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次 目

生物滴滤池对 BTEX 的去除及相应细菌群落分析

李建军1,2,3,4、廖东奇1,2,3,4、许玫英1,2,3,4、孙国萍1,2,3,4

(1.广东省微生物研究所,广州 510070; 2.广东省菌种保藏与应用重点实验室,广州 510070; 3. 广东省微生物应用新技术 公共实验室,广州 510070; 4. 广东省华南应用微生物重点实验室-省部共建国家重点实验室培育基地,广州 510070) 摘要:以预先驯化的菌群和活性污泥作为起始接种物用于生物滴滤池(BTF)中,研究评估了BTF去除苯、甲苯、乙苯和二甲 苯混合气体(BTEX)的性能,并利用变性梯度凝胶电泳(DGGE)技术分析了微生物群落结构的变化. 结果表明,BTF 能在短时 间内得到驯化,填料附着的生物量从第 10 d 的 5.7 mg·g⁻¹迅速增加至第 30 d 的 112 mg·g⁻¹. BTF 能同时有效去除混合 BTEX 中的各组分,在进气负荷和停留时间分别为 269.7 $g \cdot (m^3 \cdot h)^{-1}$ 和 39 s 时,可获得的最大去除能力为 216.6 $g \cdot (m^3 \cdot h)^{-1}$. DGGE 图谱表明,BTF 中优势微生物种群主要来源于富集菌群,微生物群落结构随着运行时间发生变化,但在 BTF 上下空间分

关键词:生物滴滤池; BTEX; DGGE; 群落结构; 菌群

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Removal of BTEX by a Biotrickling Filter and Analysis of Corresponding **Bacterial Communities**

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Abstract: The pre-acclimated microbial consortium and the activated sludge were used as start inoculums of a bench-scale biotrickling filter (BTF). The performance of the biotrickling filter on the removal of BTEX mixture was evaluated, and the changes in the bacterial community structure of the BTF were analyzed by PCR-DGGE technique. The results showed that the BTF could be acclimated within a short time, the biomass that adhered to the surface of packing materials increased rapidly from 5.7 mg·g⁻¹ at 10th day to 112 mg·g⁻¹ at 30th day. BTF could simultaneously remove all components of the BTEX mixture efficiently. The maximum removal capacity of the BTF was 216.6 g·(m³·h)⁻¹, which was achieved with an inlet loading rate of 269.7 g·(m³·h)⁻¹ and an empty bed retention time (EBRT) of 39 s. DGGE analysis indicated that the dominant microorganisms may be derived from the pre-acclimated microbial consortiums rather than the activated sludge. Although the bacterial community changed with run time, the spatial distribution was very

Key words: biotrickling filter (BTF); BTEX; DGGE; community structure; microbial consortium

苯、甲苯、乙苯和二甲苯合称为 BTEX,是一类 工业废气中常见的有机污染物,对人体健康和生态 环境具有危害作用. 生物过滤是一种高效率、低成 本、容易管理和环境友好的处理方法. 在生物过滤 反应器中接种活性污泥是一种常见的选择[1]. 污泥 中含有丰富多样的微生物,能降解广泛的微生物. 尽管有学者认为活性污泥足以用来启动生物反应 器,无需用特定的富集微生物[2]. 但对于难降解物 质,已证明利用相应的降解菌种能有效提高去除能 力,缩短微生物的驯化时间,提高生物过滤设备的去 除性能和稳定性[3~7].

生物过滤方法已经广泛应用于各种废气污染物 的去除,但有关系统中微生物群落结构的研究很少, 仅有少数生物过滤过程中的微生物群落结构得到了 研究[8~10]. 微生物在生物过滤过程中扮演着关键的 角色,研究证实利用筛选的降解菌种能提高污染去 除负荷,但有关降解菌种能否在与土著微生物的竞 争中发育为优势种群的研究有限. 因此,有必要通 过微生物群落结构的研究,分析降解菌种在生物过 滤过程中的变化规律,为工程应用提供参考.

本实验中,生物滴滤池同时接种降解菌群和活性 污泥,经短期驯化后逐步增加进气负荷. 本研究的首

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要目的是考察混合 BTEX 进气负荷对生物滴滤池去除效能的影响,分析生物滴滤池能否有效地同时去除 BTEX;其次利用 PCR-DGGE 技术分析了生物滴滤池运行过程中的细菌群落结构的变化,重点考察降解菌群能否在生物滴滤池中成长为优势微生物.

1 材料与方法

1.1 生物滴滤池及运行条件

生物滴滤池(BTF)呈圆柱形,内径8 cm,高度80 cm. 柱体由三部分构成,顶部为液体喷淋区域,底部为液体存储池,中间两段为填料柱,用多孔板隔开. 所用填料为聚氨酯泡沫(PU),立方体,边长为1 cm. 填料高度为40 cm,有效填料体积为2 L. 填料

的孔隙率、堆积密度和持水力分别为:96.0%、17 kg·m⁻³和 -1.64%·h⁻¹. 生物滴滤池运行模式为上流式,环境温度在 20~37℃之间. 废气由苯、甲苯、乙苯和二甲苯这 4 种物质人工合成,4 种苯系物的液体预先按照一定比例均匀混合,用微量注射泵注入风管,由空气吹脱. 空气由空压机产生,污染物浓度通过调节气体流速和微量注射泵的注射速率实现.

实验分4个阶段(表1). 第一阶段为驯化阶段,生物滴滤池连续运行,此后以每周运行5d,每天运行8h的间歇性模式运行. 每个阶段均持续至生物滴滤池达到拟稳定状态,即连续监测约3次的去除率波动范围小于5%.

表 1 实验程序

Table 1 Schedule of the experiment

运行参数	运行阶段						
运 们	I (1 ~7 d)	II (8~42 d)	Ⅲ (43 ~84 d)	IV (85 ~114 d)			
苯进气浓度/g·m ⁻³	0.09 ~ 0.11	0. 21 ~ 0. 33	0. 32 ~ 0. 68	0. 24 ~ 0. 49			
甲苯进气浓度/g·m ⁻³	0. 13 ~ 0. 17	0. 30 ~ 0. 46	0. 39 ~ 0. 74	0. 39 ~ 0. 72			
乙苯进气浓度/g·m ⁻³	0. 23 ~ 0. 29	0. 45 ~ 0. 57	0. 35 ~ 0. 74	0.66 ~ 0.96			
二甲苯进气浓度/g·m ⁻³	0. 17 ~ 0. 22	0. 24 ~ 0. 37	0. 35 ~ 0. 71	0. 48 ~ 0. 72			
停留时间 EBRT/s	72	72	54	39			
总进气负荷/g•(m³•h) ⁻¹	32 ~ 39. 6	66. 1 ~ 94. 2	120 ~ 212. 8	160. 9 ~ 269. 9			
运行模式	连续	间歇	间歇	间歇			

1.2 微生物与培养基

BTF 接种所用菌群的驯化过程简述如下,两份 1 g 石油污染的土壤分别加入到两份 100 mL 灭菌的 M9 无机盐培养基中,分别置于1 L 的干燥器中,加 人 50 μL 的甲苯和二甲苯溶液,密封后于 30℃培 养,10 d 后转接一次至新鲜培养基中,传代20次后 分别获得以甲苯和二甲苯为唯一碳源生长的菌群. BTF 启动前,两份新鲜培养菌群等量混合,离心浓缩 细胞至湿重 2.0 g·L-1. 活性污泥为市政污水厂一 沉池新鲜污泥,污泥浓度(MLSS)调整为 $2.0 \text{ g} \cdot \text{L}^{-1}$. 菌群和污泥接种量各为 200 mL,加入 1.6 L 的无机 盐培养基,从顶部均匀倒入填料柱.渗滤液用蠕动 泵重新滴酒回填料柱,循环6h后,通入人工合成的 含 BTEX 的废气开始驯化. 无机盐培养基每升含 有: KNO₃ 2 g, Na₂HPO₄·12 H₂O 0.6 g, NaH₂PO₄ 0.05 g, FeSO₄·7H₂O 50 mg, MgSO₄·7H₂O 120 mg, CaCl,·2H,O 10 mg. 培养基浓度根据进气负荷及时 调整,每3d更换一次,排液中污泥量(MLSS)为 0.15 g·L⁻¹ ±0.02 g·L⁻¹,始终维持培养基 C: N: P 比例为100:20:1. 培养基储存于柱子底部的液体存 储池,用蠕动泵以 $0.12 \text{ m}^3 \cdot (\text{m}^2 \cdot \text{h})^{-1}$ 的速率回流至

填料柱顶部,液体通过设置在填料上部的多孔板后均匀滴洒至填料表面.

1.3 分析方法

BTEX 检测:生物滴滤池的进气和出气样品用 1 L 的 Tedlar 采样袋在固定时刻同时采集,每周采样约 3 次. 采样均在生物滴滤池启动后 2 h 时进行,8 h 内的进口浓度波动幅度调节至 5% 以内. 样品用气密性针取 100 μ L 由气相色谱仪(GC-2010Plus, SHIMADZU)分析. 色谱仪具 FID 检测器,色谱柱为HP1NNOWAX 型毛细管柱(30 m × 0.25 mm × 0.32 μ m). 柱温采用程序升温,初始温度为 35 $^{\circ}$,保持 3 min 后,以 11° · min $^{-1}$ 的速率升温至 200° ,保持 3 min,以 20° · min $^{-1}$ 的速率再升温至 250° ,保持 1 min. 气化室温度和检测器温度分别维持在 200° 和 250° 。以氮气为载气,流速为 1.51 mL·min $^{-1}$ 。氢气流速:40.0 mL·min $^{-1}$,空气流速:400.0 mL·min $^{-1}$,是吹气流速:30 mL·min $^{-1}$.柱前压:100 kPa.

填料压降用 U 型管连接填料床上下部空间 测量.

生物量用重量法测量:定期采集的填料,用无菌

水冲洗并涡旋至少30 min,含生物膜液体用0.2 μm 的滤纸过滤,105℃烘干4h后称重,减去滤纸本身 的重量即为生物量,以每克干填料所含生物量表示.

1.4 细菌群落结构分析

填料采样孔距离底部 10 cm 和 30 cm 处,采样 日期分别为第30、60和90d,填料样品储存于 -30℃冰箱,于实验结束后一起抽提总 DNA. 12 块 聚氨酯泡沫填料与 20 mL 的磷酸缓冲液混合(137 mmol·L⁻¹ NaCl; 2. 7 mmol·L⁻¹ KCl; 4. 3 mmol·L⁻¹ Na₂HPO₄; 1.4 mmol·L⁻¹ KH₂PO₄; pH 7.3), 涡旋 30 min. 总 DNA 用氯仿-苯酚法抽提. 以总 DNA 为 模板,以 V3 区引物 341f(5'-CGC CCG CCG CGC CCC GCG CCC GGC CCG CCG CCC CCC TAC GGG AGG CAG CAG-3')和518r(5'-ATT ACC GCG GCT GCT GG-3') 扩增细菌 16S rDNA 基因片 段. PCR 反应体积为 50 μL, 含 1.5 mmol·L⁻¹ MgCl₂, 0.2 mmol·L⁻¹ dNTP,1 μmol·L⁻¹ 的引物和 2.5 U的 DNA 酶, PCR 扩增用 Mastercycler gradient thermocycler(Eppendorp, Tiangen,北京). 反应条件 为94℃ 5 min,随后94℃ 40 s, 55℃ 40 s, 72℃ 30 s,30 个循环,最后 72℃延伸 10 min. PCR 产物用 0.5 μg·mL⁻¹ 的 Gold View (Applygen Technologies Inc.,北京)染色后用1.0%(质量分数)的琼脂糖凝 胶电泳和观察.

DGGE 分析用 D-code 通用突变检测系统 (Bio-Rad Laboratories Inc., USA), PCR 产物上样于 10% (质量分数)的聚丙烯酰胺凝胶(丙烯酰胺和双丙烯 酰胺比例为 37.5:1),线性变性剂梯度为 40%~ 70% (100%的变性剂定义为7 mol·L-1尿素加 40% 的甲醛). DGGE 缓冲溶液为 1 倍的 TAE (40 mmol·L⁻¹ Tris, 20 mmol·L⁻¹ 乙酸, 1 mmol·L⁻¹ EDTA pH 7.4),上样 50 μL 的 PCR 产物. DGGE 条 件为 20 V 预电泳 20 min, 再 60℃、80 V 电泳 12 h. 胶用 Goldview 染色后用 ImageQuant 350 (GE Healthcare, USA)观察并拍照,图谱用 Quantity one 4.4(Bio-Rad, USA) 软件分析. 用直径为 50 的滚环 扣除背景值,相对丰度用软件计算. 不同阶段 DGGE 图谱的相似性系统树状图根据 Dicecoefficient 按照非加权组算数平均法 (unweighted pair-group method with arithmetio means, UPGMA)绘 制,香农指数(shannon-weiner index, SDI)由下式 计算:

$$SDI = -\sum P_i \times ln P_i$$

式中,P,为 i条带的亮度/所有条带的总亮度.

2 结果与分析

2.1 BTF 对混合 BTEX 的去除性能

生物滴滤池运行 114 d,分为 4 个阶段,通过改变气体流量和 BTEX 浓度以获得相应的进气负荷. 从第二阶段开始,生物滴滤池间歇性运行以模拟实际工业废气的排放模式(即 8 h/d、5 d/周),晚上和周末停止 BTEX 供应,但不中断空气和培养液的供应.

图 1 显示了 BTF 在不同进气负荷状态下去除气体中 BTEX 的性能,前 7 d 是生物滴滤池驯化阶段. 气体中 BTEX 进气负荷维持在 39.6 g·(m³·h) -1以下,停留时间 72 s. 结果表明,BTF 所需要的驯化期很短,在 7 d 内,对 BTEX 各成分的去除率均接近 100%,但对不同成分的去除行为略有差异. 第 1 d,BTF 对苯、甲苯和乙苯的去除率即可达到 81.0%、94.1%和 94.7%,但对二甲苯的去除率仅为 73.6%.

第二阶段,气体停留时间不变,按比例增加各组分浓度,进气负荷介于66~94 g·(m³·h)-1之间.进气负荷增加后,BTF对BTEX的去除率随即出现明显的下降,对苯、甲苯、乙苯和二甲苯的去除率分别下降至89.1%、94.4%、91.2%和89.8%,随后逐步上升.第26 d可恢复至拟稳定状态,对苯、甲苯和乙苯的去除率接近99%.二甲苯的去除率恢复较慢,于第40 d恢复至95.9%.

第三阶段缩短停留时间至 54 s,同时增加进气浓度,总进气负荷在 120~213 g·(m³·h)⁻¹之间.与第二阶段类似,各组分的去除率先下降后上升.第 78 d 达到拟稳定状态,BTF 对苯、甲苯和乙苯的去除率约为 96%、96% 和 95%,而二甲苯的去除率约为 85%,在 82 d 时可达到 87.3%.

第四阶段,停留时间缩短为39 s,乙苯和二甲苯的负荷有较大幅度的增加,而苯和甲苯的负荷变化不大,总进气负荷从205 g·(m³·h)-1逐步增加至270 g·(m³·h)-1,再逐步降低至161 g·(m³·h)-1,接近第三阶段末期的进气负荷.进气负荷的增加同样引起各组分去除率的剧烈下降,乙苯和二甲苯的去除率分别从95.1%和87.3%下降至72.8%和62.9%.值得注意的是,虽然苯和甲苯的进气负荷并没有明显增加,但去除率同样从96%分别下降至62.2%和66.9%.这种下降可能意味着乙苯和二甲苯的负荷增加可能抑制了苯和甲苯的降解.不管怎

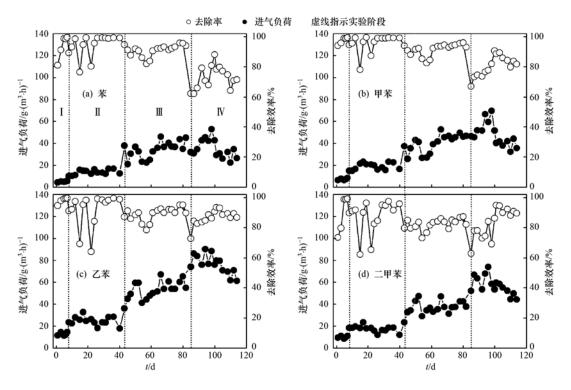


图 1 BTF 对混合 BTEX 各成分的去除效果

Fig. 1 Overall performance of the BTF in the removal of benzene, toluene, ethylbenzene and xylene

样,BTF 运行至 103 d 时,苯、甲苯、乙苯和二甲苯的去除率分别为 79.7%、89.3%、93.5%和94.5%.随后尽管进气负荷逐步降低,但各组分的去除率呈现下降,至113 d,分别下降至约70%、82%、88%和89%左右.此时的下降很可能与温度有关,环境温度从实验开始时的37℃下降至20℃左右,温度的下降影响了微生物活性和降解速率.

2.2 BTF 的去除负荷

BTF 对混合 BTEX 的最大去除能力如图 2 所示,去除能力与进气负荷在一定范围内几乎呈直线相关,当进气负荷超过 190 g·(m³·h)-1后,去除能力虽然仍在增加,但幅度降低.在整个实验过程中,BTF 所获得的最大去除能力为 216.6 g·(m³·h)-1[进气负荷和停留时间分别为 269.7 g·(m³·h)-1和 39 s],但去除率仅为 80%.而去除率为 95% 的去除能力为 176.6 g·(m³·h)-1[进气负荷和停留时间为188.5 g·(m³·h)-1和 54 s].对于混合气体中每一种组分而言,BTF 所获得的关键去除能力(即去除率为 95%)分别为 33.4、44.3、62.0 和 56.6 g·(m³·h)-1.总体而言,BTF 的去除能力随着进气负荷的增加而增加,但到一定程度后虽然去除能力仍然增加,去除率却出现下降,表明进气负荷的增加超过了相应生物量应有的降解能力.

2.3 生物滴滤池运行过程中的细菌群落结构变化

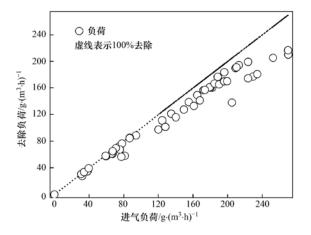


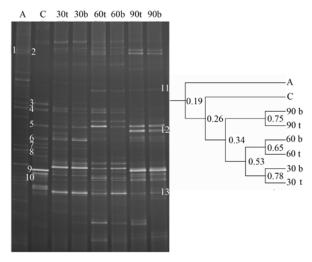
图 2 生物滴滤池去除能力与进气负荷的关系 Fig. 2 Variation in removal capacity of the BTF with

changes of inlet loading rates

为了解微生物在 BTEX 的生物过滤中的作用,利用 PCR-DGGE 技术分析了 BTF 中细菌群落结构 在不同运行阶段中的变化规律. 图 3 显示了起始接 种物以及 BTF 分别在 30、60 和 90 d 时的细菌群落 结构的 DGGE 指纹图谱,其中,第一(A)和第二(C) 泳道分别为活性污泥和降解菌群的细菌群落指纹图谱. 结果表明,细菌群落结构随着时间的迁移而发生了明显的变化. 在活性污泥中,只有条带 1、2 和 10 在 BTF 整个运行过程中出现,第 90 d 的下层填料中的丰度分别为 3.7%、5.6% 和 5.1%. 条带 4

则在第90 d 时消失,条带7和8仅出现在第30 d,但这3个条带也在菌群的图谱中出现.在菌群的图谱中,最为明显的是条带5和9,虽然在前期运行过程中亮度较弱,但在90 d 后显著增强,成为BTF中的优势细菌种群,第90 d在BTF下层填料中的丰度分别为10.8%和23.1%,远高于由污泥发育而来的种群丰度.由此可见,BTF的优势菌种主要来源于富集的菌群,尽管BTEX进气负荷的变化影响了BTF的微生物群落结构,但起始接种菌群的优势种群能够很好地在BTF中生长繁殖.因此,可以认为富集的菌群更有利于功能性微生物群落结构的形成.

分析生物多样性指数发现,活性污泥和菌群的香农指数分别为3.23和2.42(表2),与活性污泥的多样性指数相比,BTF中的多样性指数呈现逐步减低的趋势.这一结果表明,尽管活性污泥中含有丰富的微生物,但在BTF接受混合BTEX后,许多不能快速利用BTEX的微生物死亡.已有很多类似的报道,如Fu等用驯化20d的活性污泥接种沸石生物滤池,香农指数也随着时间而减低[11].另外,上



A:活性污泥 C:菌群;数字表示对应的采样日期; t和b表示柱子的上层和下层填料

图 3 BTF 不同运行阶段和位置的 DGGE 图谱和 UPGMA 树状图

Fig. 3 DGGE profile and UPGMA dendrogram of the biofilm samples from the top and bottom of the BTF

层填料的生物多样性指数均高于下层填料,原因在于 BTF 从底部进气,下层填料接受的更高浓度的混合 BTEX 对微生物有胁迫作用.

表 2 BTF 随时间变化的生物多样性指数

		Table 2 Di	io-diversities of the	DIF at different of	perating times			
A	С	30t	30b	60t	60b	90t	90b	-
3. 23	2. 42	2. 61	2. 58	3. 00	2. 68	2. 62	2. 58	-

3 讨论

一般来讲,常见工业废气中 BTEX 往往以多组 分而非单一组分的形式存在. 多组分废气污染物的 生物降解过程中经常可以观察到促进、抑制或毒性 作用等现象[12,13]. BTEX 具有相似的化学结构、代 谢酶系和代谢途径,因而在共同生物降解过程中以 竞争性抑制作用为主[14]. 如 Du Plessis 等[15]发现, 用甲苯驯化菌群接种的生物滤池中,甲苯竞争性抑 制了苯、乙苯、m-二甲苯和 o-二甲苯的去除,但却 增强了p-二甲苯的降解率,原因是p-二甲苯与其它 两种异构体降解过程中需要不同的酶系,p-二甲苯 的降解需要通过共代谢途径实现. 因此,为同时去 除 BTEX,选择合适的菌群是必要的,尤其对于二甲 苯而言,去除效果将会因相互抑制作用的存在而降 低. 本实验中,BTF 除了实验室预先驯化的菌群,另 外接种了活性污泥. 多样的微生物组合可以在一定 程度上减轻多组分废气中不同成分间的相互抑制作 用,因而获得了理想的混合 BTEX 的同时去除效果

和去除能力,至少在试验段前三阶段,没有发现明显 的相互抑制作用. 组分间的相互抑制作用程度不仅 取决于污染物种类,也与其浓度有关. 在第四阶段 起始时,虽然苯和甲苯的进气负荷没有明显增加,但 其去除率则因乙苯和二甲苯负荷的增加而降低. 经 过短暂的适应后,尽管进气负荷继续增加,但苯和甲 苯去除率逐步回升,显示抑制作用减弱. 原因可能 在于生物膜中预驯化菌群中的微生物种类占据了优 势,促进了生物降解速率. 在含有混合 BTEX 的工 业废气的生物过滤过程中,经常以活性污泥来接种 生物反应器,活性污泥中含有丰富的微生物. 而富 集菌群或纯化的菌种也是生物过滤反应器的一个重 要来源,利用驯化的微生物,不仅可以缩短驯化时 间,也能有效提高去除能力. Klapková 等[16]比较了 接种甲苯、二甲苯驯化的菌种和填料土著微生物对 堆肥生物滤池去除性能的影响,发现接种驯化菌种 的生物滤池的长期去除性能明显好于土著微生物.

BTF 能在短时间内(小于7d)完成驯化过程, 这种快速的驯化应归功于合适的接种物. 连续供应

含 BTEX 的混合气体后,预先经甲苯和二甲苯驯化的菌群无需适应即可在 BTF 中增殖并开始生物降解. 图 4显示了 BTF 实验期间上/下层填料生物量的变化,第 10 d 下层填料的生物量仅为 5.7 mg·g⁻¹,第 30 d 生物量显著增加至 112 mg·g⁻¹,生物量的迅速增加表明 BTF 所接种的微生物具有以BTEX 为碳源快速增殖的能力,也说明填料和运行条件适合微生物的生长. 而上下层填料的生物量差异较小,上层填料第 10 d 和 30 d 的生物量分别为3.1 mg·g⁻¹和 99.3 mg·g⁻¹,60 d 时,两部分生物量无显著差异,预示着微生物均匀分布在整个填料柱.

尽管生物量增加迅速,但填料床压降的增加并不明显(小于100 Pa). 本实验所用填料为 PU,是一种 BTF 常用的有效填料,具有良好的物理化学特性. 已有研究证明 PU 因具有大量开放的孔室使得其持水力、孔隙率和比表面积较高,能负载相对较高的生物量[17~19]. Ryu等[20]评估了不同生物量时的 PU-BTF 去除性能,维持有效和稳定去除效率的生物量为 2.0~2.5 g·g⁻¹,而每 m 填料层的压降仅为 300 Pa. 实际上,间歇性运行方式也是一种控制填料堵塞的有效方法. 间歇期,污染负荷为零,意味着没有碳源或能源供应,微生物细胞进入内源呼吸状态. 因此,间歇施加污染负荷的生物滴滤池可降低因生物量过度积累而堵塞填料的可能.

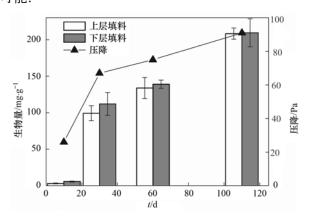


图 4 实验期间生物量和压降的变化

Fig. 4 Variation in biomass and pressure drop of the BTF during the experiment

本试验中,BTF 所获得的去除负荷高于多数类似的报道. 例如,Mathur 等[21]报道了当 BTEX 进气负荷低于 68 g·(m^3 ·h) ⁻¹时,几乎可以达到 100%的去除,而当进气负荷为 126.5 g·(m^3 ·h) ⁻¹时,仅获得 83.7 g·(m^3 ·h) ⁻¹的最大去除负荷. Lu 等[22]报道了接种活性污泥的 BTF 可以去除超过 80%的进

气负荷为 143 g·(m³·h) -1 的 BTEX. 研究表明,单 一组分的去除负荷一般高于混合 BTEX. 例如 Cho 等[4]研究了乙苯、o-二甲苯 和 BTEX 的生物过滤性 能,当EBRT为48s时,乙苯和o-二甲苯的最大去除 负荷分别为 34.3 g·(m³·h) ⁻¹和 38.6 g·(m³·h) ⁻¹, 相应的去除率分别为 61.8% 和 67.0%. 而去除 90.7% 的混合 BTEX 的最大负荷仅为 32.9 g·(m³·h)⁻¹. PCR-DGGE 的分析结果表明,本实验 虽然同时接种了活性污泥和预驯化的菌群,但在后 期稳定阶段,主要功能微生物来源于甲苯、二甲苯 富集菌群. 菌群由多种微生物组成,不仅能有效去 除去除甲苯和二甲苯,而且能获得理想的苯和乙苯 的去除效果,显示出利用预驯化菌群相对于单一菌 种的优越性. 多菌种培养物的降解能力优于单一菌 种已得到其他学者的证实,如 Jang 等[23]的研究显 示出多菌种对生物过滤效率的增强作用,接种3个 苯乙烯降解菌对苯乙烯的去除能力是单一菌株的2 倍. 接种苯甲酸降解菌,能移除苯乙烯降解中积累 的苯甲酸,生物滤池的去除性能得以维持,利用降解 菌还可以缩短驯化时间. Choi 等[24]提出利用代谢 功能互补的菌株组成的菌群处理 BTX 混合废气的 思路,虽然单菌株不能利用全部的苯系物,但组合为 菌群时不仅能有效去除全部的 BTX,去除速率也高 于单菌株.

废气中污染物的组成和浓度往往影响着微生物 群落结构的时空分布^[25, 26]. Yasuda 等^[10]分析了取 自火山岩生物滤池中两个填料层的氨氧化微生物的 空间分布,每层填料设3个采样点,结果发现,有两个 点在不同填料层的氨氧化微生物群落结构相似,但另 外一个差异较大,笔者认为这是由氨气浓度的空间分 布不同造成的. Omri 等[27] 曾经用 PCR-SSCP 技术研 究了处理 H,S 污染气体的泥炭土生物滤池中微生物 群落结构的变化,结果发现上、中、下层填料中的微 生物群落显著不同,物种多样性从下层到上层逐渐降 低,这种变化与废气浓度的垂直分布对应. 而在本研 究中,BTF上下层的群落结构非常接近,相似性分析 表明(表3),不同阶段的条带模式的差异远大于同一 阶段不同填料位置的条带模式. 同一阶段不同位置 的微生物群落结构的相似度较高. 原因应该可以归 因于填料的特性,聚氨酯泡沫是 BTF 所采用的填料, 具有较大的孔隙率,营养物质和气体污染物在其中的 传输阻力小,垂直分布较为均匀,可能是细菌群落结 构在不同垂直高度相似的原因. 同一阶段上下层填 料间生物量的微小差异也表明微生物实际上均匀分

	Table 3 Similarity of the microbial communities of the BTF during different operating stages							
	A	С	30t	30b	60t	60b	90t	90b
A	100	15. 8	21.0	18. 5	21. 7	20. 5	16. 9	20. 0
C		100	26. 2	22. 0	22. 9	21.9	33. 8	30. 9
30t			100	77. 9	49. 1	62. 1	27. 8	30. 0
30b				100	42. 7	58. 2	26. 4	27. 8
60t					100	64. 8	47. 9	42. 5
60b						100	31. 9	37. 0
90t							100	75. 1
001								100

表 3 BTF 各运行阶段微生物群落结构的相似性

布在填料柱. 微生物群落结构在不同时间的差异则 是因为进气负荷的不断增加.

4 结论

- (1)BTF 能在很短时间完成驯化过程并获得理想的对 BTEX 的去除效果,生物量的增长迅速,但未引起填料床压降的明显上升,说明实验所选择的聚氨酯泡沫是一种合适的填料.
- (2)起始接种物有助于 BTF 对混合 BTEX 各组分的 同时 去除,最大去除能力可达到 216.6 $g \cdot (m^3 \cdot h)^{-1}$.
- (3) DGGE 指纹图谱表明,BTF 中的优势微生物主要来源于富集菌群,BTF 上下层填料的细菌群落结构相似性程度高,表明 BTF 微生物的空间分布均匀.

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