好氧颗粒污泥的微生物研究进展

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摘要 好氧颗粒污泥是由微生物在一定选择压下自凝聚形成的可移动的生物膜。本文从微生物群落的组成、分布及演替3个方面对好氧颗粒污泥进行论述, 并对未来的研究方向进行展望, 为好氧颗粒污泥后续研究提供参考。主要结论如下: 好氧颗粒污泥与絮状污泥的微生物组成存在差异, γ -变形菌纲(γ -Proteobacteria)、黄杆菌纲(Flavobacteria)、鞘脂杆菌纲(Sphingobacteriia)等的微生物在好氧颗粒污泥中所占的比重不容忽视; 以聚磷菌(Accumulibacter)、亚硝化单胞菌属(Nitrosomonas)和亚硝化螺菌属(Nitrospira)为主要微生物的好氧颗粒污泥能够高效脱氮除磷; 反硝化除磷好氧颗粒污泥是聚糖菌(Competibacter)和Accumulibacter共同作用的效果, 也可以是黄单胞杆菌目(Xanthomonadales)和Tetrasphaera共同作用的效果; pH过低, DO不足或者有机负荷过高会导致好氧颗粒污泥中绿弯菌门(Chloroflexi)、球衣菌属(Sphaerotilus)、发硫菌属(Thiothrix)等丝状菌的过量生长; 红环菌属(Rhodocyclus)、生丝微菌科(Hyphomicrobiaceae)等非球状菌和产EPS的动胶菌属(Zoogloea)在好氧颗粒污泥形成过程中可起到关键性的作用。

关键词 好氧颗粒污泥, 微生物组成, 微生物分布, 微生物演替, γ -变形菌纲

好氧颗粒污泥(aerobic granular sludge, AGS)是由微生物在一定选择压下自凝聚形成的以各种微生物种群为主体的可移动的生物膜。好氧颗粒污泥技术具有污泥浓度高、剩余污泥量少、沉降速度快、耐冲击负荷能力强、所需占地面积小、低成本、低能耗、可同时实现脱氮除磷等特点^[1], 成为目前污水生物处理领域的研究热点之一。

Mishima和Nakamura^[2]首次报道在好氧上流式污泥床反应器(aerobic upflow sludge blanket, AUSB)中培养获得AGS, 该技术随后便得到广泛关注^[3,4]。荷兰代尔夫特理工大学的van Loosdrecht课题组将好氧颗粒污泥与序批式活性污泥法(sequencing batch reactor, SBR)结合形成的Nereda工艺(或称好氧颗粒污泥序批式反应器(granular sequencing batch reactor, GSBRT工艺))应用于实际工程应用并通过中试^[5]和生

产性试验^[6]。目前关于AGS的特性、影响因素、应用和形成机理等方面已有了大量的研究和论述^[7,8]。例如, 减少沉淀时间、提高水力剪切力和溶解氧浓度、高低负荷交替运行、钙镁离子的强化等有利于AGS的形成。总体说来, 提供不利于某些种类微生物生长的因素, 有利于活性污泥体系中的丝状菌群与其他菌群聚集形成共生体系即颗粒污泥。

尽管关于AGS的形成和影响因素等方面有较多论述和报道, 关于颗粒污泥微生物的论述相当不足。本文以好氧颗粒污泥的主体——微生物相为出发点, 从微生物的组成、分布和演替等方面论述AGS的污染物去除机理。

1 AGS微生物群落组成

现代分子微生物学手段近年来在环境生态学领

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域得到了快速的发展,是研究AGS微生物的重要方法,主要包括梯度凝胶电泳(denatured gradient gel electrophoresis, DGGE)、荧光原位杂交(fluorescence in situ hybridization, FISH)、实时定量聚合酶链反应(polymerase chain reaction, PCR) (实时定量PCR (real-time quantitative PCR, qPCR)), 克隆文库、末端限制性片段长度多态性(terminal-restriction fragment length polymorphism, T-RFLP)和高通量测序等手段. 基于高通量测序技术的宏基因组学^[9]和宏转录组学^[10]是当前微生物生态学分析的最新手段. 一般说来, qPCR、FISH和T-RFLP技术用于少数种类的微生物分析, 而基于PCR的克隆文库、DGGE和高通量测序的手段用于系统中较多种类的微生物群落分析.

1.1 普通工艺的微生物组成

AGS最常用的工艺为SBR工艺, 即GSBR工艺^[11], 也有采用气提式序批反应器(sequencing batch

airlift reactor, SBAR)^[12]或类似AUSB的连续流的反应器^[13]. 培养AGS的接种污泥一般来源于污水厂, 其微生物种群大多数分布在变形菌门(Proteobacteria (β -变形菌纲(β -Proteobacteria)、 α -变形菌纲(α -Proteobacteria)), 厚壁菌门(Firmicutes), 拟杆菌门(Bacteroidetes)和放线菌门(Actinobacteria)4个门^[14]. 表1展示了AGS微生物组成的代表性研究成果^[15~24]. 通过对比发现, 尽管 β -Proteobacteria的主导地位没有发生改变, 其他门的微生物跟生活污水厂中污泥微生物组成类似, 但是 γ -Proteobacteria, Flavobacteria, Sphingobacteriia等的微生物在颗粒污泥中所占的比重不容忽视.

Weissbrodt等人^[25]借助基于T-RFLP生物信息学的方法PyroTRF-ID (pyrosequencing-based T-RF identification)对AGS的微生物组成做了大量的研究, 并根据主要微生物的种群的不同将AGS微生物组成分为3大类: (1) *Accumulibacter* (典型的聚磷菌(phosphorus accumulating organisms, PAO), β -Proteobacteria),

表1 AGS微生物组成一览表
Table 1 Literature lists of microbial component of AGS

工艺及废水种类 (特殊物质)	分析手段	主要微生物	
		门、纲、目	科、属、种
SBR人工配水 ^[15]	克隆文库	β -Proteobacteria, Sphingobacteria (鞘脂杆菌门) Candidate division TM7, Flavobacteria γ -Proteobacteria	<i>Acidovorax</i> (食酸菌属), <i>Pseudomonas</i> (假单胞菌属), <i>Micropruina glycogenica</i> , <i>Comamonadaceae</i> (丛毛单胞菌科)
SBR人工配水 (甲基叔丁基醚) ^[16]	DGGE	Flavobacteria, α -Proteobacteria, γ -Proteobacteria, 放线菌门(Actinobacteria)	<i>Flavobacterium</i> , <i>Methylobacterium</i> (甲基杆菌属), <i>Pseudoalteromonas</i> (假交替单胞菌属)
SBR人工配水 (2-氟苯酚) ^[17]	DGGE	γ -proteobacteria, β -Proteobacteria, α -Proteobacteria, Actinobacteria, <i>Rhizobiales</i> (根瘤菌目), Nitrospirae (硝化螺旋菌目)	<i>Pseudoxanthomonas</i> , <i>Xanthomonas</i> (黄单胞菌属), <i>Acidovorax</i> , <i>Nitrospira</i>
SABR人工配水 (四氯苯胺) ^[18]	DGGE	β -Proteobacteria, Flavobacteriales (黄杆菌目), Planctomycetales (浮霉菌目), Clostridiales (梭菌目), Acidobacteria (酸杆菌目)	<i>Thauera</i> (陶厄氏菌属), <i>Xanthomonas</i> , <i>Acidobacterium</i>
SBR生活污水 ^[19]	DGGE	β -Proteobacteria, Bacteroidetes (拟杆菌门)	<i>Nitrosomonas</i> , <i>Candidatus Accumulibacter Phosphatis</i> , <i>Thauera</i>
SBR人工配水 (高盐) ^[20]	DGGE	β -Proteobacteria, Actinobacteria	<i>Hydrogenophaga</i> (氢嗜胞菌属), <i>Corynebacterium</i> , <i>Actinobacterium</i> (放线菌属), <i>Streptomyces</i> (链霉菌属)
SBR人工配水 ^[21]	高通量测序	γ -Proteobacteria, α -Proteobacteria, Sphingobacteriia, β -Proteobacteria, Bacilli (芽孢杆菌纲)	<i>Xanthomonadales_norank</i> , Saprospiraceae (腐螺旋菌科)
SBR畜产污水 ^[22]	高通量测序	γ -proteobacteria, β -Proteobacteria, Sphingobacteriia, Actinobacteria, α -proteobacteria	Xanthomonadaceae (黄单胞菌科), Comamonadaceae, rhodocyclaceae (红环菌科), Sphingomonadaceae
AS生活污水 (双酚A) ^[23]	高通量测序	β -Proteobacteria, Sphingomonadales (鞘脂单胞菌目), Sphingobacteriales (鞘脂杆菌目), Burkholderiales (伯克氏菌目), Nitrosomonadales (亚硝化单胞菌目), Methylophilales, Methylococcales	<i>Thauera</i> sp., <i>Azoarcus</i> sp., <i>Aquimonas</i> (水细胞菌属) sp., <i>Sphingomonas</i> (鞘氨醇单胞菌属) sp.
SBR人工配水 (吡啶) ^[24]	高通量测序	Proteobacteria (变形菌门), Bacteroidetes (拟杆菌门)	<i>Paracoccus</i> (副球菌属), <i>Comamonas</i> (丛毛单胞菌属)

*Nitrosomonas*和*Nitrospira*为主体(有机底物浓度充足); (2) *Competibacter* (典型的聚糖菌(glycogen accumulating organisms, GAO), γ -Proteobacteria), *Sphingobacteriales*, 噬细胞菌属(*Cytophaga*)和间孢囊菌科(*Intrasporangiaceae*)为主体(有机底物浓度相对不足); (3) 黄单胞菌科Xanthomonadaceae (γ -Proteobacteria)为主体(溶解氧(dissolved oxygen, DO)较高, 饱和浓度). 对于(1) *Accumulibacter*和(2) *Competibacter*而言, COD/P=20有利于*Accumulibacter*的生长(化学需氧量, chemical oxygen demand, COD), COD/P=200有利于*Competibacter*的竞争生长^[26]. 高有机负荷培养的AGS微生物主体一般主要属于 β -Proteobacteria^[27]. 另外, pH>7.3, $T<20^{\circ}\text{C}$ 和固定延时曝气2 h (饱和氧浓度)有利于PAO (*Accumulibacter*)的生长富集, 从而使得GAO (*Competibacter*)的生长得到抑制^[28]. Winkler等人^[29]报道*Nitrosomonas*是絮状污泥中氨氧化菌(ammonia oxidizing bacteria, AOB)的主要组成, 但是(1)类AGS中*Nitrosomonas*和亚硝化螺菌属(*Nitrospira*)数量相当. 相对于减少沉淀时间进行微生物选择作用而形成的

AGS, 污泥床的均匀清洗更有利于*Accumulibacter*在AGS中的富集和磷酸盐的去除^[30]. 对于第(3)类AGS中的主要微生物Xanthomonadaceae属于反硝化菌群(图1)且能产生胞外多糖^[25]. He等人^[21]报道人工配水培养的AGS样本中的Xanthomonadales_norank生物量高达45.85%; Liu等人^[22]报道的畜产污水培养的AGS的Xanthomonadaceae含量超过40%. 由于Weissbrodt等人^[25]仅考虑有机底物浓度($1.5\sim 2.9\text{ kg COD m}^{-3}\text{ d}^{-1}$)和DO浓度($>5.5\text{ mg L}^{-1}$)两个因素根据微生物组成对AGS进行的分类, 因此由于各种因子的变化, 也有报道的AGS并不属于这3类中的某一类. Lv课题组^[31]报道的AGS从微生物组成上判断属于(2)和(3)类AGS之间. Pronk等人^[32]报道当固体停留时间(solid retention time, SRT)由51 d减少至24 d, AGS中的GAO由 γ -Proteobacteria (Xanthomonadales)转为 α -Proteobacteria (*Dechloromonas*), 其微生物组成类似于但不同于第(3)类AGS. Yadav等人^[33]报道了DO=1, 2, 4 mg L^{-1} 条件下AGS的微生物组成情况, 发现DO升高会使得 α -Proteobacteria数量减少而 β -Proteobacteria数量增

图1 厌氧-好氧SBR工艺AGS中微生物的碳氮磷代谢过程示意图^[25]

Figure 1 Diagram on C, N and P microbial metabolisms of AGS from anaerobic-aerobic SBRs^[25]

多; DO=2 mg L⁻¹时, AGS中微生物群落最丰富, 主要包含 Desulfuromonadales, 虫原体目 (Entomoplasma tales), 巴斯德菌目 (Pasteurellales), 栖热菌目 (Thermales)和绿弯菌目 (Chloroflexales).

富集 PAOs 的污泥微生物组成包括 β -proteobacteria, *Cytophagia*和绿弯菌门 (Chloroflexi), 而富集 GAOs 的污泥微生物组成包括 γ -Proteobacteria, α -Proteobacteria, 酸杆菌门 (Acidobacteria)和鞘脂杆菌门 (Sphingobacteria)^[34]. 图1展示了AGS中常见微生物在碳氮磷的代谢过程中的作用. 由于 *Accumulibacter*, *Nitrosomonas*和*Nitrospira*为主体的AGS是当前被证实的最重要具有脱氮除磷功能^[35]的微生物门类. 因此, 在AGS的驯化和研究中要控制DO等因素使得其主要微生物为*Accumulibacter*, *Nitrosomonas*和*Nitrospira*的AGS. 另外, 以 *Xanthomonadales* 和 *Tetrasphaera*为主要微生物的AGS也能高效同时去除碳氮磷, 需要进一步研究.

1.2 不利条件下AGS的微生物组成

特殊的有机污染物(化工合成中间产物、农药、染料等)有一定的毒性, 对AGS微生物的组成也有影响, 一般通过污泥驯化或者生物强化等手段能够使得某种(属)的微生物能够降解这种有机物. 表2展示了在代表性有机污染物条件下, AGS中能够降解该种有机物的特定种(属)的微生物. Jiang等人^[36]证实苯酚降解的AGS以 β -Proteobacteria 和高鸟嘌呤和胞嘧啶 (guanine and cytosine, GC)含量的G⁺细菌为主, 而 *Pandoraea* sp. strain PG-01在苯酚降解中起到重要作用. Adav等人^[37]从AGS中分离的不动杆菌属 (*Acinetobacter*)的菌株能实现初始浓度1500 mg L⁻¹苯酚的高效降解(19.7 mg L⁻¹ h⁻¹), FISH-CLSM证实该菌株主要分布在小体积颗粒污泥的中心部分. Franca

等人^[38]利用 FISH 的手段研究表明, GSBP 中 *Deffluicoccus*属的细菌生长有利于偶氮染料(酸性红14)的降解. 在采用AGS处理特定有机物废水的处理中, 其特征微生物可以参考表2^[39-42].

极端环境(高盐、高碱和高温等)、重金属和纳米材料等对AGS的微生物组成也有不同程度的影响. 高盐环境对AGS中亚硝酸盐氧化菌有较强抑制作用^[43]. 林兵^[20]借助PCR-DGGE的手段对高盐胁迫下的AGS微生物种群进行研究, 发现要的优势种群为 *Hydrogenophaga*, *Corynebacterium*, β -Proteobacterium, *Actinobacterium*, *Streptomyces*, *Anaerobic bacterium*, *Psychrobacter*和芽孢杆菌属(*Bacillus*)等. 盐胁迫下AGS微生物体内Na⁺含量呈下降趋势, 而K⁺和Ca²⁺含量呈上升趋势^[20]. *Lactococcus* sp. YM05004, *Desulfopila* sp. PR5_F09和*Demequina oxidasica*等菌株可以在8%的盐度条件下培养的AGS中生长^[44]. pH越低, AGS中真菌(丝状菌)的数量越大(图2), 所需要的培养周期较短; pH越高, AGS中细菌的数量越大, 所需培养周期较长^[45,46], 但具体的微生物种属未见报道. Ebrahimi等人^[47]应用T-RFLP的手段研究了20, 30, 35℃条件下AGS的微生物组成, 发现各个温度下的微生物种群有差异, 而Sphingomonadaceae对维持AGS的结构稳定有重要作用. Zitomer等人^[48]从55℃耐热AGS中筛选出*Anoxybacillus flavothermus*和*Pseudoxanthomonas taiwanensis*两株菌. 10 mg L⁻¹以上Zn²⁺会对AGS脱氮反应速率和微生物活性产生明显抑制作用^[49]. Cu²⁺会导致AGS变得松散, 丝状菌数量增多, 当Cu²⁺浓度达到10 mg L⁻¹时AGS解体^[48]. 当Cr⁶⁺浓度超过0.5 mg L⁻¹时, 便可导致AGS系统中丝状菌过量生长, PAOs被GAOs取代, 且过程不可逆^[50]. 在Cu²⁺, Cd²⁺和Cr⁶⁺离子的胁迫下, AGS中多数菌归属于Actinobacteridae纲. 1~50 mg L⁻¹理论浓度的

表2 典型有机污染物条件下AGS中的特征微生物
Table 2 Representative microbes in AGS under conditions of typical organic pollutants

污染物	特征微生物	污染物	特征微生物
叔丁醇 ^[39]	<i>Rubrivivax gelatinosus</i>	双酚A ^[23]	<i>Sphingomonas</i> (鞘氨醇单胞菌属)
甲基叔丁基醚 ^[16,40]	<i>Methylobacterium</i> (甲基杆菌属)	吡啶 ^[24,42]	<i>Acinetobacter</i> (不动杆菌属)和 <i>Rhizobium</i> (根瘤菌属)
苯酚 ^[36,37]	<i>Pandoraea</i> 和 <i>Acinetobacter</i>	酸性红14 ^[38]	<i>Deffluicoccus</i>
2-氟苯酚 ^[17]	<i>Pimelobacter</i> 和 <i>Rhodococcus</i> (红球菌属)	四氯苯胺 ^[18]	<i>Thauera</i> (陶厄氏菌属)
五氯苯酚 ^[41]	<i>Desulfobulbus</i> (脱硫叶菌属)

图2 (网络版彩色)不同pH条件培养的颗粒污泥^[45]. (a) pH 3; (b) pH 8 (比例尺为 10 mm)

Figure 2 (Color online) AGS obtained at varied pH values^[45]. (a) pH 3; (b) pH 8 (scale bar 10 mm)

Pb²⁺对于AGS系统微生物多样性无明显影响,但相对于Bacteroidetes门微生物,β-Proteobacteria纲微生物对铅离子耐受性更强^[51].关于纳米材料对颗粒污泥的微生物的影响鲜有报道^[51].由上可知,极端环境(高盐、高碱和高温等)、重金属和纳米材料等对AGS的微生物组成研究均不足,尤其是对具体的种属微生物的数量和表达活性的影响亟待进一步的研究.

1.3 新工艺AGS的微生物组成

关于好氧条件下培养的颗粒污泥的新工艺主要包含短程硝化颗粒污泥(亚硝化颗粒污泥)和反硝化除磷颗粒污泥.短程硝化颗粒污泥(亚硝化颗粒污泥)是厌氧氨氧化的前提条件,其工艺运行被广泛关注,Isanta等人^[52]证实其驯化过程中亚硝酸盐氧化菌(nitrite oxidizing bacteria, NOB) (*Nitrobacter*)数量的减少,与絮状污泥不同的是,颗粒污泥中NOB主要的组成通常是*Nitrobacter*,而不是*Nitrospira*^[53].关于AOB具体微生物组成未见报道^[52,54].尽管反硝化除磷工艺运行被报道^[55],但是对关键性DNPAOs未作

进一步的研究.反硝化除磷可以是*Competibacter*和*Accumulibacter*共同作用的效果^[56],也可以是*Xanthomonadales*和*Tetrasphaera*协同作用的效果^[21].

2 微生物分布

Lemaire等人^[56]报道的AGS的核心部分主要为负责反硝化脱氮的聚糖菌*Competibacter*而外面包裹为聚磷菌*Accumulibacter*.Lv等人^[31]报道的AGS的核心部分为红环菌科(Rhodocyclaceae),外层包裹的部分的微生物组成为黄杆菌科(Flavobacteriaceae), Xanthomonadaceae, Rhodobacteraceae和微杆菌科(Microbacteriaceae).Winkler等人^[57]在研究SRT对AGS的影响的时候,给出了典型AGS的微生物组成示意图(图3).

丝状菌作为AGS的骨架,在AGS的自凝聚和形态保持方面起到重要作用,一般来说, pH过低, DO不足或有机负荷过高会导致AGS中丝状菌的过量生长(图4),从而导致AGS沉降性能下降,关于AGS中丝状菌的微生物组成研究较少. Figueroa等人^[58]从AGS中分离出4株丝状菌,即*Chloroflexi*, 浮游球衣菌(*Sphaerotilus natans*), 发硫菌属(*Thiothrix*)和*Meganema perideroedes*.另外,钟虫属(*Vorticella*)和独缩虫属(*Carchesium*)的带柄原生动物可附着在AGS表面,可作为实际生活污水处理工艺中健康的微生物生态系统的迹象^[6].

3 微生物演替

Zhang等人^[59]利用DGGE研究AGS的形成过程,结果表明, *Rhodocyclus*, Hyphomicrobiaceae等杆状菌和丝状菌先构成AGS的骨架,随后成熟的AGS有球状菌生长, *Accumulibacter*, *Nitrosospira*和*Thauera*是主要脱氮除磷的功能菌.具体而言, *Accumulibacter*始

图3 (网络版彩色)典型AGS微生物分布示意图^[57]. (a) SRT减少AGS解体时外层nitrifiers减少; (b) SRT不变AGS解体时各种细菌均有减少

Figure 3 (Color online) Microbial distribution diagram of typical AGS^[57]. (a) Breakage of mainly the outer layers hence decreasing the SRT of nitrifiers; (b) an equal wash-out of bacteria during granule breakage with the same SRT

图4 (网络版彩色)丝状菌FISH图^[58]. 所用探针依次为(a) Euk516和Eub338mix; (b) Alf1b; (c), (d) MEGmix和Eub338mix. 比例尺为(a), (b) 25 μm ; (c) 10 μm ; (d) 100 μm

Figure 4 (Color online) FISH images of filamentous organisms^[58]. The probes are (a) Euk516 and Eub338mix; (b) Alf1b; (c), (d) Probe MEGmix and Eub338mix. The scale bar indicates 25 μm in (a) and (b), 10 μm in (c) and 100 μm in (d)

终保持较为稳定的优势地位,以*Candidatus Nitrospira defluvii*和*Thauera*为代表的种群逐渐得到强化,而拟杆菌纲在前期占有优势地位,在后期逐渐消亡^[60].也有研究声称*Brachymonas*, *Zoogloea*和*Thauera*为AGS结构,因为这些菌株能够产生大量胞外聚合物(extracellular polymeric substances, EPS)^[61]. Lv等人^[31]保持 $\text{DO}=7.5 \text{ mg L}^{-1}$, pH 7, 利用高通量测序的手段研究了以絮状污泥为接种污泥利用人工配水培养出来的AGS的微生物演替过程:在科的水平上,Flavobacteriaceae, Xanthomonadaceae, Rhodobacteraceae, Microbacteriaceae迅速增长,随后Rhodobacteraceae, Microbacteriaceae, Xanthomonadaceae和Microbacteriaceae依次增长,接着Rhodobacteraceae再次增长,Flavobacteriaceae和噬纤维菌科(Cytophagaceae)数量增多. *Zoogloea*在絮状污泥颗粒化的

过程中可起到关键性的作用,但在AGS成熟之后数量迅速减少^[62]. Aqeel等人^[63]研究了AGS从膨胀到恢复的过程中微生物的变化:詹森菌属(*Janthinobacterium*)和*Auxenochlorella*的过量生长可以导致丝状菌膨胀,而*Chitinophaga*可以抑制*Auxenochlorella*的生长从而促使污泥颗粒物, *Rhodanobacter*是AGS的关键性微生物. 关于AGS微生物的演替方面的研究报道不足.

4 结论和展望

本文基于最新研究报道对好氧颗粒污泥AGS的微生物组成、分布和演替做了系统的论述,主要得到如下结论: (1) AGS与絮状污泥的微生物组成存在差异, γ -Proteobacteria, Flavobacteria, Sphingobacteriia等的微生物在AGS中所占的比重不容忽视; (2) 以*Accumulibacter*, *Nitrosomonas*和*Nitrospira*为主要微生物的AGS能够高效脱氮除磷; (3) 反硝化除磷AGS可以是*Competibacter*和*Accumulibacter*共同作用的效果,也可以是*Xanthomonadales*和*Tetrasphaera*共同作用的效果; (4) pH过低, DO不足或有机负荷过高会导致AGS中*Chloroflexi*, *Sphaerotilus*, *Thiothrix*等丝状菌的过量生长; (5) *Rhodocyclus*, Hyphomicrobiaceae等非球状菌和产EPS的*Zoogloea*在AGS形成过程中可起到关键性的作用.

今后的研究方向如下: (1) 进一步利用现代分子生态学手段研究各种环境因子作用下各类AGS微生物群落的组成; (2) 研究以*Accumulibacter*, *Nitrosomonas*和*Nitrospira*为主要微生物的AGS的演替过程; (3) 研究极端环境、重金属和纳米材料等条件下AGS的群体行为调控机制即群体感应; (4) 研究丝状菌在AGS中的组成和演替; (5) 系统建立微生物组成、环境因子及污染物去除效能三者之间的关系.

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Summary for “好氧颗粒污泥的微生物研究进展”

Research progress on microbes in aerobic granular sludge

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Aerobic granular sludge (AGS) is a mobile biofilm which is formed by varied microbial populations by self-coherence under certain selective pressure. Aerobic granular sludge technology has merits such as high sludge concentration, little residual sludge, fast settling velocity, strong shock resistance, small area requirement, low cost, low energy consumption, simultaneous nitrogen and phosphorus removal, which has become a research hotspot in wastewater treatment. There have been a lot of research and discussion on the characteristics, influencing factors, application and formation mechanisms of AGS. It is beneficial to the formation of AGS by reducing the settling time, increasing the hydraulic shear force and the concentration of dissolved oxygen, and using low load alternating operation, adding calcium and magnesium salt. As a result, it is not conducive to the growth of some kinds of microorganisms, but favors the aggregation of the filamentous bacteria and other bacteria to form a symbiotic system, namely, granular sludge. This article discusses the three aspects of composition, distribution and succession of microbial communities from the microbial perspective of aerobic granular sludge, and the future research directions are prospected, which provides references for further research of aerobic granular sludge. Generally speaking, qPCR, FISH and T-RFLP are used for the analysis of a few kinds of microorganisms, and the PCR based cloning library, DGGE and high-throughput sequencing methods are used to analyze the complex microbial communities in the system. Metagenomics and metatranscriptomics analyses are the latest methods on microbial ecology. Extreme environment, heavy metal and nano materials have different effects on the microbial composition of AGS. As the framework of AGS, filamentous bacteria plays an important role on the AGS self-aggregation and morphology. A low value of pH or DO, insufficient or high organic loading will lead to excessive growth of filamentous bacteria in AGS, resulting in AGS deposition performance degradation, microbial AGS on filamentous bacteria composition research. The main conclusions are as follows: (1) microbial compositions of aerobic granular sludge differs from activated sludge, microorganisms as γ -Proteobacteria, *Flavobacteriia*, *Sphingobacteriia* are remarkable in aerobic granular sludge; (2) study on efficient bacteria in nitrogen and phosphorus removal mainly including *Accumulibacter*, *Nitrosomonas* and *Nitrospira*; (3) denitrifying phosphorus removal for aerobic granular sludge is the results of interaction of *Competibacter* and *Accumulibacter*, as well as *Xanthomonadales* and *Tetrasphaera*; (4) low pH, low DO and high organic load will lead to excessive growth of filamentous bacteria such as *Chloroflexi*, *Sphaerotilus* and *Thiothrix* in aerobic granular sludge; (5) *Rhodocyclus*, *Hyphomicrobiaceae* and other non-spherical bacteria and *Zoogloea* with EPS production can play key role in the formation of aerobic granular sludge. The directions of future research as follows should be researched: (1) impacts of various environmental factors on microbial communities components of AGS by using modern molecular ecology such as metagenomics and metatranscriptomics analyses; (2) research on microbial population dynamics of AGS when *Accumulibacter*, *Nitrosomonas* and *Nitrospira* as the main succession of microbial AGS; (3) quorum sensing mechanism of AGS under extreme environment, heavy metal and nano materials; (4) study on the composition and succession of filamentous bacteria in AGS; (5) the relationship among systematic microbial composition, environmental factors and pollutants removal efficiency.

aerobic granular sludge, microbial component, microbial distribution, microbial dynamics, γ -Proteobacteria

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