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Research article

Biofiltration of trimethylamine in biotrickling filter inoculated with *Aminobacter aminovorans*

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ABSTRACT

Background: Trimethylamine (TMA) is the main responsible for the odor associated with rotting fish and other annoying odors generated in many industrial activities. Biofiltration has proved to be efficient for treating odorous gaseous emissions. The main objective of this work was to determine the removal capacity of TMA of a biotrickling filter inoculated with *Aminobacter aminovorans* and to evaluate the effect of H_2S on its performance.
Results: The maximum specific growth rate of *A. aminovorans* in a liquid culture was 0.15 h^{-1}, with a TMA to biomass yield of 0.10 ($g\,g^{-1}$) and a specific consumption rate of 0.062 $g \cdot g^{-1} \cdot h^{-1}$. The initial specific consumption rate of TMA was highly influenced by the presence of H_2S in liquid culture at concentrations of 20 and 69 ppm in heading space of the flasks. A BTF inoculated with *A. aminovorans* showed removal efficiencies higher than 98% in a range of loading rate of 0.2 to 8 $g \cdot m^{-3} \cdot h^{-1}$ at empty bed residence time (EBRT) of 85 and 180 s. No effect on the elimination capacity and efficiency was detected when H_2S was added at 20 and 50 ppm to the inlet gaseous emission, though the fraction of *A. aminovorans* measured by qPCR in the biofilm decreased.
Conclusions: A biotrickling filter inoculated with *A. aminovorans* can remove efficiently the TMA in a gaseous stream. The elimination capacity of TMA can be negatively affected by H_2S, but its effect is not notorious when it is forming part of a biofilm, due to its high specific consumption rate of TMA.
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1. Introduction

Volatile amines are one of the main responsible of odor nuisances in many industrial activities; usually they are generated by the decay or biological degradation of organic material. In particular, trimethylamine ($(CH_3)_3N$), is the main responsible for the odor associated with rotting fish and is one of the major sources of annoying odors generated in many industrial activities like fish-meal manufacturing processes, wastewater treatment plant, waste disposal landfills, livestock farming and hog manure, and rendering plants [1]. The source of trimethylamine (TMA) is not fully established, but there is evidence that it is produced by the action of microorganisms on choline, betaine or trimethylamine N-oxide [2]. The reported TMA odor threshold is in the range of 0.00021–0.00058 ppm while characteristic concentrations of TMA emitted in such discharges between 5 and 100 ppm [3,4,5].

In the last decade there has been an increased concern related to the presence of amines in gaseous emissions due to their toxic effects on human health because of its potentially toxic and carcinogenic effects [6]. The cost of using physical–chemical operations for depleting their presence in gaseous streams and the potential adverse effects resulting from the presence of residually persistent unknown by-products in the treated stream, have made that biological systems have been preferentially adopted [7,8,9].

Biological removal of amines could be accomplished by aerobic and anaerobic microorganisms. In aerobic conditions, TMA is oxidized to diethylamine (DMA) and formaldehyde by a TMA dehydrogenase. A second pathway for utilization of TMA is due to a TMA monooxygenase that oxidize TMA to TMA N-oxide that is subsequently demethylated by a TMA demethylase to DMA and formaldehyde. DMA is oxidized to methylamine (MA) and formaldehyde by a DMA monooxygenase. MA

Abbreviations: BTF, biotrickling filter; c_{in}, inlet TMA concentration; c_{out}, outlet TMA concentration; DGGE, denaturing gradient gel electrophoresis; DMA, diethylamine; EBRT, empty bed residence time; EC, elimination capacity ($gTMA \cdot m^{-3} \cdot h^{-1}$); F, flow ($m^3 \cdot h^{-1}$); H, height (m); ID, inside diameter (m); L, loading rate ($gTMA \cdot m^{-3} \cdot h^{-1}$); MA, methylamine; OD, outside diameter (m); PVC, polyvinyl chloride; qPCR, quantitative polymerase chain reaction; RE, removal efficiency (%); TMA, trimethylamine; V, volume (m^3).

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is oxidized by a MA dehydrogenase or by a MA oxidase to formaldehyde and ammonia that can be used as a carbon and nitrogen source for some microorganisms present in a biological treatment system. There are other routes proposed for the conversion of MA to formaldehyde through glutamate by a *N*-methylglutamate synthase, g-glutamylmethylamide synthase and a *N*-methyl glutamate dehydrogenase [10]. Thus, microbial degradation would be an efficient way of eliminating TMA in industrial gaseous emissions. There are a few reports about biofiltration of amines as individual compounds or in complex mixtures. Chang et al. [11] used a biofiltration system containing a mix of microorganisms obtained from an activated sludge of a wastewater treatment plant to treat a TMA-containing waste gas, obtaining a removal efficiency higher than 90% at TMA inlet loads below 27.2 $mgN \cdot h^{-1}$, using a long retention time of 318 s. Ding et al. [12] showed the complete oxidation of TMA to NO_3^- in the compost biofilter due to the presence of nitrifying bacteria. Ho et al. [13] also showed that a biofilter inoculated with a nitrifying microorganism *Arthrobacter* sp. removes efficiently TMA and NH_3 from the exhaust air of a swine waste storage pit. The inoculation of *Paracoccus* sp. CP2 and *Arthrobacter* sp. CP1 as inoculum into a biofilter allowed the removal of TMA in a mixture with DMA and MA at EBRT of 60 s treating emissions containing TMA in a range of 10–100 ppm [14]. Wan et al. [15] reported the biofiltration of waste gas containing high concentration of TMA using a Biotrickling filter (BTF) packed with ceramic particles and inoculated with B350 a mixture of microorganisms that contains 28 species and several enzymes (Biosystems Co., USA) showing a maximum EC of 13.13 $g \cdot m^{-3} \cdot h^{-1}$ with a RE of 64.7% at 55 s EBRT. Liffourrena and Lucchesi [9] have shown that *Pseudomonas putida* A immobilized in calcium alginate is capable of degrading higher concentrations of TMA than free cells. Understanding of microbial community compositions in biofilters plays an important role in seeking biological limiting factors related to the removal efficiencies of TMA and other compounds from waste gas and further enhancing the performance of biofilters [16,17]. Molecular fingerprints methods such as Denaturing gradient gel electrophoresis (DGGE) has been successfully used for showing the presence of specific microorganisms [13], and other techniques like qPCR allows to quantify the presence of an specific microorganism in a biofilter.

Aminobacter aminovorans is a microorganism known for its ability to use TMA as carbon and energy source. Rappert and Muller [18] reported that the degradation of TMA is strongly inhibited by reduced volatile sulfur compounds that are usually present in industrial emissions causing odor nuisance where TMA is also present. The main objective of this work was to determine the removal capacity of TMA of a biotrickling filter inoculated with *A. aminovorans* and to evaluate the effect of H_2S on its performance.

2. Materials and methods

2.1. Microorganism and preparation of the inoculum

Aminobacter aminovorans (DSM 7048) was used in all the experiments. The liquid culture medium used was the Colby and

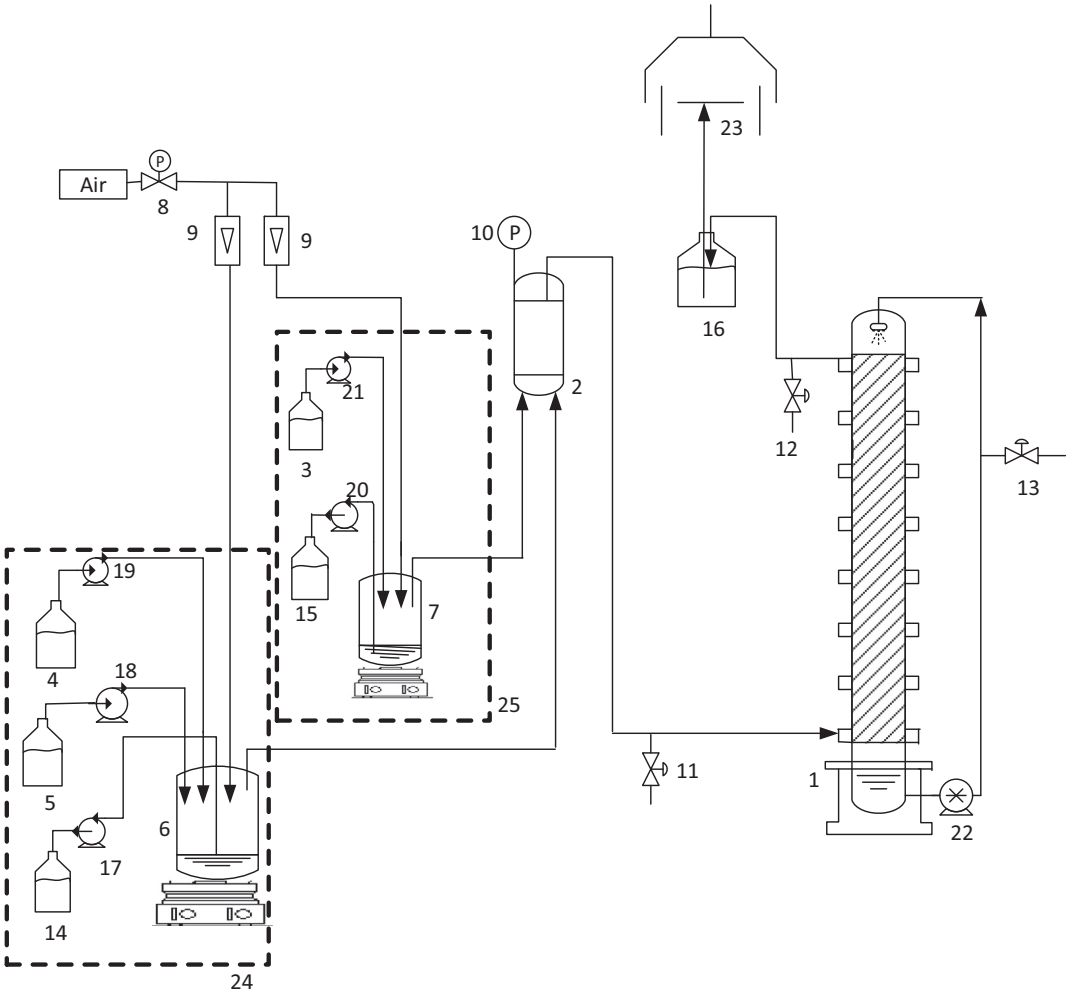

Fig. 1. Experimental set up. 1: Biotrickling filter; 2: Gas mixer; 3: Solution of trimethylamine; 4: Solution of HCL; 5: Solution of Na_2S; 6–7: Heating plate with magnetic stirring; 8: Manifold; 9: Rotameter; 10: Manometer; 11–12–13: Sampling ports; 14: Container for disposal of H_2S generation solution; 15: Container for disposal of Trimethylamine generation solution; 16: Acid solution for TMA absorption; 17–18–19–20–21–22: Peristaltic pumps; 23: Gas extraction system; 24: Generation of gaseous H_2S; 25: Generation of gaseous TMA.