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污水处理系统中微生物群落结构及其对环境因子响应研究进展

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摘　要　**【目的】**　文章旨在探讨不同污水处理系统中微生物群落的结构及其功能,分析环境因子(进水成分、处理工艺和运行参数)对微生物群落的影响,以期为污水处理系统的优化提供理论支持。**【方法】**　综述了不同城镇污水处理系统中微生物群落的结构及功能,结合束缚性排序分析和曼特尔检验分析,探讨了微生物群落对进水成分、处理工艺和运行参数等环境因子的响应。重点分析了脱氮、除磷及其他功能菌属在不同环境条件下的相对丰度变化。**【结果】**　结果表明,污水处理系统中的微生物群落在门水平上表现出相似性,其中变形菌门、拟杆菌门、放线菌门和绿弯菌门为主要的优势菌门。相比生活污水处理系统,以工业废水为进水的活性污泥中,硝化螺旋菌属等脱氮功能菌属的相对丰度有所降低。不同处理工艺的运行效能有所差异,其微生物群落结构也会受到设计结构的影响有所变化。此外,运行参数如温度、溶解氧、水力停留时间和污泥停留时间会影响特定功能微生物的生长环境,从而影响其活性和丰度。**【结论】**　微生物群落结构与污水处理系统的运行效果密切相关,进水成分、处理工艺和运行参数等环境因子显著影响微生物群落的组成和功能。通过优化这些环境因子,可有效提高污水处理系统的运行效率。未来的研究应加强对核心微生物和稀有微生物的鉴定与识别,在多组学技术与数学模型基础上进一步揭示微生物群落、环境因子以及污水处理系统运行效能之间的关系,为优化污水处理系统运行效能和提供理论基础。

关键词　污水处理　微生物群落　环境因子　功能菌属　运行效能
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Research Progress on Microflora Structure and Its Response to Environmental Factors in Wastewater Treatment Systems

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Abstract　[**Objective**]　This study aims to explore the structure and functions of microflora in different wastewater treatment systems and to analyze the effects of environmental factors, including influent composition, treatment processes, and operating parameters, on these communities. The findings are intended to provide theoretical support for the optimization of wastewater treatment systems. [**Methods**]　Microflora in various urban wastewater treatment systems are analyzed. The responses of microflora to environmental factors such as influent composition, treatment processes, and operating parameters are investigated using constrained ordination analysis and Mantel tests. The changes in the relative abundance of nitrogen-removing, phosphorus-removing, and other functional bacteria genus under different environmental conditions are also examined. [**Results**]　The result reveals that microflora in wastewater treatment systems exhibited similarity at the phylum level, with Proteobacteria, Bacteroidota, Actinobacteriota, and Chloroflexi

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identified as the dominant phyla. The relative abundance of nitrogen-removing functional bacteria genus, such as *Nitrospira*, is found to be reduced in activated sludge treating industrial wastewater compared to domestic wastewater treatment systems. The operational efficiency of different treatment processes varied, and the microbial community structures are influenced by system design. Furthermore, operating parameters, including temperature, dissolved oxygen, hydraulic retention time, and sludge retention time, are observed to affect the growth environment, activity, and abundance of specific functional microorganisms. [**Conclusion**] The structure of microflora is found to be closely associated with the operational performance of wastewater treatment systems. Environmental factors such as influent composition, treatment processes, and operating parameters significantly influenced the composition and function of microflora. Optimizing these factors can effectively improve the operational efficiency of wastewater treatment systems. Future research should focus on the identification and functional analysis of core and rare microorganisms. In addition, multi-omics techniques and mathematical modeling should be employed to further elucidate the relationships between microflora, environmental factors, and the operational efficiency of wastewater treatment systems, thereby providing a theoretical basis for system optimization and improve pollutant removal efficiency.

Keywords　wastewater treatment　microflora　environmental factor　functional bacteria genus　operational efficiency

微生物群落是污水处理系统去除污染物的主体,与碳、氮、磷等污染物去除过程密切相关[1],而微生物群落结构受进水成分、处理工艺和运行参数等环境因子影响[2]。如,生活污水和工业废水组成差异较大,进水成分是影响微生物群落组成的重要因素[3];当进水成分相似时,厌氧/缺氧/好氧(AAO)工艺中与脱氮除磷有关的功能菌属相对丰度要远高于氧化沟(OD)工艺[4];适当延长水力停留时间(HRT)有利于脱氮功能菌属的富集,提升污水处理系统脱氮效能[5]。本文综述了不同污水处理系统中微生物群落的结构及其功能,分析了微生物群落对不同环境因子的响应情况,总结了微生物群落与环境因子关联性分析方法,旨在为污水处理系统处理条件的优化以及运行效率的提升提供理论基础。

1　微生物群落结构分析

1.1　优势菌门

不同城镇污水处理系统中微生物群落结构组成,在门水平上基本相似但相对丰度略有差异(表1)。优势菌门主要包含变形菌门(Proteobacteria)、拟杆菌门(Bacteroidetes)、放线菌门(Actinobacteria)和绿弯菌门(Chloroflexi)等。其中,Proteobacteria 为革兰氏阴性菌,在绝大部分生物处理系统中占据主导地位,包含大部分与生物脱氮除磷和有机物降解作用相关的功能菌属。Bacteroidetes 可以促进含氮污染物的转化,参与有机碳和蛋白质循环过程并将大分子物质转化成小分子物质。Actinobacteria 和 Chloroflexi 均能够有效降解复杂的有机物,在有机物去除过程中发挥重要作用。

表1　不同城镇污水处理系统中的优势菌门组成

Tab. 1　Composition of Dominant Bacteria Phyla in Different Urban Wastewater Treatment Systems

污水处理系统	优势菌门	参考文献
苏州市2个污水处理系统	Proteobacteria(25.5%~31.8%)、Actinobacteria(12.8%~22.2%)、Chloroflexi(8.2%~21.0%)、Bacteroidetes(4.3%~18.8%)、厚壁菌门(2.6%~16.5%)等	[6]
深圳市2个污水处理系统	Proteobacteria(58.2%)、Bacteroidetes(22.1%)、厚壁菌门(5.3%)、硝化螺旋菌门(2.8%)、Actinobacteria(1.9%)等	[7]
广东省某污水处理系统	Proteobacteria(58.5%)、Bacteroidetes(21.6%)、Chloroflexi(7.1%)、浮霉菌门(2.9%)、髌骨菌门(1.4%)等	[8]
天津市某污水处理系统	Proteobacteria(47.0%~52.0%)、Bacteroidetes(8.0%~22.0%)、Chloroflexi(3.0%~11.0%)、Actinobacteria(4.0%~9.0%)、解糖微小寄生菌门(2.0%~7.0%)等	[9]
我国东部3个污水处理系统	Proteobacteria(12.3%~58.5%)、Chloroflexi(2.8%~37.7%)、酸杆菌门(1.8%~35.1%)、硝化螺旋菌门(1.7%~52.0%)、Bacteroidetes(0.7%~19.2%)等	[10]

1.2　功能菌属

1.2.1　脱氮功能菌属

硝化菌属包括氨氧化菌(AOB)和亚硝酸盐氧化菌(NOB),污水处理系统中常见的 AOB 有亚硝化单胞菌和亚硝螺菌,NOB 有硝化螺旋菌属(*Nitrospira*)和硝化杆菌属(*Nitrobacter*)[11]。NOB 比 AOB 更容易

受到外界环境变化的影响,如随着温度的增高 AOB 的生长速度高于 NOB。此外,通过控制曝气时间可以在抑制 NOB 繁殖的同时,有选择性地富集 AOB 实现短程硝化过程,再结合厌氧氨氧化(PN/A)工艺,可在节省碳源情况下提高脱氮效果[12]。

反硝化菌属多为兼性菌,相对丰度占微生物总量的 10.0%~15.0%,可以通过多种途径参与生物代谢过程。污水处理系统中常见的缺氧反硝化菌属为陶厄菌属(*Thauera*)和从毛单胞菌属(*Comamonas*)等,好氧反硝化菌属为假单胞菌属(*Pseudomonas*)和葡萄球菌属(*Staphylococcus*)等(表 2)。这类菌属基本都是异养菌,生长速率比自养菌高,可以利用有机物作为碳源将不同形态的氮转为氮气,具备同步脱氮除碳的能力[13]。硫弧菌属(*Sulfurimonas*)、硫杆菌属(*Thiobacillus*)和红环菌属(*Rhodocyclus*)等自养反硝化菌属可以在不额外投加碳源的情况下实现对含氮污染物的去除,有利于降低工艺运行成本[14]。除了硝化菌属与反硝化菌属,厌氧氨氧化菌(AnAOB)可以在无需碳源和氧气的情况下实现自养型生物脱氮,典型的 AnAOB 包括布罗卡菌属(*Candidatus brocadia*)和库宁菌属(*Candidatus kuenenia*)[15]。

表 2 污水处理系统中常见的反硝化菌属

Tab. 2 Denitrifying Bacteria Commonly Found in Wastewater Treatment Systems

优势菌属	功能	参考文献
Thauera	反硝化菌属,可降解多种有机物	[16]
Comamonas	反硝化菌属,以乙酸为碳源进行反硝化	[17]
Pseudomonas	好氧反硝化菌属	[18]
Staphylococcus	好氧反硝化菌属,可去除硝酸盐氮(NO_3^--N)和亚硝酸盐氮(NO_2^--N)	[19]
Sulfurimonas	硫自养反硝化菌属	[20]
Thiobacillus	硫自养反硝化菌属,分布范围广泛,可以同步脱氮除硫	[14]

1.2.2 除磷功能菌属

生物除磷作用指聚磷菌属在厌氧条件下把细胞内聚磷水解为正磷酸盐并从中获得能量,吸收污水中的易降解有机物如挥发性脂肪酸,同化为胞内碳能源存贮物聚β-羟基丁酸或聚β-羟基戊酸等,在缺氧和好氧条件下吸磷来实现的[21]。城镇污水处理系统中常见的聚磷菌属包括拟集胞菌属(*Candidatus_accumulibacter*)、不动杆菌属(*Acinetobacte*)和四球菌属(*Tetrasphaera*)等,用荧光原位杂交探针技术对聚磷菌属进行鉴定,发现拟集胞菌属(*Candidatus_accumulibacter*)含量极高,后续也有研究表明 *Candidatus_accumulibacter* 为一种重要的聚磷菌属[22]。污水处理系统中常见的反硝化聚磷菌属包括偶氮弧菌属(*Azoarcus*)、*Thauera* 和枯草芽孢杆菌(*Bacillus subtilis*)等,可以同步发挥脱氮除磷的作用。反硝化聚磷菌属的相对丰度变化受碳源、pH、NO_3^--N 浓度和 NO_2^--N 浓度等因素的影响[23]。

1.2.3 其他功能菌属

此外,污水处理系统中还有其他类型功能菌属。如微丝菌属小细胞种(*Microthrix parvicella*)、硫丝菌属(*Thiothrix*)和水生哈氏菌(*Haliscomenobacter hydrossis*)等丝状菌属大量繁殖,会导致活性污泥沉降性能变差,发生丝状菌膨胀[24]。*Thauera*、动胶菌属(*Zoogloea*)和黄杆菌属(*Flavobacterium*)等胞外聚合物(EPS)分泌菌属可以吸附抗生素,保护细胞免受抗生素的毒害[25]。但是,EPS 分泌菌属过度繁殖则会导致细胞表面产生大量 EPS,引发活性污泥黏性膨胀。当诺卡氏丝状菌(*Nocardioform filamentous bacteria*)和拟微丝菌属小细胞种(*Candidatus microthrix parvicella*)相对丰度过高时,则会引起污泥泡沫现象恶化出水水质。

2 微生物群落对环境因子的响应

了解环境因子对微生物群落结构的影响,有助于调控微生物群落结构,提高污水处理系统的运行效能。本文主要从进水成分、处理工艺和运行参数 3 个方面论述了污水处理系统中微生物群落对环境因子的响应。

2.1 进水成分

生活污水中主要包括日常生活中排放的蛋白质、糖类、纤维等污染物,以生活污水为进水的污水处理系统中优势菌门主要是 Proteobacteria 和 Bacteroidetes[26]。不同类型的废水处理系统的微生物群落组成有所差异。在纺织废水处理系统中,浮霉菌门、Chloroflexi、绿菌门和酸杆菌门等为优势菌门[27]。在含油废水处理系统中,Proteobacteria 和厚壁菌门等为优势菌门[28]。在含高浓度大蒜废水的处理系统中,Bacteroidetes 和 Proteobacteria 等为优势菌门[29]。工业废水中大部分有机物难以被微生物降解,混合一定比例的生活污水将其作为微生物

生长和繁殖的营养物质,可以提高微生物对难降解有机污染物的去除能力。如南方某城镇污水处理系统将生活废水和印染废水按 5∶1 的比例混合,对污染物的去除效果明显提高[30]。

2.2　处理工艺

不同的处理工艺对污染物的去除效果不同。OD 工艺结构简单,适用于在氧气充分的条件下去除含碳污染物[31]。厌氧/好氧工艺和 AAO 工艺结构相对 OD 工艺复杂一些,在生物脱氮除磷过程中更有优势[32]。不同工艺的运行效能有所差异,微生物群落结构也会受到设计结构的影响有所差异[33]。AAO 工艺中设计了好氧环境和缺氧环境,为硝化菌属和反硝化菌属提供适宜的生长条件,进一步实现系统稳定脱氮。AAO+移动床生物膜工艺中投加了填料,有利于以未分类菌属(*norank_o__Run-SP*154)为主的反硝化聚磷菌属富集,反硝化聚磷菌属的相对丰度占总聚磷菌属相对丰度的 65.3% ~ 83.9%[34]。增强型生物除磷工艺可以选择性富集聚磷菌属进而提高除磷率,该工艺中优势聚磷菌属为不动杆菌属(*Acinetobacter*)、*Pseudomonas*、*Tetrasphaera* 和产碱杆菌属(*Alcaligenes*)等,其中部分聚磷菌属具有反硝化除磷和异养硝化的能力[35]。

短程硝化-反硝化工艺和 PN/A 工艺均因其具备出色的脱氮性能,成为污水处理领域研究的热点。短程硝化-反硝化工艺可以在节省曝气量和碳源的情况下实现高效脱氮。采用序批式反应器通过控制曝气时间可以实现稳定的短程硝化,*Comamonas* 是其中的优势 AOB。PN/A 工艺因其无需供氧并且无需外加碳源,被认为是一项高效可持续的脱氮技术引起人们关注。PN/A 系统中存在多种功能菌属的协同和竞争作用,当 NOB 处于优势地位,会导致 AnAOB 相对丰度下降,出水 NO_3^--N 浓度过高[36]。NO_2^--N 生成速率是影响 PN/A 污水处理系统中 AnAOB 和 NOB 竞争优势的关键因素。将短程硝化耦合 PN/A 工艺,在曝气阶段向系统中投加一定量的 NO_2^--N,AnAOB 相对丰度提高为原系统的 1.2 倍,NOB 相对丰度下降,并且产氢单胞菌属(*Hydrogenophaga*)、*Thauera* 和盐单胞菌属(*Halomonas*)等脱氮功能菌显著富集,化学需氧量和 NO_3^--N 去除率维持在 80%以上[37-38]。

2.3　运行参数

温度会影响污水处理系统微生物群落的组成和多样性[39],温度降低微生物群落的多样性下降[40]。温度与 *Nitrospira*、水栖生物菌属(*Aquihabitans*)和脱氯单胞菌属(*Dechloromonas*)等核心脱氮功能菌属呈显著正相关,当运行温度低于 15 ℃时,核心脱氮功能菌属相对丰度下降会导致系统脱氮效果不佳[41]。城镇污水处理厂为了保证冬季正常运行,一般可能会采取降低污泥负荷和增加污泥回流量等措施提高核心脱氮功能菌属的相对丰度。污水处理系统低温运行还可能导致丝状菌属分泌过多,活性污泥污泥容积指数(SVI)上升至 254 mL/g,引发污泥膨胀现象[42]。研究表明[43],在低温引发污泥膨胀现象的序批式反应器中投加 120 mg/L 的氯化铁并且采用交替曝气的方法,成功抑制了丝状菌属拟糖细菌属(*Candidatus saccharibacteria*)的繁殖,其相对丰度降低了 66.5%,SVI 值从 274 mL/g 降低至 56 mL/g,改善了活性污泥的沉降性能。

溶解氧(DO)浓度对污水处理系统微生物群落结构有显著影响。污水处理系统长期在 DO 质量浓度为 0.5 mg/L 条件下运行会导致硝化菌属明显富集,系统对氨氮去除率达到 90%,脱氮性能没有受到较大影响[44]。也有研究[45]进一步证实,DO 质量浓度维持在 0.5~2.0 mg/L 有利于 *Nitrospira* 的生长,这是污水处理系统在低 DO 条件下脱氮性能没有受到影响的主要原因。调节 DO 浓度有利于抑制部分丝状菌属繁殖,改善活性污泥沉降性能。某座大型造纸废水处理系统发生污泥膨胀现象后,通过提高 DO 质量浓度为 1.5 mg/L 和在选择池加大预曝气等措施,成功抑制了红球菌属(*Rhodococcus*)和 *Thiothrix* 等丝状菌属的繁殖,其相对丰度分别从 2.9%和 0.2%下降至 0.2%和 0.01%,SVI 值从 198 mL/g 降低至 80 mL/g,该厂污泥膨胀的问题得到了解决[46]。

HRT 会影响微生物的生存环境并且改变微生物的群落结构。过长的 HRT 会增加污水处理系统的经济成本,过短的 HRT 会导致出水 NO_3^--N 和 NO_2^--N 浓度上升,系统脱氮效果变差。某移动床生物膜反应器的 HRT 大于等于 9 h 时,有利于产氢单胞菌属(*Hyddrogenophaga*)、*Thauera*、*Pseudomonas* 和 *Flavobacterium* 等脱氮功能菌属的富集,小于 9 h 时系统 *Thauera* 的相对丰度显著下降,系统脱氮效果变差[47]。污泥停留时间(SRT)会影响微生物的生长和繁殖从而影响菌群的丰度。为了避免功能菌群

的流失率大于繁殖率,SRT 不能小于 3~5 d。当采用膜生物反应器处理高浓度奶牛养殖污水时,SRT 从 30 d 延长至 45 d,丰富度指数和多样性指数分别从 2 673 和 7.4 上升至 2 928 和 9.3,适当地延长 SRT 有利于微生物的生长[48]。过长的 SRT 会引起微生物发生内源呼吸作用,从而抑制硝化菌属的生长代谢[49]。

3 微生物群落与环境因子关联性分析方法

3.1 束缚性排序分析

束缚性排序分析能够有效评估不同环境因子对微生物群落结构组成的影响,并通过坐标轴直观展示微生物群落结构组成随环境因子的变化情况(图 1)。常用的束缚性排序方法为冗余性分析。Zheng 等[50]通过冗余性分析研究了污水处理系统中的微生物群落对环境因子的响应,表明优势脱氮功能菌属 *Nitrospira* 与混合液悬浮固体浓度和 SRT 呈正相关,而与 DO 浓度呈负相关。Zhu 等[51]采用冗余性分析研究高海拔城镇污水处理系统中微生物群落和环境因子之间的相互作用,结果表明,低温、海拔、紫外线指数、pH、DO 和总氮是影响污水处理系统中微生物群落组成的主要环境因子,其中低温和强紫外线是导致高海拔地区活性污泥微生物群落多样性下降的关键因素。

3.2 曼特尔检验分析

曼特尔检验分析常用于评估环境因子矩阵与微生物群落矩阵之间的相关性。通过计算皮尔逊或斯皮尔曼相关系数,分析 2 个矩阵之间的关联性(图 2)。当相关系数的绝对值接近 1 且概率(P)值小于 0.05 时,表明 2 个矩阵之间存在显著的相关性。Xie 等[52]利用曼特尔检验分析方法探究了深圳 2 座污水处理系统的运行效果与进水成分、温度、pH 等环境因子的关联性,发现进水化学需氧量、总氮和 NO_3^--N 浓度与微生物群落结构显著相关。Yang 等[53]分析了我国 60 座污水处理系统的微生物群落组成与其地理位置、运行条件和污水水质指标等环境因子进行了曼特尔检验分析,结果表明,污水水质指标是影响微生物群落结构的重要因素,而且由于丰富微生物群落占据了较窄的生态位,其对环境因子的响应强于稀有微生物群落。

4 结论与展望

污水处理系统中的微生物群落在污染物去除过程中发挥重要作用,了解微生物群落结构并且筛选出功能菌属有利于从微观角度对污水处理系统运行效能进行提升。研究不同污水处理系统中微生物群落结构,能够深入了解其在不同环境条件下的动态变化及其对污水处理效果的影响。微生物群落的结构与进水成分、处理工艺和运行参数等环境因子密切相关,这些因子会影响微生物的种群组成、代谢途径以及功能分布。进水水质的变化,特别是污染物的种类和浓度,可能会促使某些微生物群落的增殖或抑制,进而影响系统的处理效率。不同的处理工艺和运行参数,如水力停留时间、污泥负荷、氧气供应量等,也会显著改变微生物的群落结构。通过调整这些环境因子,可以有效地优化污水处理系统中的微生物群落结构,从而提升系统的污染物去除效率。针对目前污水处理系统微生物群落研究进展,未来的相关研究工作可以从以下 2 个方面展开。

(1)核心微生物和稀有微生物的鉴定与识别

污水处理系统中高丰度和高频率的核心微生物对污染物去除贡献较大,其鉴定与识别可为优化微生物群落结构提供理论支持。稀有微生物虽低丰度且难以检测,但在特定环境下可能会转化为优势微生物,同样对污染物去除贡献较大,高通量测序技术虽有助于识别这些微生物,但目前对绝大多数稀有微生物的生态作用仍不清晰。深入研究核心与稀有微生物的生理生态特性,能够有助于全面理解微生物群落结构,并为更加准确地评估与预测污水处理系统运行效能提供重要支撑。

(2)微生物群落、环境因子以及污水处理系统运行效能的关联

污水处理系统中微生物群落组成直接影响系统的运行效能。由于环境因子对微生物群落组成具有显著影响,通过系统性分析微生物群落组成与环境因子的关联,可以有针对性地调控微生物群落,进而优化系统的运行效能。可将宏基因、宏蛋白、宏转录等多组学技术与数学模型相结合,深入研究微生物学信息及其与污水处理系统效能之间的关联,为污水处理系统运行效能的提升提供科学依据。

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(上接第 18 页)

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