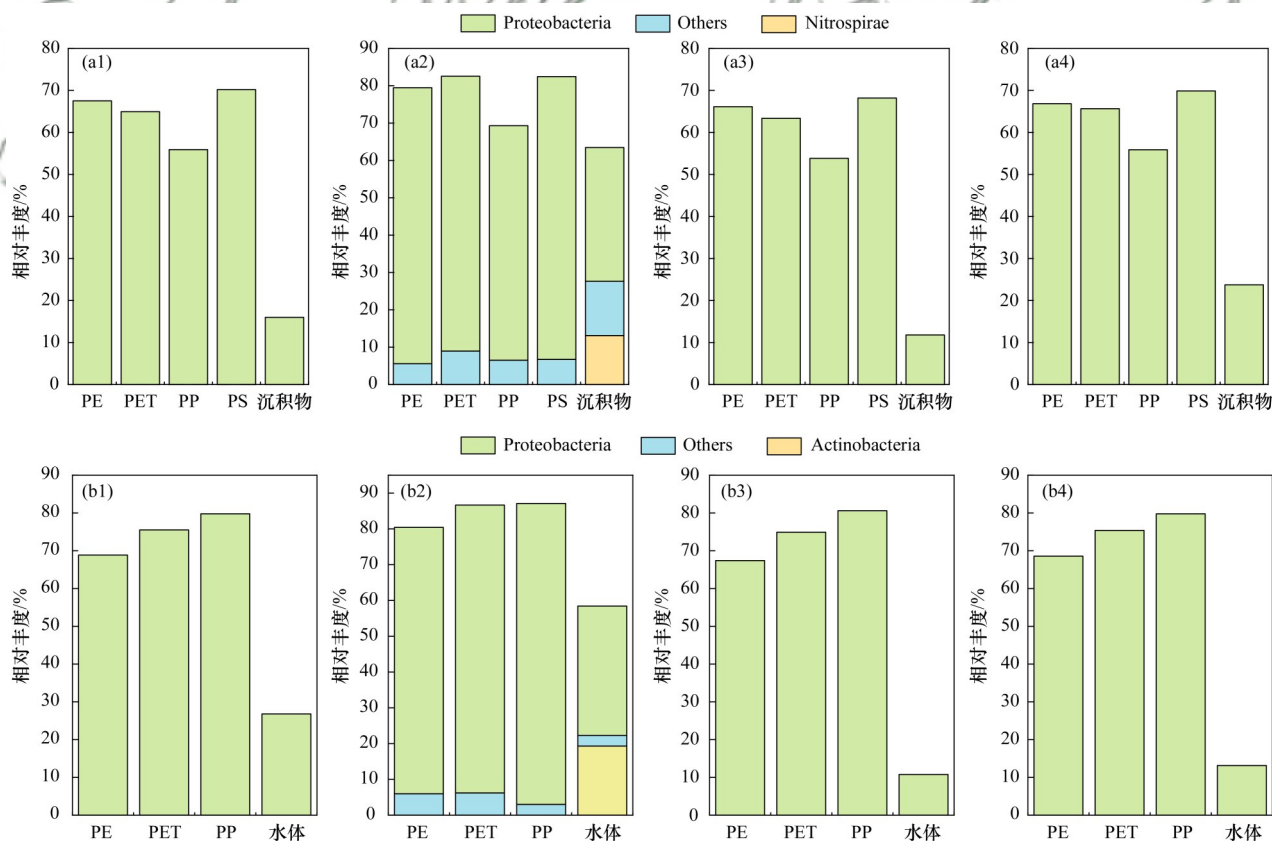
图6 BugBase表型预测

Fig. 6 BugBase phenotype prediction

种微生物表型.较沉积物而言,微塑料表面细菌群落的可移动基因元件含量、潜在致病性及胁迫耐受能力明显升高,厌氧表型明显降低[图6(a)].可移动基因元件含量、生物膜形成、革兰氏阴性、潜在致病性及胁迫耐受等5个功能表型在水体微塑料表面细菌群落中较水体细菌群落存在上升,而在好氧和革兰氏阳性功能表型上水体微塑料表面细菌群落

却明显降低[图6(b)].

经图7进一步分析发现,可移动基因元件含量、生物膜形成、潜在致病性及胁迫耐受等4个功能表型相关的细菌主要由变形杆菌组成.在这4个功能表型贡献上,变形菌门对微塑料的贡献明显高于沉积物和水体,而在微塑料样品之间差异不大.在生物膜形成表型贡献上,硝化螺菌门对沉积物和放线菌



(a1)~(a4)沉积物中采集的样品,(a1)可移动基因元件含量,(a2)生物膜形成,(a3)潜在致病性,(a4)胁迫耐受;(b1)~(b4)水体中采集的样品,(b1)可移动基因元件含量,(b2)生物膜形成,(b3)潜在致病性,(b4)胁迫耐受;细菌表型贡献表示特定表型的主要物种组成,即反映物种与表型的对应关系;横坐标为所有样品,不同颜色表示不同的物种,纵坐标为该样本中不同物种对此表型的贡献

图7 物种表型贡献

Fig. 7 Species phenotypic contribution

门对水体均存在一定贡献,但在微塑料样品上并没有发现其二者的功能表型贡献。

3 讨论

3.1 环境与微塑料表面细菌群落物种多样性特征

本研究中微塑料表面细菌群落物种多样性与周围水体和沉积物存在显著差异.微塑料表面细菌群落丰富度和多样性皆低于周围水体和沉积物,与此前的研究结果相一致^[3].Frère等^[24]在布雷斯特湾的研究显示,微塑料表面物种多样性高于环境与天然介质,研究结果间的差异可能与研究区地理位置、研究的季节差异以及研究区环境不同存在一定关联^[12,25].沉积物和水体中几种微塑料丰富度最低的是PP微塑料,这可能是因为相较于其他几种微塑料而言,PP表面相对光滑从而影响细菌定殖.已有报道指出微塑料表面的粗糙程度是细菌吸附在不同微塑料上的主要因素,即粗糙表面为细菌附着提供更多表面积,增强了细菌的附着力^[26].

早前研究表明微塑料表面的细菌主要来源于周围环境^[1],但由于微塑料特殊的性质使其在环境中形成了特殊的生态位^[10,27],从而于其表面形成了一套异于周围环境和自然介质的独特细菌群落组成^[28].本研究也发现微塑料表面细菌群落结构与周围水体和沉积物存在较大差异.有研究认为不同聚合物微塑料之间细菌群落差异显著^[29],而本研究中没有得到上述结论,Tagg等^[30]和Oberbeckmann等^[31]与笔者持相同看法.不同研究结果之间的悖论可能是由于野外采样无法确定微塑料在环境中的留存时间^[32],且难以准确追溯微塑料的来源与运转过程造成的。

3.2 环境与微塑料表面细菌群落结构特征

变形菌门、拟杆菌门以及厚壁菌门是微塑料表面细菌群落常检测到的主要菌门^[33],本研究亦发现变形菌门在微塑料表面占到绝对优势,相对丰度明显高于周围沉积物与水体,且在水体微塑料表面占比高于沉积物微塑料.有研究认为变形菌门是微塑料表面的早期定殖者^[34],而后是拟杆菌门等一些次级定殖者^[35].拟杆菌门是本研究中微塑料表面仅次于变形菌门的优势菌门,其于沉积物微塑料表面相对丰度较周围沉积物明显升高,而于水体微塑料却与沉积物得出相反结果.可能由于本研究中采集到的微塑料表面“微塑料圈”尚处于一个较为初始的演化阶段,且水体微塑料表面微生物群落发展可能较沉积物微塑料处于一个更早的时期。

属水平上,假单胞菌属、马赛菌属以及紫色杆菌属是微塑料表面的优势菌属,相对丰度较周围环境明显升高.假单胞菌是海洋中人工表面的早期定

殖菌属之一^[36],在已有研究中常于微塑料上检测到^[37],是目前微塑料细菌群落研究的重点.有研究证实假单胞菌属对于动植物和人类具有致病潜力,如机会病原体铜绿假单胞菌可引起多种感染与炎症^[38],对于人类健康存在较大威胁.较环境而言微塑料表面显著富集了一些人类致病假单胞菌,如防御假单胞菌(*Pseudomonas protegens*)和旋氏假单胞菌(*Pseudomonas stutzeri*)^[39],此外Wu等^[40]还在微塑料生物膜上检测到两种自然基质上不存在的人类机会致病假单胞菌[蒙氏假单胞菌(*Pseudomonas monteilii*)和门多萨假单胞菌(*Pseudomonas mendocina*)].因此,需谨慎对待微塑料表面高丰度的假单胞菌,未来研究应更进一步探讨微塑料表面假单胞菌的致病潜力.马赛菌属在环境中分布广泛,适应多种生存环境,具有溶磷、降解多环芳烃菲和抗重金属等功能,在土壤修复方面具有重要意义^[41].Jiang等^[42]从Mellonella幼虫肠道中分离出来一种可以降解聚苯乙烯(PS)的马赛菌属细菌(*Massilia* sp. FS1903),通过30 d的培养使PS失重(12.97 ± 1.05)%,具有相当大的塑料降解潜力.紫色杆菌属在环境中广泛存在,耐受极端环境,在医疗领域发挥着重要作用,可以合成具有抑菌、抗癌、抗病毒与抗肿瘤等多种有益功能的紫色杆菌素^[43];还有研究发现紫色杆菌属具有在低温下强氮代谢的能力,在水污染处理方面具有巨大的应用前景^[44].

3.3 微塑料污染生态风险预测

为了进一步探讨微塑料对细菌群落功能性状的影响,评估微塑料污染在微生物层面对环境的生态威胁,通过BugBase表型预测发现微塑料表面菌群的功能性状与周围环境存在差异,可移动基因元件含量、生物膜形成、潜在致病性以及耐受胁迫等4个功能性状在微塑料表面有明显的提升.细胞内的抗生素抗性基因位于染色体或可移动基因元件上^[45],现有报道声称与浮游细菌相比,塑料相关细菌含有更高丰度的可移动遗传元件^[46].此外,有研究发现微塑料表面可移动基因元件与抗生素抗性基因的绝对和相对丰度均显著相关^[47],可移动基因元件含量的升高会促进微塑料表面抗生素抗性基因的富集传播^[48].目前已有研究证明抗生素抗性基因丰度相较于无机基质和自然水环境,在微塑料表面呈现更高的富集趋势^[49].生物膜是由包裹在胞外聚合物中的表面相关微生物细胞组成的集合^[50],可提高细菌对抗菌药物的耐受性、加快抗生素抗性基因的进化速度和在病原体中的传播速度^[51],增强细菌对不利环境变量如紫外线、热量和有毒金属等的抵抗力^[33].在许多微塑料研究中都有致病菌的发现^[9],如

弧菌^[11]和假单胞菌^[52],且有研究认为相较于一些自然介质微塑料具有更强的致病菌富集能力^[53].本研究发现微塑料表面细菌群落潜在致病性的提高进一步验证了微塑料对致病菌的富集作用,这对于人类卫生安全和生态稳定维护都是潜在的挑战.耐受胁迫是评估细菌群落生态风险的一个重要指标^[10],微塑料表面细菌群落耐受胁迫能力的升高意味着细菌群落可以更好地适应和抵抗不利环境,加重微塑料的生态环境威胁.

4 结论

(1)鄱阳湖白沙湖区微塑料表面细菌群落丰富度和多样性均低于周围水体和沉积物.NMDS分析结果表明,微塑料与水体和沉积物之间细菌群落结构具有明显差异.

(2)在门水平上,变形菌门和拟杆菌门在水体、沉积物与微塑料样品中均呈优势状态,变形菌门在微塑料表面的相对丰度较周围水体和沉积物有明显升高.水体和沉积物中微塑料表面细菌在属水平上以马赛菌属、假单胞菌属与紫色杆菌属占有较大优势,相对丰度明显高于周围水体和沉积物.

(3)BugBase表型预测分析结果显示,微塑料表面细菌群落的可移动基因元件含量、生物膜形成、潜在致病性及胁迫耐受能力较周围水体、沉积物明显有所增强,且其主要贡献菌门为变形菌门.

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