微生物学通报
Microbiology China
tongbao@im.ac.cn
http://journals.im.ac.cn/wswxtbcn

Dec. 20, 2021, 48(12): 4918−4931
DOI: 10.13344/j.microbiol.china.210265

专论与综述

水生植物-微生物联合去除水体有机污染物的研究进展

王秀璞　张慧　王语萱　李彦*　杜道林*

江苏大学环境与安全工程学院 环境健康与生态安全研究院　江苏 镇江　212013

摘　要：近年来，随着经济的快速发展，大量有机化合物随着工业废水和生活污水排放进入水体，严重破坏了水环境的生态平衡，威胁着水生生物及人类健康。植物-微生物联合修复技术因具有修复效率高、持续时间长、投入成本低，而且不会产生二次污染等特点，在水体有机污染治理中受到了人们的广泛关注。本文综述了近年来水生植物-微生物联合去除水体有机污染物的应用现状，详细阐述了水生植物-微生物联合修复过程中的研究方法、作用机制及影响因素。以期不断完善和优化水生植物-微生物联合修复技术，为实现水环境有机物污染的统筹高效治理提供参考。

关键词：生物降解，有机污染物，水生植物-微生物，人工湿地

Application of aquatic plant-microbe association in removal of organic pollutants in water bodies: a review

WANG Xiupu　ZHANG Hui　WANG Yuxuan　LI Yan*　DU Daolin*

Institute of Environmental Health and Ecological Security, School of the Environment and Safety Engineering, Jiangsu University, Zhenjiang, Jiangsu 212013, China

Abstract: With the rapid economic growth, a large amount of organic compounds has been released into water bodies, which seriously damages the eco-balance of aquatic system and threatens aquatic life and human health. Remediation via plant-microbe association has attracted wide attention, because of its high efficiency, long duration, low cost, and environmental friendliness. We reviewed the recent advance in the application, research methods, mechanism, and influencing factors of aquatic plant-microbe association in the removal of organic pollutants in water bodies. This review will facilitate the performance optimization of remediation via aquatic plant-microbe association and provide an effective way for the removal of organic pollutants in water bodies.

Keywords: biodegradation, organic pollutants, aquatic plant-microbe association, constructed wetlands

---

Foundation items: National Natural Science Foundation of China (31700108, 31770446); Senior Talent Scientific Research Initial Funding Project of Jiangsu University (17JDG017)

***Corresponding authors:** E-mail: LI Yan: liyanhellen@ujs.edu.cn; DU Daolin: daolindu@163.com

Received: 17-03-2021; **Accepted:** 21-05-2021; **Published online:** 04-06-2021

基金项目：国家自然科学基金(31700108，31770446)；江苏大学高级人才科研启动基金(17JDG017)

*通信作者：E-mail：李彦：liyanhellen@ujs.edu.cn；杜道林：daolindu@163.com

收稿日期：2021-03-17；接受日期：2021-05-21；网络首发日期：2021-06-04

1 有机污染物危害及去除技术

有机污染物是指排入环境中直接或间接对生态系统造成不良影响的有机物质，根据来源可分为天然有机污染物和人工合成有机污染物 2 大类。其中，人工合成的有机物普遍存在于食品、添加剂、香水、药物、化妆品、明胶、塑料、油漆、农药和其他工业产品的生产、加工过程中，通过工业废水、农业径流、城市径流、垃圾渗滤液、大气沉降等方式进入环境，因此是环境中有机污染物的主要来源[1]。在人类活动频繁的沿海海水区域，主要为氨氮、活性磷酸盐和石油的污染[2]；而在地表水、地下水、河流及底泥等淡水区域，主要为烷烃、多环芳烃、卤代烃、有机农药等有机物污染[3]。环境中的有机污染物质被生物摄入后，在体内被逐级累计放大，产生毒性、致癌、致畸、致突变和干扰内分泌等效应，严重威胁着生态平衡和人类健康[4]。因此，治理水体有机污染，解决人民饮用水安全的问题迫在眉睫。

生物修复技术是一种利用生物(植物、动物、微生物)的特性，通过吸收、降解或转化等方式原位去除污染物的技术[5]，省去了物理修复、化学修复技术的中间转移、运输等环节，节约了成本，而且生物降解过程可以达到对污染物的完全矿化，无二次污染生成，近年来成为人们关注的热点[6]。目前生物修复技术中研究较多的主要包括植物修复、微生物修复、植物-微生物联合修复技术。传统的植物修复和微生物修复技术中，由于植物一般缺乏降解有机物的酶，单一利用植物修复去除环境有机污染物的去除效率很低[2]；而单纯依靠添加降解微生物虽然可以高效降解目标污染物，但由于环境中的营养不足，微生物菌剂在寡营养环境中难以长时间存活，成为制约该技术应用的瓶颈[7]。植物-微生物联合修复，利用植物-微生物互惠共生、相互协作关系，共同降解有机污染物。植物作为一个太阳能驱动下的生物能量泵，通过光合作用源源不断地供给根际微生物生长和维持活性所必需的营养与氧气。根际微生物则通过对污染物的降解，降低污染物的环境毒害作用，或促进植物生长、增强植物对外界环境胁迫的抵抗力[8-9]。植物-微生物联合修复技术是在植物修复和微生物修复技术基础上进行优势互补、整合形成的技术，可以实现长时间、高效率、低成本地去除环境污染物，因而受到了广大环境工作者的关注。本文综述了近年来水生植物-微生物联合修复水体有机污染物的研究进展、作用机制及影响因素，以期为高效去除环境中难降解和有毒有机物质提供借鉴。

2 水生植物-微生物联合修复技术及其应用现状

目前在植物-微生物联合修复技术中常用的水生植物主要有：(1) 挺水植物(如芦苇、菖蒲)，(2) 浮叶植物(如睡莲)，(3) 漂浮植物(如浮萍)，(4) 沉水植物(如金鱼藻、黑藻)；微生物则主要包括环境土著微生物或者引入的外源高效功能微生物菌剂。

2.1 水生植物-土著微生物

利用水生植物-微生物联合去除有机污染物的过程中涉及非生物去除(如有机物的蒸发、光降解、水解)与生物去除(如微生物的降解及植物的吸收、积累、固定等)这 2 方面因素的作用[10]。生物作用是其中的主导因素。在植物根际存在着根际激发效应，即根际是一个氧气充足、营养丰富的环境，使得该区域聚集了比非根际区更多的微生物，而且微生物代谢活性更为活跃[11]。微生物在植物-微生物耦合降解有机污染物的过程中起着举足轻重的作用[12]。大量研究表明，革兰氏阴性菌为植物根际主要富集的微生物菌群，通常这种类型微生物在植物根系分泌物的利用及分泌降解酶去除环境污染物方面表现更高效，主要包括根瘤菌(*Rhizobium*)、固氮菌(*Azotobacter*)、假单胞菌(*Pseudomonas*)等细菌，以及一些与植物共生的真

菌[13]。Han 等研究发现，漂浮植物荇菜(*Nymphoides peltata*)和欧菱(*Trapa natans*)植物表面生物膜中 *nirK*、*nirS*、*cnorB*、*nosZ* 这 4 类反硝化基因的大量富集，可能在修复富营养化水体过程中发挥重要作用[14]。植物根系分泌物的释放改善了根际环境的理化性质(pH、溶解氧、氧化还原电势等)及微生物群落结构，直接或间接影响根际有机污染物的去除效率[15]。Meng 等研究结果显示根际微生物的数量和活性与污染物的去除效率呈正相关[16]。Yin 等研究发现由于根系分泌氧，使得 4 种水生植物[金鱼藻(*Ceratophyllum demersum*)、黑藻(*Hydrilla verticillata*)、菹草(*Potamogeton crispus*)、睡莲(*Nymphaea tetragona*)]根际氨氧化古细菌的 *amoA* 基因相对丰度显著高于非根际区[17]。Yan 等将菖蒲和沉积物微生物样品联合用于降解沉积物中多环芳烃(Polycyclic Aromatic Hydrocarbons，PAHs)，发现菖蒲根际的氧化还原电势、含氧量及多环芳烃厌氧降解菌的数量明显高于非根际区域，PAHs 降解率较单独的沉积物微生物处理或植物处理组相比至少增加了 70%[18]。

大量难降解的有机污染物被发现在植物和土著微生物的共同作用下被有效去除(表 1)。Ogata 等研究发现，浮萍在根际效应的驱动下，根际细菌可以加速水体中对叔丁基苯酚的去除[29]。Toyama 等则报道了，芦苇根际沉积物中的微生物可以加速芘和苯并[a]芘的去除[19]。Qu 等研究发现农药阿特拉津在种植有穗状狐尾藻(*Myriophyllum spicatum*)沉积物中的残余率显著低于未种植对照组[20]。同时，Teeratitayangkul 等发现生长成熟的香根被一层可以降解苯酚的由细菌[肠杆菌(*Enterobacter* spp.)、假单胞菌(*Pseudomonas* spp.)、红球菌(*Rhodococcus* spp.)、不动杆菌(*Acinetobacter* spp.)]和真菌[念珠菌(*Candida* spp.)、根霉菌(*Rhizopus* spp.)、曲霉菌(*Aspergillus* spp.)、镰刀菌(*Fusarium* spp.)]组成的生物膜覆盖，加速了废水中苯酚的去除[21]。

近年来受到广泛关注的人工湿地(Constructed Wetland，CW)正是植物-根际微生物联合修复技术在水体污染治理中的应用。CW 是经人为设计、建造并可监督控制的污水生态处理工程，是由基质、植物、微生物和水体组成的复合生态系统[30]。目前主要用于对富营养化水体、工农业废水、城市污水等有机废水的治理过程。Vymazal 等研究发现 3 个水平潜流人工湿地对农业废水中总氮平均去除率分别为 61.2%、62.6%和 70.9%，表明水平潜流人工湿地是修复农业废水的有用工具[31]。Stefanakis 等研究利用水平地下流人工湿地处理被石油烃和酚类物质混合污染的地下水，发现不仅地下水中的甲基叔丁基醚、苯、氨等污染物被有效去除，水中的苯酚、间甲酚这 2 种酚类化合物还可以完全被去除[32]。Dan 等发现垂直流人工湿地可以对人工合成的垃圾渗滤液中的苯酚、双酚 A 和对叔丁基苯酚的去除率分别达到 88%−100%、9%−99%和 18%−100%[33]。Toro-Vélez 等利用热带水平地下流人工湿地可以有效去除污水处理厂废水中约 73.39%的双酚 A 和 62.8%的壬基酚[34]。Zhang 等研究发现采用小规模的地下水流人工湿地可以去除废水中 40%−80%的药品和个人护理产品[35]。

然而在不同环境下，传统 CW 对不同有机污染物的去除效率存在较大的差异，有时对一些难降解有机物质不能有效去除。因此，需要改进人工湿地的设计，通过选择合适的宿主植物、添加吸附剂或者载体等途径，提高 CW 去除有机污染物的能力。Saggaï 等研究发现，具有 C4 光合途径的单子叶植物与其他物种相比，具有良好的污染物耐受性，更适合用于构建人工湿地治理有机废水[36]。Zhang 等研究了种植不同植物[天山泽芹(*Berula erecta*)、黄菖蒲(*Iris pseudacorus*)、灯心草(*Juncus effusus*)、芦苇(*Phragmites australis*)、香蒲(*Typha latiflolia*)]的湿地去除布洛芬和碘海醇的效果，结果发现仅天山泽芹和灯心草对该污染物

表 1　水生植物-土著微生物组合

Table 1　Aquatic-indigenous microbes association

水生植物 Aquatic plant	土著微生物 Indigenous microbes	有机污染物 Organic pollutants	修复效果 Removal efficiency	文献 References
Acorus calamus	Aerobes (including *Vogesella*, *Pseudomonas*, *Flavobacterium*, *Rhizobium*) and anaerobes (including *Longilinea*, *Bellilinea*, *Desulfobacca*, *Anaeromyxobacter*) were the main bacterial communities in the rhizosphere	Pyrene, BaP	Microorganisms in the rhizosphere sediments accelerated the removal of PAHs	[18]
Phragmites australis	Rhizospheric microorganism	Pyrene, BaP	Removal of pyrene and BaP was observed in sediments containing plants, while contaminants persisted in sediments without plants	[19]
Myriophyllum spicatum	*Acetobacter*	Atrazine	The residual rate of atrazine was significantly reduced in vegetative sediments	[20]
Vetiver	Phenol-degrading bacterial community in rhizosphere (including *Enterobacter*, *Pseudomonas*, *Rhodococcus*, *Acinetobacter*)	Phenol	The phenol of 500 mg/L was degraded to 1 mg/L in 249 h	[21]
Typha angustifolia	*Cytophaga* sp.	Ibuprofen	*Typha angustifolia* strongly promoted the rhizodegradation of ibuprofen	[22]
Lemna minor	Naturally occurring microbial of duckweed	Phenol	Removal of 70% of phenol from the highest initial concentration of 100 mg/L, in mixed cultures of duckweed and bacteria	[23]
Lemna minor	Naturally occurring microbial of duckweed	Benzotriazole	The highest BZT concentration decreases were thus in 0 g/L NaCl, 0.1 mg/L BZT, and in the presence of microbes	[24]
Algae	Activated sludge bacteria	The synthetic municipal wastewater	The amelioration of microbial activity after introducing algae resulting in high nutrients removal in the combined system	[25]
Microalgae	Activated sludge bacteria	Olive washing water	Removal of phenols, COD and BOD_5 is 94.84%, 85.86%, 99.12%	[26]
Phragmites australis	Rhizospheric microorganism	PTBP	Bacteria can accelerate the biodegradation of PTBP through co-metabolism in the rhizosphere	[27]
Phragmites australis	Rhizospheric microorganism	BPA, BPF, 3-nitrophenol, POP	*Phragmites australis*-bacteria combination can accelerate the biodegradation of pollutants	[28]

表现出较高的去除效率[37]。Kadam 等则发现将 2 种水生植物[香根草(*Chrysopogon zizanioides*)和狭叶香蒲(*Typha angustifolia*)]混合培养构建的人工湿地比单一植物的湿地系统对纺织废水的处理效果更好[38]。杜甫义等研究发现 3 种水生植物[水葱(*Scirpus tabernaemontani*)、黑三棱(*Sparganium*)和芦苇(*Phragmites australis*)]混合种植对污水中化学需氧量、氨氮、总氮和总磷的去除效果及稳定性优于单一植物覆盖的人工湿地[39]。Wirasnita 等在湿地体系中添加活性炭作为湿地基质后，发现与不添加活性炭的对照组对双酚 A (35%−93%)、双酚 F (45%−95%)、双酚 S (0%−78%)、对叔丁基苯酚(25%−93%)的降解能力相比，添加活性炭的处理组可以持续、稳定地去除上述 4 种有机物

质，去除率达到 98%–100%[40]。

2.2 水生植物-外源高效功能菌(群)

在利用植物-土著微生物联合降解污染物的过程中，由于降解功能菌在环境微生物群落中的丰度一般较低且降解能力有限，导致有机物降解效率受到限制。然而通过接种外源高效降解菌株或功能菌群到植物的根际，可以有效解决上述问题，大大提高污染物的降解效率。目前已经分离得到大量能够降解难降解有机物的高效降解菌株(表 2)。Li 等从浮萍根际筛选出的双酚 A 高效降解菌株新鞘氨醇杆菌(*Novosphingobium* sp. FID3)接种到浮萍(*Spirodela polyrhiza*)根际，发现 FID3 可以稳定地定殖在浮萍根表面，*Spirodela*-FID3 组合可以在 120 h 内持续、高效、完全去除污水中的双酚 A[41]。Wang 等将微囊藻毒素降解菌株接种至种植黄菖蒲(*Iris pseudacorus* L.)的小型人工湿地中，发现与未接菌的人工湿地相比，对微囊藻毒素的去除速率提高了 110%。体系内降解基因 *mlrA* 的丰度显著高于未生物强化的人工湿地[60]。

部分外源高效功能菌株不仅具有降解污染物活性，还具有促进植物生长的作用。Singh 等发现从芦苇根际分离的微杆菌(*Microbacterium* sp. P27)不仅可以降解林丹，还具有产吲哚-3-乙酸、氨和 1-氨基环丙烷-1-羧酸脱氨酶(ACC 脱氨酶)等植物促生属性[61]。Toyama 等发现分离自浮萍(*Lemna aoukikusa*)根际的醋酸钙不动杆菌(*Acinetobacter*

表 2 水生植物-功能菌联合

Table 2 Aquatic and functional microbe association

水生植物 Aquatic plant	降解菌 Functional microbes	降解菌株来源 Source of microbes	有机污染物 Organic pollutants	修复效果 Removal efficiency	文献 References
Leptochloa fusca	*Acinetobacter* sp. ACRH82, *Acinetobacter* sp. BRRH61, *Bacillus niabensis* ACSI85	The rhizosphere or root of a plant	Hexadecane	Plants-bacteria combination significantly improved pollutant removal and reduced toxicity	[7]
Spirodela polyrrhiza	*Novosphingobium* sp. FID3	*Spirodela polyrrhiza* rhizosphere	BPA	*Spirodela*-FID3 combination can remove BPA in wastewater many times	[41]
Selenastrum capricornutum	*Mycobacterium* sp. strain A1-PYR	The mangrove surface sediment	Pyrene	Bacteria accelerate the degradation of pyrene	[42]
Typha domingensis	*Klebsiella* sp. strain LCRI87, *Pseudomonas* sp. strain BRRI54, *Acinetobacter* sp. CYRH21	Plant internal	Industrial wastewater	COD and BOD decreased by 87.0% and 87.5% respectively	[43]
Scenedesmus obliquus GH2	*Sphingomonas* GY2B *Burkholderia cepacia* GS3C *Pseudomonas* GP3A *Pandoraea pnomenusa* GP3B	PAH, oil contaminated soil	Crude oil	Degradation of hydrocarbons in crude oil by a combination of sterile GH2-bacteria community	[44]
Phragmites australis	*Acinetobacter junii* strain NT-15, *Rhodococcus* sp. strain NT-39, *Pseudomonas indoloxydans* strain NT-38	Activated sludge, root interior and rhizosphere of *Polygonum aviculare* and *Poa labillardierei*	Textile industry wastewater	Combined application of plants and bacteria further enhanced the removal performance	[45]
Typha domingensis, *Leptochloa fusca*	*Bacillus cerus*, *Aeromonas salmonicida*, *Pseudomonas gessardii*	The rhizosphere of *Cyperus laevigatus*, root interiors and the rhizosphere of *T. domingensis*	Polluted river water	Significantly greater decrease in COD, $BOD_5$and TOC was observed in inoculated FTWs than in the wetlands without bacterial inoculation.	[46]

(待续)

(续表 2)

Spirodela polyrhiza, *Lemna minor*, *Lemna aequinoctialis*, *Wolffia arrhiza*	*Pseudomonas* spp., *Delftia* spp., *Azospirillum* spp., *Acinetobacter* spp., *Zoogloea* spp.	From *Spirodela polyrhiza*, and *Wolffia arrhiza*	Phenol	Extract from the duckweed paints promoted the cell growth and rate of phenol degradation by degrading bacteria.	[47]
Phragmites australis	*Acinetobacter* sp. BRRH61, *Bacillus megaterium* RGR14, *Acinetobacter iwoffii* AKR1	The rhizosphere or root of a plant	Hydrocarbon	Bacterial inoculation improved the degradation efficiency of hydrocarbons in water	[48]
Cyperus laevigatus L.	*Acinetobacter* sp. 61KJ620863, *Bacillus megaterium* 65 KF478214, *Acinetobacter* sp. 82 KF478231	The rhizosphere or root of a plant	Diesel oil contaminated water	73.48% reduction in hydrocarbons was exhibited by the joint application of both plant and bacteria in FTWs.	[49]
Phragmites australis	*Pseudomonas veronii* JB1 *Pseudomonas plecoglossicida* JB2	Oil contaminated soil	BaP	69.3% BaP was degraded	[50]
Acorus calamus	*Ochrobactrum* sp. strain A15	*Acorus calamus* rhizosphere	Lindane	The root exudates of *Acorus calamus* increased the degradation efficiency by 10.7%	[51]
Chlorella sp.	*Raoultella ornithinolytica*, *Pseudomonas aeruginosa*, *Pseudomonas* sp., *Stenotrophomonas* sp.	Sewage outlet and waste water	Mixture of analgesics	The removal rate of analgesic mixture reached 95%	[52]
Brachiara mutica, *Phragmites australis*	*Bacillus subtilis* strain LORI66, *Klebsiella* sp. strain LCRI87, *Acinetobacter Junii* strain TYRH47, *Acinetobacter* sp. strain LCRH81	Oil contaminated soil	Oil field wastewater	The *Phragmites*-bacteria combination significantly improved the efficiency of the plant to reduce the oil content (97%) in the wastewater	[53]
Typha domingensis, *Leptochloa fusca*	*Bacillus subtilis* LORI66, *Klebsiella* sp. LCRI87, *Acinetobacter Junii* TYRH47, *Acinetobacter* sp. BRSI56	Plant internal and rhizosphere	Hydrocarbon	The *Typha*-bacteria combination showed the highest reduction in hydrocarbons (95%)	[54]
Typha domingensis	*Acinetobacter lwofii* ACRH76, *Bacillus cereus* LORH97, *Pseudomonas* sp. LCRH90	Plant internal and rhizosphere	Phenol	The addition of bacteria significantly improved the removal ability	[55]
Scirpus triqueter	*Bacillus subtili* HD-1	Activated sludge	Pyrene	Pyrene degrading bacteria may be an important cause of the removal of pyrene from wetlands	[56]
Phragmites australis	*Acinetobacter lwofii* ACRH76, *Bacillus cereus* LORH97, *Pseudomonas* sp. LCRH90	Plant internal	Phenol	The removal efficiency of phenol in Phragmites-degrading bacteria combination was obviously higher	[57]
Spirodela polyrhiza	*Pseudomonas* sp. E1, *Klebsiella terrigena* E42, *Pseudomonas* sp. E46	Plant internal	Fenpropathrin	*Spirodela polyrhiza* increased the degradation of fenpropathrin by strain E46	[58]
Brachiaria mutica	*Acinetobacter* sp. strain BRSI56, *Bacillus cereus* strain BRSI57, *Bacillus licheniformis* strain BRSI58	*Brachiaria mutica* stem	Organic wastewater	The plant-bacterial combination resulted in maximum reductions in COD, BOD_5, N, and PO_4	[59]

calcoaceticus P23)，不但具有苯酚降解功能，还可以促进 3 种浮萍(*L. aoukikusa*、*Lemna minor*、*Spirelet polyrhiza*)的生长，在废水体系中保护浮萍免受其他病原微生物的抑制作用[62]。Luo 等发现从红树林表面沉积物中筛选的多环芳烃高效降解菌株分枝杆菌(*Mycobacterium* sp. strain A1-PYR)，降解芘过程中形成的代谢产物酚酸可以作为植物激素促进水体羊角月牙藻(*Selenastrum capricornutum*)生长[42]。植物与微生物之间的这种互惠共生的关系，有助于实现植物-微生物耦合体系的稳定性、持久性和高效性。

此外，部分植物内生菌也被发现具有污染物降解活性和促进植物生长的作用，可以协助植物去除环境有机污染物[63]。Ijaz 等将具有烃降解能力的 3 株内生菌[克雷伯氏菌(*Klebsiella* sp. strain LCRI87)、假单胞菌(*Pseudomonas* sp. strain BRRI54)、不动杆菌(*Acinetobacter* sp. CYRH21)]接种到水生植物香蒲(*Typha domingensis*)植株后，与不接菌对照组相比，工业废水中化学需氧量、生化需氧量分别下降了 87.0%、87.5%[43]。Shehzadi 等从香蒲、大藻和凤眼莲的根、芽中分离出 41 株内生菌，其中 8 株显示出降解纺织废水的能力，并具有植物生长促进活性(产吲哚乙酸、铁载体、ACC 脱氨酶、溶磷)[64]。Wu 等研究发现从芦苇根内分离的一株内生菌铜绿假单胞菌(*Pseudomonas aeruginosa* L10)不仅对多环芳烃萘、菲和芘具有较强的降解能力，通过产生吲哚乙酸、铁载体、ACC 脱氨酶等促进植物生长[65]。Hussain 等发现具有染料降解能力和促进植物生长的 3 种内生菌株[树状微杆菌(*Microbacterium arborescens* TYSI04)、泛菌(*Pantoea* sp. TYRI15)、内生芽孢杆菌(*Bacillus endophyticus* PISI25)]投加到种植双稃草(*Leptochloa fusca*)的人工湿地，可以去除废水中大部分有机和无机污染物，在 48 h 内化学需氧量、生化需氧量去除率分别为 86%、78%[66]。

对于一些结构复杂的难降解有机物质或者污染物成分复杂的环境，单一的功能菌株不能实现对污染物的完全降解，有时需要添加几种不同功能微生物，构建功能菌群，通过微生物功能互补或者功能强化等作用共同完成。Tang 等将从多环芳烃和石油污染土壤中分离的 4 株石油烃降解菌[鞘氨醇单胞菌(*Sphingomonas* GY2B)、洋葱伯克霍尔德菌(*Burkholderia cepacia* GS3C)、假单胞菌(*Pseudomonas* GP3A)、*Pandoraea pnomenusa* GP3B]，分别以单菌或混菌的方式与无菌斜生栅藻(*Scenedesmus obliquus* GH2)进行组合，结果发现当与单菌组合时可以提高原油中部分组分的降解，而接种 4 株菌的混合处理则显著增强了原油所有组分(特别是难降解的多环芳烃组分)的生物降解[44]。Hussain 等将具有原油降解能力和植物生长促进活性的根际细菌[不动杆菌(*Acinetobacter* sp. ACRH82)]和内生菌株[不动杆菌(*Acinetobacter* sp. BRRH61)、芽孢杆菌(*Bacillus niabensis* ACSI85)]以单菌或混菌的方式分别接种到双稃草(*Leptochloa fusca*)根部联合去除十六烷烃，结果发现与单菌接种组相比，混合接种的十六烷烃去除率提高了 72.8%−76.4%[7]。由此可见，构建功能菌群，将不同的功能微生物混合接种到水生植物，有助于增强植物-微生物的修复效率。

同时，添加功能菌剂的人工湿地在有机污染水体的大规模修复中也表现出显著的效果。Afzal 等将 10 株碳氢化合物降解菌添加到由 4 种水生植物[芦苇(*Phragmites australis*)、香蒲(*Typha domingensis*)、双稃草(*Leptochloa fusca*)、巴拉草(*Brachiaria mutica*)]构建的人工湿地中处理受原油污染的矿井水，结果显示接种细菌使人工湿地具有了更高、更持久的代谢活性，化学需氧量、生化需氧量、总溶解固体、碳氢化合物含量和重金属分别降低了 97.4%、98.9%、82.4%、99.1%和 80.0%[67]。

3 植物-微生物联合修复技术的方法

近年来，伴随着陆生植物-微生物联合修复技

术研究的不断深入与分析手段的飞速发展，也带动了水环境中植物-微生物联合修复技术的不断进步，由原来简单的植物-土著微生物群落的湿地系统到接种高效功能微生物菌剂的湿地系统，研究手段也由传统的分离培养、克隆文库、变性梯度凝胶电泳、末端限制性片段长度多态性分析等一代测序技术发展到宏基因组、转录组等技术的广泛应用。

首先在微生物群落结构分析方面，准确率高、成本低的高通量测序技术逐渐取代了原来的 Sanger 一代测序技术，使得对环境微生物群落组成的分析更加快速、准确、全面。李蒙等利用高通量测序技术分析不同污染物浓度处理下水葱根际微生物群落变化，结果发现变形菌门(*Proteobacteria*)是在所有污染物浓度处理下植物根际细菌中处于绝对优势地位的细菌门类[68]。Huang 等利用高通量测序，对 2 种常见挺水植物[菰米(*Zizania latifolia*)、芦苇(*Phragmites australis*)]根际和非根际沉积物微生物群落的组成进行了比较，结果发现根际沉积物富集了以 α 变形菌(*Alphaproteobacteria*)、γ 变形菌(*Gammaproteobacteria*)、放线菌(*Actinobacteria*)、拟杆菌(*Bacteroidetes*)、蓝细菌(*Cyanobacteria*)、浮霉菌(*Planctomycetes*)和疣微菌(*Verrucomicrobia*)等为主的微生物群落，而且比非根际区微生物群落种类更为丰富、多样性更高[69]。其次在微生物的分离培养方面，以前的研究主要是利用选择性合成培养基进行菌株分离，然后降解菌在没有植物存在情况下进行的离体降解研究。然而目前提出的用毛状根或宿主植物共培养的技术，不仅扩大了分离功能菌株的范围，还更有利于研究植物-微生物之间的相互作用。Tanaka 等利用浮萍-微生物共培养方法从浮萍根部分离得到的微生物菌株种类更为多样，其中新型微生物的比例也有所增加，约占分离菌株的 23%−40%[70]。Iwashita 等研究则进一步补充证明了共培养后浮萍整个植株，包括叶状体和根，均可能是富集、分离难培养微生物或微生物新种的良好基质来源[71]。Sauvêtre 等研究了辣根(*Armoracia rusticana*)毛状根植物模型与根瘤菌(*Rhizobium radiobacter*) Cb58 和 *Diaphorobacter nitroreducens* Cb55 共培养条件下对马卡西平的降解，清晰地解析了其中植物与菌株之间的相互作用：植物的存在激发了共生体系在修复过程中的代谢活性，并提出了在植物中马卡西平代谢的新途径——吖啶代谢途径[63]。稳定同位素探测技术(Stable Isotope Probing，SIP)、转录组等技术的应用更有助于研究功能微生物群落结构的变化，而无需传统的分离工艺识别污染物降解菌，还可用于追踪污染物的代谢途径[72]。Linhares 等利用 DNA-SIP 技术鉴定红树林沉积物中参与甲烷氧化的微生物，结果显示活性最高的微生物与甲烷氧化菌[甲基单孢菌(*Methylomonas*)、甲基杆菌(*Methylobacter*)和甲基营养型细菌(*Methylotenera*)]有关[73]。Wang 等利用转录组观察绿藻(*Desmodesmus* sp.) WR1 对双酚 A 应激反应和耐受机制，结果显示绿藻显著上调氧化还原酶和糖基转移酶编码基因，用于双酚 A 氧化生物降解和糖基解毒[74]。

4 植物-微生物联合修复的作用机制

植物-微生物联合去除水体有机污染物的能力受到宿主植物、微生物及环境因素等多方面因素的影响[75]。因此了解和把握水生植物-微生物在水体修复过程中的相互作用机制，有助于深入挖掘水生植物-微生物联合的潜力，实现对水体有机污染物有的放矢地高效治理。

目前，有关植物-微生物联合修复机制的研究主要集中于陆生环境，水生植物-微生物之间的相互作用类似于陆生植物和微生物。根际微生物通常以生物膜的形式紧密包裹在植物的根部，被称为植物体的“第二基因组”。植物提供微生物生长所赖以生存的营养物质与 O_2，反过来微生物的存在可以促进植物矿质营养吸收，同时增强植物的抗胁迫能力，影响植物的生长及代谢[76]。根际降

解微生物的数量及其降解活性的高低是决定该耦合体系降解能力的关键所在[75]。植物通过释放组织凋落物、根系分泌物、释放 O_2 等方式富集大量微生物于根际，并且诱导或者激发微生物的降解活性，从而有助于各种化学物质的降解。

植物的组织凋落物以及分泌物中含有大量有机物质，包括糖类、氨基酸、有机酸、酚类和其他的次级代谢物[77]，其中一些有机质组分可以被根际微生物吸收、利用，成为微生物细胞结构的重要组分或者维持新陈代谢、生命活性的重要物质基础。Toyama 等发现当芦苇暴露于芘中时，根系分泌的酚类化合物增加，含有酚类化合物的芦苇根系分泌物可以作为芘降解菌生长的碳源，并诱导该菌株降解苯并[a]芘[19]。Jin 等发现，植物根系分泌物中糖类物质可能与细菌生长和携带降解基因的质粒转移有关，氨基酸组分可以维持细菌邻苯二酚 2,3-双加氧酶活性，有机酸异羟肟酸可以降低细菌活性氧水平[78]。

同时，根系分泌物中含有大量的酚类、柠檬烯、类黄酮类物质，许多化合物具有与污染物相似的结构[79]，这类物质可以激发根际微生物代谢活性，通过诱导或共代谢作用对水体中的难溶性有机物质进行降解[80]。在植物根际环境中，大量的胞外酶活性，例如纤维素酶、果胶酶、几丁质酶、谷胱甘肽 S-转移酶、过氧化物酶等被检出。Dan 等发现芦苇根系分泌物中的酚类组分，具有类似对叔丁基苯酚的单羟基结构，可以诱导微生物羟化酶催化酚环羟基化，从而加速对叔丁基苯酚的生物降解[27]。根系分泌物中的类黄酮和香豆素，在结构上与多氯联苯、多环芳烃相似，可以诱导或加速根际微生物对环境中多氯联苯的降解[79]。根系分泌物中的有机酸可以改变根系周围环境的酸碱度，调节植物、微生物对矿质元素的营养吸收状况[81]。

植物根部释放的氧气增加了水中的溶解氧浓度，有助于一些好氧微生物的生长及有机污染物降解反应的发生[57]。根际微生物可以以氧气作为电子受体，在一些根系分泌物组分存在的情况下，通过共代谢方式对环境中持久性有机物质进行降解[82]，这一点在水体环境中尤为重要。Toyama 等发现芦苇的存在为根际沉积物区域创造了有利于壬基酚(Technical Nonylphenol，tNP)有氧降解的环境，从而刺激 tNP 降解菌的细胞生长和 tNP 降解活性，从而加速 tNP 从沉积物中的去除[28]。

另外，植物根部是基因的水平转移(Horizontal Gene Transfer，HGT)的热点区域。细菌多环芳烃分解代谢基因通常位于质粒上，携带有降解基因的质粒在根际细菌群落间的转移，可以更有助于提高污染物去除效率[80]。Jin 等将携带含有降解基因质粒的 P7 菌株、P13 菌株与植物共培养，结果发现质粒可以从 P7 菌株转移至 P13 菌株，质粒在植物根际转移频率的增加可能是苯酚降解加速的主要原因之一[78]。

水体中的植物促生菌可以通过分泌植物生长激素、铁载体等促进植物生长，或分泌抗生素、ACC 脱氨酶等增强植物的抵抗病原菌以及环境胁迫的能力，间接达到净化水体的效果。Ishizawa 等研究发现接种醋酸钙不动杆菌 (*Acinetobacter calcoaceticus*) P23 到浮萍根际，可以通过分泌植物生长激素等促进浮萍生长，从而加速浮萍对氮和磷的去除[83]。

5 问题与展望

与传统水体修复技术相比，利用水生植物-微生物联合治理水体有机污染具有高效、经济、无二次污染等诸多优势。但另一方面，植物-微生物联合修复技术的利用受多种因素的制约。首先，选择合适的植物-微生物耦合体系是决定水生植物-微生物的联合修复效果的决定性因素。根际微生物在植物根部的定殖能力及对污染降解能力是衡量植物-微生物体系稳定性的首要条件。不同宿主植物因其所分泌物质的组成成分不同，决定了

根际所富集的微生物群落组成会有所差异，最终导致对污染物的去除效果也不同。Rehman 等研究发现,芦苇可以比巴拉草更好地促进根际微生物的生长和降解活性，因此芦苇-微生物处理组较巴拉草-微生物组合显著提高了植物降低废水中油含量的效率[53]。因此选择合适的植物-微生物组合是决定该技术效率的关键因素。其次，水环境的理化性质(pH、电导率、盐浓度、溶解氧、可溶性有机物浓度、氧化还原势能以及营养状况等)及其土著微生物群落都会影响水体中植物-微生物的联合修复效果[82]。Liu 等研究中发现，随着盐胁迫增加和培养时间延长，浮萍对氮和磷的去除能力显著降低，100 mmol/L 的盐胁迫下甚至会诱导浮萍释放氮和磷[84]。Ishizawa 等研究发现在铜和锌胁迫下，接种促生菌株 H3 可以增强浮萍积累和耐受重金属的能力，但是在高盐度和营养不良条件下，接种菌株 H3 反而会抑制浮萍的生长[85]。

因此，基于对目前水体有机污染修复过程中存在的问题以及水生植物-微生物联合修复技术的影响因素的考虑，今后在对该技术的开发与利用过程中应该着重在以下几个方面有所突破：首先要继续筛选高效降解菌，构建广谱的植物、微生物资源库，有助于优化植物-微生物组合，深入挖掘其中植物和微生物相互作用机制、微生物降解机制、植物-微生物联合降解机制，优化植物-微生物体系的构建，为后期水生植物-微生物联合治理水体的推广应用奠定基础。其次，结合基因工程技术对植物或微生物的基因进行改造，通过扩大植物根系的影响范围、提高降解菌在环境中的生存能力或者增强降解基因在根际表达水平等，提高其污染物的去除效率。再有，可以通过添加激活剂或者辅助材料等优化或者改良植物生长的环境，提高修复效率及其持久性。

近年来，大量新型有机污染物不断涌入环境中,给水体修复工作提出新的挑战,但是另一方面,随着基因组、蛋白组、代谢组、转录组学、宏基因组学、宏转录组学、培养组学等技术的不断发展，以及生物信息学等研究领域的不断拓展,势必将有助于对水生植物-微生物联合修复技术研究的不断深入和突破，有助于水生植物-微生物联合修复技术在治理水体有机污染的进一步推广应用。

REFERENCES

[1] Ali S, Anjum MA, Nawaz A, Naz S, Ejaz S, Ahmad S, Hussain S. Role of reactive nitrogen species in mitigating organic pollutant-induced plant damages[J]. Handbook of Bioremediation, 2021: 493-503

[2] Bao LJ, Maruya KA, Snyder SA, Zeng EY. China's water pollution by persistent organic pollutants[J]. Environmental Pollution, 2012, 163: 100-108

[3] Han DM, Currell MJ. Persistent organic pollutants in China's surface water systems[J]. Science of the Total Environment, 2017, 580: 602-625

[4] Adithya S, Jayaraman RS, Krishnan A, Malolan R, Gopinath KP, Arun J, Kim W, Govarthanan M. A critical review on the formation, fate and degradation of the persistent organic pollutant hexachlorocyclohexane in water systems and waste streams[J]. Chemosphere, 2021, 271: 129866

[5] Giovanella P, Vieira GAL, Ramos Otero IV, Pellizzer EP, Fontes BDJ, Sette LD. Metal and organic pollutants bioremediation by extremophile microorganisms[J]. Journal of Hazardous Materials, 2020, 382: 121024

[6] Zhuo R, Fan FF. A comprehensive insight into the application of white rot fungi and their lignocellulolytic enzymes in the removal of organic pollutants[J]. Science of the Total Environment, 2021, 778: 146132

[7] Hussain F, Tahseen R, Arslan M, Iqbal S, Afzal M. Removal of hexadecane by hydroponic root mats in partnership with alkane-degrading bacteria: bacterial augmentation enhances system's performance[J]. International Journal of Environmental Science and Technology, 2019, 16(8): 4611-4620

[8] Santos JJD, Maranho LT. Rhizospheric microorganisms as a solution for the recovery of soils contaminated by petroleum: a review[J]. Journal of Environmental Management, 2018, 210: 104-113

[9] Arora NK, Kumar N. *Phyto* and Rhizo Remediation[M]. Singapore: Springer Singapore, 2019

[10] Hijosa-Valsero M, Reyes-Contreras C, Domínguez C, Bécares E, Bayona JM. Behaviour of pharmaceuticals and personal care products in constructed wetland compartments: influent, effluent, pore water, substrate and plant roots[J]. Chemosphere, 2016, 145: 508-517

[11] Kotoky R, Rajkumari J, Pandey P. The rhizosphere microbiome: significance in rhizoremediation of polyaromatic hydrocarbon contaminated soil[J]. Journal of Environmental Management, 2018, 217: 858-870

[12] Saravanan A, Jeevanantham S, Narayanan VA, Kumar PS, Yaashikaa PR, Muthu CMM. Rhizoremediation——a promising tool for the removal of soil contaminants: a review[J]. Journal of Environmental Chemical Engineering, 2020, 8(2): 103543

[13] Anderson TA, Coats JR. An overview of microbial degradation in the rhizosphere and its implications for bioremediation[A]//SSSA Special Publications[M]. Madison, WI, USA: Soil Science Society of America, American Society of Agronomy, and Crop Science Society of America, 2015: 135-143

[14] Han B, Zhang SH, Zhang LS, Liu KH, Yan LY, Wang PF, Wang C, Pang S. Characterization of microbes and denitrifiers attached to two species of floating plants in the wetlands of Lake Taihu[J]. PLoS One, 2018, 13(11): e0207443

[15] Shahid MJ, Al-Surhanee AA, Kouadri F, Ali S, Nawaz N, Afzal M, Rizwan M, Ali B, Soliman MH. Role of microorganisms in the remediation of wastewater in floating treatment wetlands: a review[J]. Sustainability, 2020, 12(14): 5559

[16] Meng FB, Chi J. Dissipation gradient of *Pyrene* in the rhizosphere of *Potamogeton crispus* L.[J]. Ecological Engineering, 2017, 106: 10-16

[17] Yin XJ, Liu GL, Peng L, Hua YM, Wan XQ, Zhou WB, Zhao JW, Zhu DW. Microbial community of nitrogen cycle-related genes in aquatic plant rhizospheres of Lake Liangzi in winter[J]. Journal of Basic Microbiology, 2018, 58(11): 998-1006

[18] Yan ZS, Jiang HL, Cai HY, Zhou YL, Krumholz LR. Complex interactions between the macrophyte *Acorus calamus* and microbial fuel cells during *Pyrene* and benzo[a]*Pyrene* degradation in sediments[J]. Scientific Reports, 2015, 5: 10709

[19] Toyama T, Furukawa T, Maeda N, Inoue D, Sei K, Mori K, Kikuchi S, Ike M. Accelerated biodegradation of *Pyrene* and benzo[a]*Pyrene* in the *Phragmites australis* rhizosphere by bacteria-root exudate interactions[J]. Water Research, 2011, 45(4): 1629-1638

[20] Qu MJ, Li N, Li HD, Yang TW, Liu W, Yan YP, Feng XH, Zhu DW. Phytoextraction and biodegradation of atrazine by *Myriophyllum spicatum* and evaluation of bacterial communities involved in atrazine degradation in lake sediment[J]. Chemosphere, 2018, 209: 439-448

[21] Teeratitayangkul P, Phutthasimma C, Wichai S, Phenrat T. Rhizomicrobial-augmented mature vetiver root system rapidly degrades phenol in illegally dumped industrial wastewater[J]. Desalination and Water Treatment, 2019, 159: 40-52

[22] Li YF, Zhang JF, Zhu GB, Liu Y, Wu B, Ng WJ, Appan A, Tan SK. Phytoextraction, phytotransformation and rhizodegradation of ibuprofen associated with *Typha angustifolia* in a horizontal subsurface flow constructed wetland[J]. Water Research, 2016, 102: 294-304

[23] Radulovic O, Petrić M, Raspor M, Tadić V, Jovanović P, Zečević V. Assessment of *in vitro* multiplication of *Lemna minor* in the presence of phenol: plant/bacteria system for potential bioremediation-part I[J]. Polish Journal of Environmental Studies, 2019, 28(2): 803-809

[24] Sauvêtre A, Schröder P. Uptake of carbamazepine by rhizomes and endophytic bacteria of *Phragmites australis*[J]. Frontiers in Plant Science, 2015, 6: 83

[25] Sun L, Tian Y, Zhang J, Li LP, Zhang J, Li JZ. A novel membrane bioreactor inoculated with symbiotic sludge bacteria and algae: performance and microbial community analysis[J]. Bioresource Technology, 2018, 251: 311-319

[26] Maza-Márquez P, González-Martínez A, Rodelas B, González-López J. Full-scale photobioreactor for biotreatment of olive washing water: structure and diversity of the microalgae-bacteria consortium[J]. Bioresource Technology, 2017, 238: 389-398

[27] Dan A, Zhang NC, Qiu RL, Li C, Wang SZ, Ni ZB. Accelerated biodegradation of p-tert-butylphenol in the *Phragmites australis* rhizosphere by phenolic root exudates[J]. Environmental and Experimental Botany, 2020, 169: 103891

[28] Toyama T, Murashita M, Kobayashi K, Kikuchi S, Sei K, Tanaka Y, Ike M, Mori K. Acceleration of nonylphenol and 4-tert-octylphenol degradation in sediment by *Phragmites australis* and associated rhizosphere bacteria[J]. Environmental Science & Technology, 2011, 45(15): 6524-6530

[29] Ogata Y, Toyama T, Yu N, Wang X, Sei K, Ike M. Occurrence of 4-tert-butylphenol (4-t-BP) biodegradation in an aquatic sample caused by the presence of *Spirodela polyrrhiza* and isolation of a 4-t-BP-utilizing bacterium[J]. Biodegradation, 2013, 24(2): 191-202

[30] Hu XJ, Xie HJ, Zhuang LL, Zhang J, Hu Z, Liang S, Feng KS. A review on the role of plant in pharmaceuticals and personal care products (PPCPs) removal in constructed wetlands[J]. Science of the Total Environment, 2021, 780: 146637

[31] Vymazal J, Sochacki A, Fučík P, Šereš M, Kaplická M, Hnátková T, Chen ZB. Constructed wetlands with subsurface flow for nitrogen removal from tile drainage[J]. Ecological Engineering, 2020, 155: 105943

[32] Stefanakis AI, Seeger E, Dorer C, Sinke A, Thullner M. Performance of pilot-scale horizontal subsurface flow constructed wetlands treating groundwater contaminated with phenols and petroleum derivatives[J]. Ecological Engineering, 2016, 95: 514-526

[33] Dan A, Fujii D, Soda S, Machimura T, Ike M. Removal of phenol, bisphenol A, and 4-tert-butylphenol from synthetic landfill leachate by vertical flow constructed wetlands[J]. Science of the Total Environment, 2017, 578: 566-576

[34] Toro-Vélez AF, Madera-Parra CA, Peña-Varón MR, Lee WY, Bezares-Cruz JC, Walker WS, Cárdenas-Henao H, Quesada-Calderón S, García-Hernández H, Lens PNL. BPA

and NP removal from municipal wastewater by tropical horizontal subsurface constructed wetlands[J]. Science of the Total Environment, 2016, 542: 93-101

[35] Zhang XM, Jing RY, Feng X, Dai YY, Tao R, Vymazal J, Cai N, Yang Y. Removal of acidic pharmaceuticals by small-scale constructed wetlands using different design configurations[J]. Science of the Total Environment, 2018, 639: 640-647

[36] Saggaï MM, Ainouche A, Nelson M, Cattin F, El Amrani A. Long-term investigation of constructed wetland wastewater treatment and reuse: selection of adapted plant species for metaremediation[J]. Journal of Environmental Management, 2017, 201: 120-128

[37] Zhang Y, Lv T, Carvalho PN, Zhang L, Arias CA, Chen ZH, Brix H. Ibuprofen and iohexol removal in saturated constructed wetland mesocosms[J]. Ecological Engineering, 2017, 98: 394-402

[38] Kadam SK, Watharkar AD, Chandanshive VV, Khandare RV, Jeon BH, Jadhav JP, Govindwar SP. Co-planted floating *Phyto*-bed along with microbial fuel cell for enhanced textile effluent treatment[J]. Journal of Cleaner Production, 2018, 203: 788-798

[39] Du FY, A Q, Dong FC, Baima WD, Du DL, Xie QJ. Purification effect of different wetland plant configuration on sewage in Tibet[J]. Environmental Engineering, 2017, 35(1): 26-30,40 (in Chinese)
杜甫义, 阿琼, 董凡超, 白玛旺堆, 杜道林, 解清杰. 西藏地区不同湿地植物配置对污水的净化效果[J]. 环境工程, 2017, 35(1): 26-30,40

[40] Wirasnita R, Mori K, Toyama T. Effect of activated carbon on removal of four phenolic endocrine-disrupting compounds, bisphenol A, bisphenol F, bisphenol S, and 4-tert-butylphenol in constructed wetlands[J]. Chemosphere, 2018, 210: 717-725

[41] Li Y, Toyama T, Furuya T, Iwanaga K, Tanaka Y, Mori K. Sustainable biodegradation of bisphenol A by *Spirodela polyrhiza* in association with *Novosphingobium* sp. FID3[J]. Journal of Water and Environment Technology, 2014, 12(1): 43-54

[42] Luo SS, Chen BW, Lin L, Wang XW, Tam NFY, Luan TG. *Pyrene* degradation accelerated by constructed consortium of bacterium and microalga: effects of degradation products on the microalgal growth[J]. Environmental Science & Technology, 2014, 48(23): 13917-13924

[43] Ijaz A, Iqbal Z, Afzal M. Remediation of sewage and industrial effluent using bacterially assisted floating treatment wetlands vegetated with *Typha domingensis*[J]. Water Science and Technology, 2016, 74(9): 2192-2201

[44] Tang X, He LY, Tao XQ, Dang Z, Guo CL, Lu GN, Yi XY. Construction of an artificial microalgal-bacterial consortium that efficiently degrades crude oil[J]. Journal of Hazardous Materials, 2010, 181(1/2/3): 1158-1162

[45] Tara N, Arslan M, Hussain Z, Iqbal M, Khan QM, Afzal M. On-site performance of floating treatment wetland macrocosms augmented with dye-degrading bacteria for the remediation of textile industry wastewater[J]. Journal of Cleaner Production, 2019, 217: 541-548

[46] Shahid MJ, Tahseen R, Siddique M, Ali S, Iqbal S, Afzal M. Remediation of polluted river water by floating treatment wetlands[J]. Water Supply, 2019, 19(3): 967-977

[47] Li Y, Toyama T, Tanaka Y, Tang YQ, Wu XL, Mori K. Effects of various duckweed species on phenol degradation in environmental waters[J]. Japanese Journal of Water Treatment Biology, 2014, 50(3): 95-103

[48] Fahid M, Arslan M, Shabir G, Younus S, Yasmeen T, Rizwan M, Siddique K, Ahmad SR, Tahseen R, Iqbal S, et al. *Phragmites australis* in combination with hydrocarbons degrading bacteria is a suitable option for remediation of diesel-contaminated water in floating wetlands[J]. Chemosphere, 2020, 240: 124890

[49] Fahid M, Ali S, Shabir G, Rashid Ahmad S, Yasmeen T, Afzal M, Arslan M, Hussain A, Hashem A, Abd Allah EF, et al. *Cyperus laevigatus* L. enhances diesel oil remediation in synergism with bacterial inoculation in floating treatment wetlands[J]. Sustainability, 2020, 12(6): 2353

[50] Jin X, Tian WJ, Qiao KL, Gong XX, Zhao J, Liu SH. Remediation of benzo[a]*Pyrene* in Jiaozhou bay wetland soil by using reed-immobilized microorganism technology[J]. Periodical of Ocean University of China, 2018, 48(12): 56-61,104 (in Chinese)
金鑫, 田伟君, 乔凯丽, 龚晓希, 赵婧, 刘淑惠. 芦苇-固定化微生物联合修复胶州湾湿地土壤中苯并[a]芘的研究[J]. 中国海洋大学学报: 自然科学版, 2018, 48(12): 56-61,104

[51] Singh T, Singh DK. Enhanced lindane degradation in the presence of root exudates of *Acorus calamus* and plant growth promoting rhizobacteria *Ochrobactrum* sp. strain A15[J]. Environmental and Experimental Biology, 2019, 17(4): 193-199

[52] Ismail MM, Essam TM, Ragab YM, El-Sayed AEKB, Mourad FE. Remediation of a mixture of analgesics in a stirred-tank photobioreactor using microalgal-bacterial consortium coupled with attempt to valorise the harvested biomass[J]. Bioresource Technology, 2017, 232: 364-371

[53] Rehman K, Imran A, Amin I, Afzal M. Inoculation with bacteria in floating treatment wetlands positively modulates the phytoremediation of oil field wastewater[J]. Journal of Hazardous Materials, 2018, 349: 242-251

[54] Rehman K, Imran A, Amin I, Afzal M. Enhancement of oil field-produced wastewater remediation by bacterially-augmented floating treatment wetlands[J]. Chemosphere, 2019, 217: 576-583

[55] Saleem H, Rehman K, Arslan M, Afzal M. Enhanced degradation of phenol in floating treatment wetlands by plant-bacterial synergism[J]. International Journal of Phytoremediation, 2018, 20(7): 692-698

[56] Liu XY, Hu XX, Zhang XY, Chen XP, Chen J, Yuan XY. Effect of *Bacillus subtilis* and NTA-APG on *Pyrene* dissipation in phytoremediation of nickel co-contaminated wetlands by *Scirpus triqueter*[J]. Ecotoxicology and Environmental Safety, 2018, 154: 69-74

[57] Saleem H, Arslan M, Rehman K, Tahseen R, Afzal M. *Phragmites australis*—a helophytic grass—can establish successful partnership with phenol-degrading bacteria in a floating treatment wetland[J]. Saudi Journal of Biological Sciences, 2019, 26(6): 1179-1186

[58] Xu XJ, Sun JQ, Nie Y, Wu XL. *Spirodela polyrhiza* stimulates the growth of its endophytes but differentially increases their fenpropathrin-degradation capabilities[J]. Chemosphere, 2015, 125: 33-40

[59] Ijaz A, Shabir G, Khan QM, Afzal M. Enhanced remediation of sewage effluent by endophyte-assisted floating treatment wetlands[J]. Ecological Engineering, 2015, 84: 58-66

[60] Wang R, Tai YP, Wan X, Ruan WF, Man Y, Wang JX, Yang YF, Yang Y. Enhanced removal of *Microcystis* bloom and microcystin-LR using microcosm constructed wetlands with bioaugmentation of degrading bacteria[J]. Chemosphere, 2018, 210: 29-37

[61] Singh T, Singh DK. Rhizospheric *Microbacterium* sp. P27 showing potential of lindane degradation and plant growth promoting traits[J]. Current Microbiology, 2019, 76(7): 888-895

[62] Toyama T, Kuroda M, Ogata Y, Hachiya Y, Quach A, Tokura K, Tanaka Y, Mori K, Morikawa M, Ike M. Enhanced biomass production of duckweeds by inoculating a plant growth-promoting bacterium, *Acinetobacter calcoaceticus* P23, in sterile medium and non-sterile environmental waters[J]. Water Science and Technology, 2017, 76(6): 1418-1428

[63] Sauvêtre A, May R, Harpaintner R, Poschenrieder C, Schröder P. Metabolism of carbamazepine in plant roots and endophytic rhizobacteria isolated from *Phragmites australis*[J]. Journal of Hazardous Materials, 2018, 342: 85-95

[64] Shehzadi M, Fatima K, Imran A, Mirza MS, Khan QM, Afzal M. Ecology of bacterial endophytes associated with wetland plants growing in textile effluent for pollutant-degradation and plant growth-promotion potentials[J]. Plant Biosystems-an International Journal Dealing With All Aspects of Plant Biology, 2015, 150(6): 1261-1270

[65] Wu T, Xu J, Xie WJ, Yao ZG, Yang HJ, Sun CL, Li XB. *Pseudomonas aeruginosa* L10: a hydrocarbon-degrading, biosurfactant-producing, and plant-growth-promoting endophytic bacterium isolated from a reed (*Phragmites australis*)[J]. Frontiers in Microbiology, 2018, 9: 1087

[66] Hussain Z, Arslan M, Malik MH, Mohsin M, Iqbal S, Afzal M. Integrated perspectives on the use of bacterial endophytes in horizontal flow constructed wetlands for the treatment of liquid textile effluent: phytoremediation advances in the field[J]. Journal of Environmental Management, 2018, 224: 387-395

[67] Afzal M, Rehman K, Shabir G, Tahseen R, Ijaz A, Hashmat AJ, Brix H. Large-scale remediation of oil-contaminated water using floating treatment wetlands[J]. Npj Clean Water, 2019, 2: 3

[68] Li M. The soil reinforcement capability and high-throughput sequencing analysis of decabromodiphenyl ether-degrading bacteria of the rhizosphere of macrophytes[D]. Wuhan: Master’s Thesis of Central China Normal University, 2018 (in Chinese)

李蒙. 水生植物根际的固土能力及十溴联苯醚降解菌的高通量分析[D]. 武汉: 华中师范大学硕士学位论文, 2018

[69] Huang R, Zeng J, Zhao DY, Cook KV, Hambright KD, Yu ZB. Sediment microbiomes associated with the rhizosphere of emergent macrophytes in a shallow, subtropical lake[J]. Limnology and Oceanography, 2020, 65(S1): S38-S48.

[70] Tanaka Y, Tamaki H, Tanaka K, Tozawa E, Matsuzawa H, Toyama T, Kamagata Y, Mori K. “Duckweed-microbe co-cultivation method” for isolating a wide variety of microbes including taxonomically novel microbes[J]. Microbes and Environments, 2018, 33(4): 402-406

[71] Iwashita T, Tanaka Y, Tamaki H, Yoneda Y, Makino A, Tateno Y, Li Y, Toyama T, Kamagata Y, Mori K. Comparative analysis of microbial communities in fronds and roots of three duckweed species: *Spirodela polyrhiza*, *Lemna minor*, and *Lemna aequinoctialis*[J]. Microbes and Environments, 2020, 35(3): ME20081

[72] Jin JN, Yao J, Zhang QY, Liu JL. Biodegradation of *Pyrene* by *Pseudomonas* sp. JPN2 and its initial degrading mechanism study by combining the catabolic nahAc gene and structure-based analyses[J]. Chemosphere, 2016, 164: 379-386

[73] Linhares DDC, Saia FT, Duarte RTD, Nakayama CR, Melo ISD, Pellizari VH. Methanotrophic community detected by DNA-SIP at bertioga’s mangrove area, southeast Brazil[J]. Microbial Ecology, 2021, 81(4): 954-964

[74] Wang R, Diao PP, Chen Q, Wu H, Xu N, Duan SS. Identification of novel pathways for biodegradation of bisphenol A by the green alga *Desmodesmus* sp.WR1, combined with mechanistic analysis at the transcriptome level[J]. Chemical Engineering Journal, 2017, 321: 424-431

[75] Stout L, Nüsslein K. Biotechnological potential of aquatic plant-microbe interactions[J]. Current Opinion in Biotechnology, 2010, 21(3): 339-345

[76] Ishizawa H, Kuroda M, Morikawa M, Ike M. Evaluation of environmental bacterial communities as a factor affecting the growth of duckweed *Lemna minor*[J]. Biotechnology for Biofuels, 2017, 10(1): 62

[77] Haichar FEZ, Santaella C, Heulin T, Achouak W. Root exudates mediated interactions belowground[J]. Soil

Biology and Biochemistry, 2014, 77: 69-80

[78] Jin JR, Wang M, Lu WW, Zhang L, Jiang QY, Jin YQ, Lu KH, Sun SR, Cao Q, Wang YJ, et al. Effect of plants and their root exudate on bacterial activities during rhizobacterium-plant remediation of phenol from water[J]. Environment International, 2019, 127: 114-124

[79] Musilova L, Ridl J, Polivkova M, Macek T, Uhlik O. Effects of secondary plant metabolites on microbial populations: Changes in community structure and metabolic activity in contaminated environments[J]. International Journal of Molecular Sciences, 2016, 17(8): 1205

[80] Vergani L, Mapelli F, Zanardini E, Terzaghi E, Di Guardo A, Morosini C, Raspa G, Borin S. *Phyto*-rhizoremediation of polychlorinated biphenyl contaminated soils: an outlook on plant-microbe beneficial interactions[J]. Science of the Total Environment, 2017, 575: 1395-1406

[81] Hoang SA, Lamb D, Seshadri B, Sarkar B, Choppala G, Kirkham MB, Bolan NS. Rhizoremediation as a green technology for the remediation of petroleum hydrocarbon-contaminated soils[J]. Journal of Hazardous Materials, 2021, 401: 123282

[82] Srivastava JK, Chandra H, Kalra SJS, Mishra P, Khan H, Yadav P. Plant-microbe interaction in aquatic system and their role in the management of water quality: a review[J]. Applied Water Science, 2017, 7(3): 1079-1090

[83] Ishizawa H, Ogata Y, Hachiya Y, Tokura KI, Kuroda M, Inoue D, Toyama T, Tanaka Y, Mori K, Morikawa M, et al. Enhanced biomass production and nutrient removal capacity of duckweed via two-step cultivation process with a plant growth-promoting bacterium, *Acinetobacter calcoaceticus* P23[J]. Chemosphere, 2020, 238: 124682

[84] Liu CG, Dai Z, Sun HW. Potential of duckweed (*Lemna minor*) for removal of nitrogen and phosphorus from water under salt stress[J]. Journal of Environmental Management, 2017, 187: 497-503

[85] Ishizawa H, Tada M, Kuroda M, Inoue D, Ike M. Performance of plant growth-promoting bacterium of duckweed under different kinds of abiotic stress factors[J]. Biocatalysis and Agricultural Biotechnology, 2019, 19: 101146