Gas Dimethyl Sulfide Removal in Biotrickling Filtration

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The biotrickling ýlter packed with ceramsite was set up to study the removal of dimethyl sulýde (DMS). The DMS removal efýciency in the biotrickling ýlter was up to 99% based on experimental results. The optimal spray density, empty bed residence time (EBRT) and pH are 100 mL.min^{-1}, 38 s and 6.0, separately. The microbial community composition taken from packing material samples in the biotrickling ýlter for removal of DMS developed, which were assessed by polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE) of eubacterial 16S rDNA followed by clone library analysis, revealed four distinct bands. Phylogenetic analysis showed that the sequences of these bands were closest to sequences of species of the *Bacillus sp, Rhodobacteraceae bacterium, proteobacterium, delta proteobacterium.*

Keywords: Biotrickling lter; Odour; Dimethyl sul de (DMS); PCR-DGGE; Microbial community; Biodegradation

Introduction

Odours emitting industrial activities, such as sewage treatment plants, waste treatment or disposal facilities, paint facilities, petroleum re neries, rendering plants, pulp mills, plastic and resin manufacturers and chemical industries, and that cause an odour nuisance problem, are o en classi ed as contaminants and are subject to regulation [1]. Odours may cause a variety of undesirable reactions in people, ranging from annoyance to documented health e ects [2]. Volatile organic sulfur compounds (VOSC) are main environmental odour contaminants, which includes methanethiol (CH3SH), dimethyl sul de (CH_3SCH_3, DMS), dimethyl disul de ($CH_3S_2CH_3$, DMDS). VOSC are characterized by their hightoxicity, potential corrosive e ect, and very low odour threshold values (OTV), e.g. 0.6–40 ppbv for dimethyl sul de (CH_3SCH_3, DMS) [3,4].

Bio ltration has been known as an e cient waste gas control technology for treatment VOSC at low cost of maintenance, and produces harmless by-products. Two [illegible] *Bacill s sphae ic s* [7]. Dimethyl sul de was removal in a thermophilicbiotrickling lter operated at 52°C, using an enriched sludge inoculum [8]. e membrane bioreactor contained a polydimethylsiloxane/Zirfon composite membrane and inoculated with *H ph ic bi* VS, a methylotrophic micro-organism was used to remove dimethyl sul de from waste air [9]. e bio lter process and bacterial community composition are key elements for biodegrading of dimethyl sul de (DMS). Hydrogen sul de, methanethiol, dimethyl sul de and dimethyl disul de was degradated by *H ph ic bi* DW44 isolated from peat bio lter [10]. Dimethyl sul de was conversed by *Me h l phagas l d a* in a microbial mat [11]. A PCR-DGGE approach and constructed a dendrogram had been used to illustrate the diversity of the bacterial community in a bio lter at di erent operating conditions. e diversity of the bacterial community in the bio lter is dynamic and varies with inlet DMS loads, the addition of glucose, and uctuating temperature [12].

In this study, experimental investigations were conducted to remove of the odor containing dimethyl sul de (DMS) in bio lter lled with the ceramsite as a medium. e study analysis bacterial community composition in bio lters assessed by polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE) followed by clone library analysis, and evaluates the factors such as the in uence of inlet concentration, empty bed residence time (EBRT), inlet concentration, biological oxidation on the performance of the bio lter system.

Materials and Methods

Experimental procedure

e ow loop used in the study is shown schematically in gure 1. e dimethyl sul de supplied from the gas cylinders, was rst diluted with the compressed air, passed through an air mixture bottle, then owed upwards the bottom of the bio lter. e bio lter column (internal diameter of 90 mm and 1200 mm long) was packed with ceramsite (external diameter of 8 to 15 mm) to a height of 510 mm, which was set up to study removal of dimethyl sul de from stimulated waste gas. It was divided into three sections with the lter medium at each section was supported on a stainless steel sieve plate that ensured homogeneous distribution of gas ow over the entire cross section of the lter bed; biodegrading bacterials adhere to the surface of ceramsite to form the bio lm, the microbial inoculum culture was obtained by acclimating the activated sludge taken from the local wastewater treatment plant.

Dimethyl sul de concentrations were monitored by the analysis device of MiniRAE PLUS PGM-7600 Photo-Ionization Detector, and gas ow rate was monitored by the rotameter and the mass ow controllers. Gas ow rates were measured using Model LZB^{-1} ow

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meters with units of 1 l/h. e pH values were measured by a Model pHB-3 pH Tester (Sanxin Instrument Company, Shanghai, China). In the process of the biodegradation of dimethyl sul de experiments, nutrient-containing aqueous solutions was sprayed downward at a rate of 3 ~ 18 $L.h^{-1}$ with a peristaltic pump from the top of column to maintain the moisture of the bio lter and supply nutrients to the microbial population. e simulated dimethyl sul de-containing waste gas was supplied to the bio lter, at a ow rate of 100 to 600 $L.h^{-1}$ (EBRT, 19 to 114s).

Bacterial community analysis by PCR-DGGE

Bacterial community compositions in the biotricking lter were assessed by polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE). Following cell lysis, DNA extraction, and PCR ampli cation were as described by Ho et al. (2008). Two primers, P1(5'>CGCCC GCCGC GCGCG GCGGG CGGGG CGGGG GCACG GGGGG CCTAC GGGAG GCAGC AG<3') and P2 (5'>ATTAC CGCGG CTGCT GG<3') were used to amplify the segment of eubacterial16S rDNA. Samples (0.5g) of packing material were removed from the biotrickling lter, mixed with 10 ml distilled water, and vortexed for 20 min. e samples were run on an 8% acrylamide gelwith a 30-68% denaturant gradient using a Bio-Rad DGGE apparatus, at 60°C and a constant voltage of 180 V for 300 min.

e DGGE bands chosen for cloning were excised, and then eluted, re-ampli ed, and sequenced. e sequencing products were analyzed with an Applied Biosystems 377 DNA sequencer. e BLASTN program was used to search for nucleotide sequence similarityin the NCBI website. Sequences recovered from excised bands were analyzed for chimeric character using the Ribosomal Database ProjectII (RDP II) Chimera.

Results and Discussion

Performance of the bio lter system

Figure 2 shows the removal performance of the biotricking lter for DMS gas removal during the 36-d continuous running test. e conversion of dimethyl sul de biodegradation e ciency increases from 5.7% with one day to 98.8% at 36^{th} d, showing good dimethyl sul de degradation e ect. Dimethyl sulphide biodegradation e ciencies were 97-99% with inlet concentrations of 12.8-63 $mg.m^{-3}$ from 24 to 36-day operating time. In the bio lter, dimethyl sul de air stream is forced to pass through a ceramsite support material on which pollutant degrading cultures are immobilized. Dimethyl sul de and oxygen di use from the gas phase to the wet layer of the bio lm and then are consumed by the microorganism communities. Under aerobic conditions in a bio lter, dimethyl sul de is oxidized to carbon dioxide, sul de (SO_4^{2-}), water vapors by biological oxidation; dimethyl sul de solubility is small in water due to its low Henry's constants, mass transfer limitation may play an important role during biological treatment; gas-phase dimethyl sul de should rst di use through a thin aqueous layer surrounding the lter medium, and then dimethyl sul de is directly adsorption to the surfaced of bio lm, biological oxidation is the process in which dimethyl sul de is oxidized to CO_2 and H_2O.

e in uence of dimethyl sul de concentration

Keeping EBRT of 36 s, and sprinkling amount (6.0 $L.h^{-1}$), pH of 6.0 xed, the in uence of dimethyl sul de concentration in inleton removal of dimethyl sul de with the bio lter are presented in gure 0 L.h0

than 80% dimethyl sul de is biological oxidized for less than the initial concentration of 60 $mg.m^{-3}$ dimethyl sul de. is illustrates that the biological reactor is e cient in purifying the waste gas whose dimethyl sul de concentration is between 5.5 $mg.m^{-3}$ and 249 $mg.m^{-3}$.

e bio lter to photocatalytic reactor eliminates gas-phase dimethyl sul deto produce CO_2, H_2O.

e in uence of empty bed residence time (EBRT)

e e ect of EBRT on removal of dimethyl sul de is presented in gure 4, under the conditions of pH of 6.0, inlet concentration of

structures in the biotrickling lter for dimethyl sul de removal were assessed by polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE). Denaturing gradient gel electrophoresis of eubacterial 16S rDNA samples taken from packing material revealed four distinct bands (Figure 8). Based on 16SrDNA sequence data, results show that the predominant bacterias for degradation of DMSare Bacillussp, *Rh d bac e aceae bac e i* , *p e bac e i* , *del a p e bac e i* . e dominant bacteria, *Bacill s* sp., takes up 68.6%; while *Rh d bac e aceae bac e i* , *p e bac e i* and *del a P e bac e i* are take up 14.8%, 2%, 2.8%, respectively. *Bacill s* sp. was very predominant in its role of DMS-degrader, enhancing the metabolism of DMS in the bio lter. *Bacill s* sp., sulfur-oxidizing bacteria, was able to degrade H_2S [13,14]. *P e bac e i* [15], oxidizing inorganic sul de and mercaptans, and *Rh d c cc s*, deodorizing domestic animal feces [16] have been described as sul de oxidizers. Since DMS can be metabolized to dimethyl sulfoxide, methyl and m/Span <</MCID 411 >>BD330.16 Tw -0 -1.21 metEMrs. SinmethycarbTjdimethyl de