

海洋环境异养硝化-好氧反硝化菌的研究进展

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摘要: 异养硝化-好氧反硝化(heterotrophic nitrifying- aerobic denitrification, HN-AD)菌的发现打破了传统的脱氮理论, 可以在有氧条件下同时进行硝化和反硝化, 成为近年来的研究热点。HN-AD细菌在海洋氮循环中发挥着重要作用。本文对海洋环境中 HN-AD 菌的多样性和部分已知氮代谢途径及相关酶系进行了介绍, 分析了盐度、碳氮比、溶解氧、pH 等环境因素对 HN-AD 菌脱氮效果的影响, 对其工艺和技术应用、前景和发展方向进行了综述和展望。

关键词: 异养硝化-好氧反硝化; 代谢途径; 生物脱氮

Advances in heterotrophic nitrifying-aerobic denitrifying bacteria in marine environment

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Abstract: The discovery of heterotrophic nitrifying-aerobic denitrifying (HN-AD) bacteria updates the conventional theory of nitrifying. The HN-AD bacteria capable of simultaneous nitrification and denitrification under aerobic conditions have become a research hotspot in recent years. These bacteria play a key role in the marine nitrogen cycle. We introduced the diversity, nitrogen metabolic pathways, and related enzymes of marine HN-AD bacteria and analyzed the effects of environmental factors (salinity, C/N ratio, dissolved oxygen, pH, etc.) on the denitrifying performance of HN-AD bacteria. Furthermore, we summarized the functioning processes and applications of these bacteria and made an outlook on the

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development directions of this field.

Keywords: heterotrophic nitrification-aerobic denitrification; metabolic pathway; biological removal of nitrogen

氮循环主要由微生物介导的多种生物地球化学循环驱动,涉及生物固氮、氨化、厌氧氨氧化、硝化和反硝化等多个环节^[1]。传统生物脱氮过程包括好氧自养硝化和厌氧异养反硝化。硝化作用是在有氧条件下,自养微生物将氨氮依次氧化为亚硝态氮和硝酸氮;反硝化过程是在严格厌氧条件下,异养型微生物将硝酸氮还原为氮气。在传统认识中,两个过程发生于不同微生物,但异养硝化-好氧反硝化(heterotrophic nitrification-aerobic denitrification, HN-AD)菌的发现突破了传统的脱氮理论,在有氧的环境中实现了同步硝化和反硝化(simultaneous nitrification and denitrification, SND)。与传统脱氮工艺相比,HN-AD 处理含氮废水有如下优点^[2]:(1) 硝化和反硝化过程同时进行,简化了工艺流程,减少了设备占地面积,缩减了运行成本,获得了更大的经济和时间效益;(2) HN-AD 菌的多样性导致它对盐度、温度和重金属等环境胁迫有较高的抗逆性,扩大了适用环境范围;(3) 将氨氮($\text{NH}_4^+\text{-N}$)最终转化为气态产物,脱氮过程中几乎无硝酸盐($\text{NO}_3^-\text{-N}$)和亚硝酸盐($\text{NO}_2^-\text{-N}$)的积累,氮去除效率较高;(4) 异养硝化作用的各种底物和产物有助于与多种细菌的混合培养。

氮元素是浮游植物生长所需要的常量元素,作为海洋初级生产力的限制因子,对生物泵的调节和控制生态系统群落结构起关键作用^[3-4]。氮循环作为海洋生态系统中物质与能量循环的关键组成部分,对维持海洋生态系统功能同样具有重要意义^[5]。然而近年来,随着城市化工业化进程的加快和集约化水产养殖业的快速发展,排入水体的含氮污染物大量增加,引起海

洋生态系统中富营养化和赤潮的发生,导致生态环境失衡,威胁人类健康^[6]。由于 HN-AD 菌的高效脱氮潜力,海洋来源的 HN-AD 菌物种多样性和代谢功能得到研究人员的关注,尤其是海洋特殊的生态环境造就了丰富的 HN-AD 菌多样性^[7],使该菌在高盐度、低溶解氧等特殊环境的适用性范围扩大,并在高盐度含氮废水处理、海洋生态修复中具有独特的应用前景。本文就海洋环境 HN-AD 菌的特性、代谢途径、影响因素、技术应用和研究热点方面进行综述,并阐述目前 HN-AD 菌的在海洋氮循环中的意义,展望未来的研究方向。

1 异养硝化-好氧反硝化菌的发现及其多样性

1983 年 Robertson 等^[8]首次发现了一株具有异养硝化-好氧反硝化能力的细菌 *Thiospharera pantotropha*, 后更名为泛养副球菌(*Paracoccus pantotrophus*), 并首次提出 HN-AD 的概念。此后,越来越多的 HN-AD 菌被发现,其中以细菌居多。海洋来源的 HN-AD 菌已分离鉴定出至少 16 个属,如卓贝尔氏菌属(*Zobellella*)^[9-10]、弧菌属(*Vibrio*)^[9,11]、盐单胞菌属(*Halomonas*)^[12-15]和芽孢杆菌属(*Bacillus*)^[16-17]等。上述细菌主要来源于海洋沉积物^[11,18-19]、海水养殖区^[12-13,20]、红树林湿地系统^[9]和河口^[10]等环境。部分真菌也可以进行 HN-AD 作用,如 Fang 等^[21]从珠江口表层沉积物分离的酵母菌 *Barnettozyma californica* K1 对氨氮的去除效率可达 99.11%,总氮去除率可达 81.48%。部分海洋 HN-AD 菌的相关信息及脱氮特性见表 1。其中,多数 HN-AD 菌的盐度适

表 1 部分海洋环境的异养硝化-好氧反硝化菌的脱氮特性

Table 1 Nitrogen removal characteristics of some marine original heterotrophic nitrification-aerobic denitrifying bacteria

Genus	Strain	Source	Carbon source	C/N	Salinity (%)	Ammonia removal (%)	References
<i>Zobellella</i>	B307	Bay sediment	Sodium succinate	5	7.5	98.35	[10]
	A36	Mangrove wetland	/	/	2	/	[9]
<i>Vibrio</i>	SF16	Marine sediment	Sodium acetate	10	1-5	91.82	[11]
	W37	Mangrove wetland	/	/	2	/	[9]
<i>Halomonas</i>	X ₃	Aquaculture wastewater	Glucose	10	3	98.29	[13]
	SD136WN1	Mariculture water	Sodium succinate	5	3	64.00	[22]
	GYL	Activated sludge	Saccharose	/	2-7	98.30	[14]
	HN2	Activated sludge	Sodium citrate	15-20	3	100.00	[15]
<i>Bacillus</i>	N31	Mariculture water	Sodium succinate	5-20	3-4	86.30	[16]
	SLWX2	Mariculture water	Glucose	/	3	100.00	[17]
<i>Exiguobacterium mexicanum</i>	SND-01	Estuarine sediments	Glucose	12	3-5	93.60	[23]
<i>Pseudomonas</i>	ADN-42	<i>Hymeniacidon perleve</i>	Sodium succinate	12	4	75.80	[24]
	F2	Mangrove wetland	/	/	2	/	[9]
	8-C	Marine sediment	sodium acetate	7.5	3-8	93.6	[25]
	DN13-1	Deep-sea sediment	/	/	/	98.89	[18]
<i>Paracoccus versutus</i>	LYM	Sea sludge	Sodium lactate	/	/	75.40	[26]
<i>Marinobacter</i>	F6	Mariculture water	Sodium succinate	15	3.2-3.5	48.62	[20]
<i>Serratia marcescens</i>	CL1502	Deep-sea sediment	Glucose	20	1-5	76.70	[19]
<i>Klebsiella</i>	y6	Sediment of Jiaozhou Bay	Sodium succinate	17	/	99.67	[27]
<i>Marinomonas</i>	SR148SN9	Mariculture water	Sodium succinate	5	3	65.00	[22]
	SD167SA1	Mariculture water	Sodium succinate	5	3	59.00	[22]
<i>Achromobacter</i>	E43	Mangrove wetland	/	/	2	/	[9]
	J1	Mangrove wetland	/	/	2	/	[9]
<i>Photobacterium</i>	NNA4	Mariculture water	Sodium succinate	>10	1-4	>70.00	[28]
<i>Stutzerimonas frequens</i>	TF18	Mariculture water	Sodium acetate	10	1-4	89.21	[29]
<i>Acinetobacter</i>	2-1-H	Marine sediment	Sodium acetate	10	3-8	89.1	[25]
<i>Dietzia maris</i>	W023a	Marine sediment	/	/	/	97.6	[30]

/表示在原文中未提及

/ indicates that the data was not mentioned in the reference.

应范围在 3%–5% 之间,少数可以达到 6.5% 以上,大部分 HN-AD 菌在无 NaCl 的环境中无法生长。HN-AD 菌所需的碳源以丁二酸钠等非糖类有机物为主,部分也可以利用葡萄糖,可能与

其分离环境以及不同种属有关,呈现不同的碳源偏好性。对 C/N 的适应范围在 5–20 之间。对氨氮的去除率在不同培养条件下的差异较大(48.62%–100%),但多数可达 80% 以上。

2 异养硝化-好氧反硝化菌的代谢途径和相关酶系

传统的异养硝化是指在好氧条件下异养微生物将还原态氮素氧化为亚硝酸氮和硝酸氮的过程。反硝化是指微生物将亚硝酸氮和硝酸氮转化成含氮气体的过程。HN-AD 菌可以将各种氮源通过同化作用转化为胞内有机氮,也可以通过异化作用将氮素转化为含氮气体。对于异化作用,HN-AD 菌目前被普遍认可的代谢途径有两种:一种为典型完全硝化和反硝化通路,认为硝化作用和反硝化作用的结合点在亚硝酸氮,氨氮首先转化为羟胺,再由羟胺转化为亚硝酸盐氮(与硝酸盐可互相转化),进而经反硝化作用转化为氮气;另一种途径认为,氨氮转化为羟胺后,羟胺氧化酶直接将羟胺反硝化为气体产物,不产生亚硝酸盐的积累。

异养硝化-好氧反硝化过程中可能参与的酶主要有氨单加氧酶(ammonia monooxygenase, AMO)、羟胺氧化还原酶(hydroxylamine oxidoreductase, HAO)、硝酸盐还原酶(nitrate reductase, NAR)、亚硝酸盐还原酶(nitrite reductase, NIR)、一氧化氮还原酶(nitric oxide reductase, NOR)和氧化亚氮还原酶(nitrous oxide reductase, NOS)等。在不同菌株中,氮代谢相关酶基因的表达存在较大差异,导致氮代谢途径有所不同^[31]。部分相关酶的功能基因和主导过程如表 2 所示^[32-33]。

尽管有许多菌株基于氮平衡分析表现出 HN-AD 功能,但通过基因组和酶活性分析缺失了许多涉及硝化作用或反硝化作用的功能基因和关键酶。相较于其他环境,更多海洋环境分离菌株的代谢途径可能异于传统代谢途径。Liu 等^[29]通过 qPCR 的方式探究 *narG*、*narA*、*norB* 和 *nirB* 等基因在 *Stutzerimonas frequens* TF18 中

表 2 部分酶的功能基因和作用过程

Table 2 Functional genes and action processes of some enzymes

Processes		Enzymes	Genes
Nitrification	$\text{NH}_4^+\text{-N} \rightarrow \text{NH}_2\text{OH}$	AMO	<i>amo</i>
	$\text{NH}_2\text{OH} \rightarrow \text{NO}_2^-\text{-N}$	HAO	<i>hao</i>
		POD	<i>pod</i>
Denitrification	$\text{NO}_2^-\text{-N} \rightarrow \text{NO}_3^-\text{-N}$	NXR	<i>nxrAB</i>
	$\text{NO}_3^-\text{-N} \rightarrow \text{NO}_2^-\text{-N}$	NAP	<i>napAB</i>
		NAR	<i>narGHI</i>
	$\text{NO}_2^-\text{-N} \rightarrow \text{NO}$	Cu-NIR	<i>nirK</i>
		Cd1-NIR	<i>nirS</i>
	$\text{NO} \rightarrow \text{N}_2\text{O}$	NOR	<i>norBC</i>
	$\text{N}_2\text{O} \rightarrow \text{N}_2$	NOS	<i>nosZ</i>

的表达,验证了完整的异化硝酸盐还原($\text{NO}_3^- \rightarrow \text{NO}_2^- \rightarrow \text{NH}_4^+$)和反硝化($\text{NO}_3^- \rightarrow \text{NO}_2^- \rightarrow \text{NO} \rightarrow \text{N}_2\text{O} \rightarrow \text{N}_2$)途径,却并未发现硝化过程对应的 *hao*、*amo* 基因。Huang 等^[34]在 *Halomonas venusta* SND-01 的基因组中未发现 HAO、NAP 和 NIR 相对应的功能基因,但菌株具有 HN-AD 功能,并根据 *amoC* 基因的存在推测可能存在新的 AMO 在菌株 SND-01 中。Zhou 等^[35]分离的 *Acinetobacter oleivorans* AHP123 培养 24 h 时对 $\text{NH}_4^+\text{-N}$ 的去除率可以达到 97.93%,但通过基因组注释未检测到 *amo*、*nap* 和 *nos* 等相关酶基因,推测可能存在其他代谢通路实现其 HN-AD 功能。

截至目前已分离得到的异养硝化-好氧反硝化菌株种类繁多,分布于不同的分类单元、不同种属。菌种的生理多样性导致其代谢途径和机理尚不明确,尚无明确破译其氮代谢途径的模式菌株^[36]。目前主要通过功能基因挖掘、相关酶系酶活测定、反应过程中间产物测定和氮平衡分析等手段来推断代谢途径。因此,发现更多的 HN-AD 菌物种多样性,了解它们在生理和代谢性状上的相似性和差异性,从基因调控的角度找到代谢途径的模式,是一个重要的研究方向。

3 异养硝化-好氧反硝化菌生长及脱氮效果的影响因素

3.1 盐度

目前对于 HN-AD 菌的研究和应用主要集中在低盐环境中,而实际应用场景下存在更高的氮含量和高盐的环境^[37]。高盐环境(盐度 $\geq 1\%$)下,渗透压发生变化,会导致细菌内部生物化学反应环境发生变化,对微生物的生长代谢有抑制和毒害作用;同时,脱氢酶出现盐析作用,活性降低,细胞脱水质壁分离甚至破裂死亡,使微生物的降解能力下降^[23],因此导致普通微生物在高盐环境下的脱氮效率会显著降低^[11]。

海洋来源的 HN-AD 细菌有耐高渗的优势,对其脱氮特性、机制和最适环境条件进行深入研究,对高盐浓度的含氮废水处理具有重要意义。白洁等^[10]从胶州湾沉底物中分离出 *Zobellella* sp. B307,在盐度为 75 g/L 时,其 $\text{NH}_4^+\text{-N}$ 和 $\text{NO}_3^-\text{-N}$ 去除率分别可达到 97.67%和 94.39%。说明该菌株在高盐度条件下仍生长良好并且脱氮效率较高,表明该菌株具有较广的盐度适应范围。Duan 等^[11]从海洋沉积物中分离的魔鬼弧菌(*Vibrio diabolicus*) SF16 在盐度 1%–5%时能去除 91.82%的 $\text{NH}_4^+\text{-N}$ 和 99.71%的 $\text{NO}_3^-\text{-N}$,而在无氯化钠的环境下几乎不能去除 $\text{NH}_4^+\text{-N}$ 。Guo 等^[38]从盐碱湖分离的 *Halomonas campisalis* ha3 可以在 20%的高盐度条件下进行脱氮。

3.2 碳源

碳源是影响微生物生长代谢的主要营养物质,承担提供能源和电子的功能,并且微生物以碳元素构成的有机物组成基本骨架^[39]。因此,碳源的种类和相对含量会对微生物的生长和脱氮效率产生显著影响。目前筛选出的 HN-AD 细菌利用的碳源主要有乙酸钠、葡萄糖、蔗糖、柠檬酸钠、丁二酸钠、醋酸钠和乙酸钠等。Zheng

等^[20]分离的 *Marinobacter* sp. F6 在以酒石酸钾钠、柠檬酸钠为碳源时细菌几乎不生长,以丁二酸钠为碳源时细菌生长量最大且总氮脱氮率可以达到 48.29%。这可能与丁二酸钠容易进入三羧酸循环快速提供能量和还原力有关。Liu 等^[29]分离的 *Stutzerimonas frequens* TF18 在以琥珀酸钠作为碳源时 $\text{NH}_4^+\text{-N}$ 的去除率为 98.96%,而以蔗糖为碳源时 $\text{NH}_4^+\text{-N}$ 的去除率仅有 59.62%,更倾向于使用分子量小的碳源^[40]。

3.3 C/N

C/N 通过电子传递链和酶活影响 HN-AD 过程^[41],同时影响菌株的生长和脱氮效率。多数 HN-AD 菌株对 C/N 的适应范围比较广,略大于 Redfield 常数。Cui 等^[23]分离的 *Exiguobacterium mexicanum* SND-01 当 C/N 从 4 上升到 20 时, $\text{NH}_4^+\text{-N}$ 的去除率从 51.4%提高到 99.9%;但当 C/N 大于 12 时,反应结束后仍然有大量碳源残留,成本效益下降。Huang 等^[16]分离的 *Bacillus litoralis* N31 在 C/N 范围为 5–20 时, $\text{NH}_4^+\text{-N}$ 的去除率都可以保持在 90%以上,其对 C/N 范围的耐受性扩大了其应用范围。

3.4 pH

大多数报道的 HN-AD 细菌在中性或碱性条件下脱氮活性更高^[42]。张培玉等^[14]分离的菌株 *Halomonas* sp. GYL 在 pH 7.5 时达到最大脱氮效率,但 $\text{NO}_2^-\text{-N}$ 的积累量随 pH 值的升高逐渐增加。Dong 等^[15]分离的 *Halomonas piezotolerans* HN2 在初始 pH 6.0–9.0 时,24 h 内可以去除几乎所有的 $\text{NH}_4^+\text{-N}$,但在 pH 6.0 时, $\text{NO}_2^-\text{-N}$ 积累量较高。亚硝酸盐还原酶可能比氨氧化酶对 pH 的变化更敏感,因此 pH 对好氧反硝化过程的影响更显著^[12]。

3.5 温度

目前报道的多数 HN-AD 细菌为嗜温菌,脱氮效率在 25–37 °C 范围内较高^[43]。胡锦涛等^[44]

从土壤中分离的黄褐假单胞菌(*Pseudomonas fulva*) K3 的在 30–35 °C 温度范围内氨氮去除率可达 90% 以上, 适宜温度范围较窄。但通常温度每降低 10 °C, 脱氮速率降低^[45], 且细菌的生长和酶活均受到严重影响。然而有些海洋环境分离的 HN-AD 细菌在保持较高脱氮效率的同时具有耐低温性, 如 Wang 等^[46]分离的 *Vibrio* sp. LY1024 菌株可以在 15 °C 时对 $\text{NH}_4^+\text{-N}$ 和 $\text{NO}_3^-\text{-N}$ 的去除率分别达到 97.3% 和 76.4%。筛选高效耐低温的 HN-AD 菌株有利于打破冬季低温时生物脱氮效率低的约束^[47]。

3.6 其他

其他影响因素如溶解氧(dissolved oxygen, DO)、重金属等对细菌的脱氮效率也有较大影响。Jin 等^[24]研究发现一定程度的 DO 增加可能会促进菌株的生长和反硝化作用, 持续低 DO 时脱氮效率最佳, 他们分离的 *Pseudomonas* sp. AND-42 在 $\text{DO} < 3 \text{ mg/L}$ 持续曝气的条件下对 $\text{NH}_4^+\text{-N}$ 的去除率可达 100%。Huang 等^[19]分离的 *Serratia marcescens* CL1502 对 Cr^{3+} 有良好的耐受性。

4 异养硝化-好氧反硝化菌脱氮技术应用和研究热点

4.1 废水处理和生态修复

近年来对 HN-AD 菌的研究得到快速发展, 虽然在脱氮性能的研究还主要停留在实验室研究阶段, 但也逐渐开始应用于废水处理系统和人工湿地的生态修复^[48]。目前研究工艺主要方式包括与反应器结合、菌株固定化和结合污泥颗粒等, 主要通过简化工艺流程、控制条件和优化过程等来提高脱氮效率^[45]。李秋芬等^[49]将 3 株从海水养殖环境分离的 HN-AD 组合菌群在模拟生物滤器进行强化挂膜, 在脱氮的同

时可去除部分有机物, 提高了海水养殖尾水的净化效率。陈昊^[25]采用以盐度为 3% 的序批式反应器, 加入菌种 *A. johnsonii* 2-1-H 和 *P. kunmingensis* 8-C 构成的 HN-AD 菌群, 对 $\text{NH}_4^+\text{-N}$ 的去除率比对照组提高 78.40%, 显著提升了耐高盐度性能及脱氮效果。Wu 等^[50]优化曝气式固相脱氮工艺 (solid phase denitrification, SPD), 将 *Acinetobacter* sp. TAC-1 吸附于生物可降解聚合物, HN-AD 细菌利用聚合物作为载体和电子供体进行生长和脱氮, 经降解后 HN-AD 菌在表面形成生物膜, 形成更稳定的同步硝化反硝化(simultaneous nitrification and denitrification, SND)过程, 经生物增强改变群落结构后, 在 DO 为 3 mg/L 条件下, 总脱氮效率提高了 50.46%。Xiang 等^[51-52]通过在移动床生物膜反应器(moving bed biofilm reactor, MBBR)添加 *Zobellella* B307, 在高盐度 (65‰) 养殖废水中 COD、 $\text{NH}_4^+\text{-N}$ 和 $\text{NO}_3^-\text{-N}$ 的去除率分别可达到 95.6%、94.4% 和 85.7%, 并提高了体系内 HN-AD 菌株和参加氮代谢功能基因的相对丰度, 在实验室中证明低 COD/TN 条件下添加 HN-AD 菌的 MBBR 工艺具有更稳定的氮去除性能。

4.2 HN-AD 菌的群体感应

近期, 研究人员开始关注 HN-AD 菌的群体感应系统(quorum sensing, QS)。部分 HN-AD 细菌可以利用信号分子或自诱导物调节基因表达水平和代谢途径, 以应对环境变化^[53]。Zhao 等^[9]研究发现 *Vibrio sinoalensis* strain W37 可以产生 C8-HSL 信号分子以及 SMP 产物, 对 *Achromobacter pulmonis* strain E43、*Zobellella denitrificans* strain A36 等 HN-AD 细菌的生长、反硝化和生物膜的形成有促进作用。Zhu 等^[54]研究发现, *P. aeruginosa* PAO1 的 QS 缺陷突变体表现出更高的脱氮能力, 自分泌的 n-酰基-L-高丝氨酸内酯或喹诺酮类信号达到一定浓度会抑制

NOR 和 NAR 的表达阈域,表明群体感应系统可以通过改变酶活来调节 HN-AD 过程。Wang 等^[55]研究发现, *Acinetobacter* sp. JQ1004 可以通过外源分子提高硝化效率和 *amoA* 基因表达效率并促进细菌的生长速率;同时其异养硝化过程中, AHL 分子驱动了细菌间通讯,为在废水中脱氮提供了新的调控方式。由于添加到生物反应器中的天然分子信号和合成分子信号之间的结果不同,因此有必要研究自分泌信号分子在 HN-AD 中的功能,以模拟微生物的实际脱氮环境。Huang 等^[56]研究发现 $\text{NH}_4^+\text{-N}$ 的去除主要由 *Marinomonas*、*Marinobacterium*、*Halomonas* 和 *Cobetia* 所属菌株之间的协同作用驱动,由于种间共存,其菌群的 $\text{NH}_4^+\text{-N}$ 去除效率和稳定性明显优于单株菌。为了保持高效的脱氮性能,在污水处理系统中添加特定的复杂菌群能提高功能细菌的活性,复杂的生物增强菌群比纯菌株更适应高氮含量环境^[57]。

4.3 联合去除碳和磷

除氮元素外,过量的有机物和磷元素也可以导致水体富营养化^[58]。部分 HN-AD 菌可以在脱氮的过程中同步实现去除碳和磷。王骁静等^[27]分离的 *Klebsiella* sp. y6 在生长对数期可以实现同步脱氮除碳,在混合氮源的系统中 COD 去除率最高可以达到 95.71%。*Exiguobacterium mexicanum* SND-01 能够在实际高盐度生活废水中脱氮的同时降解有机物,对 $\text{NH}_4^+\text{-N}$ 和 COD 的去除率达到 27.9%和 21.9%^[23]。磷可以通过增加表层水体中较高的初级生产力来促进富营养化,通常以磷酸盐($\text{PO}_4^{3-}\text{-P}$)的形式存在于水溶液中。Yang 等^[59]分离的 *Pseudomonas* sp. Y1 可以在 $\text{NH}_4^+\text{-N}$ 去除率达到 92.04%的同时吸附和共沉淀磷酸盐,去处理率可达 99.98%,为同步磷酸盐回收和异养硝化在好氧环境下

处理复杂污染背景废水的实际应用提供了新的视角。

5 结语与展望

海洋是全球生态系统中主要的氮通量场所,对地球系统氮循环有着重要的影响。海洋来源的 HN-AD 菌,其丰富的物种多样性、较强的环境抗逆性和独特的代谢途径使其在海洋氮污染治理中具备良好的发展潜力,然而目前对于海洋来源 HN-AD 菌的研究尚处于起步阶段,未来的研究应重点关注 3 个方面。

(1) HN-AD 菌虽然是参与海洋生态系统氮循环的重要微生物之一,但它对海洋环境的适应性研究仍处于基础阶段。因此,为深入研究 HN-AD 菌在全球典型海洋生态系统(如湿地、河口、大洋、深海和沉积环境等)中的分布特征以及种群多样性,仍需进一步探究不同环境下 HN-AD 菌的胞内胞外代谢反馈机制,以此明确 HN-AD 菌群落组成与环境相关性的实质分子机制。

(2) 目前已发现多种海洋来源 HN-AD 菌,但对它们的脱氮途径和机制尚不明晰。因此仍需进一步结合多组学手段加强对海洋环境 HN-AD 菌的特异性酶和脱氮代谢机制的研究,尤其是关键功能基因、代谢途径和关键酶活特征等,以便从分子水平探究其代谢途径和机理,这对深入理解 HN-AD 菌在海洋氮循环过程中的作用有重要意义。

(3) 为应对愈发严重的海水养殖尾水环境问题,仍需加强海洋环境 HN-AD 菌的脱氮去污技术研发,尤其是与其他环境工程技术方法(如电化学、燃料电池等)的综合集成,为 HN-AD 菌在海洋环境污染治理方面的应用提供技术支撑。

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