

# Odor removal efficiency and microbial profiling of the biofilter <sup>(1)</sup>

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## Abstract

The purpose of the study aims to evaluate the odor removal efficiency and microbial composition of biofilters applied to ventilating compost depots. The biofilters were divided into four groups, namely A: fern chips, Group B: mixture of fern chips Group C: matured compost, fern chips with humidifying, and Group D: mixture of fern chips and matured compost with humidifying. The odor of inlet and outlet gas were measured, and the microorganisms in the filter samples were identified. The results showed ammonia removal efficiencies of the all treatments were nearly 100% without significant difference during 220 days of operations. The odor concentrations detected in the outlet of the four treatments were 55.4, 55.5, 44.2 and 42.4 OU/m<sup>3</sup>, respectively, while the latter two biofilters with humidify were lower in odor emission. The data from ssu rRNA gene sequence analysis of the four biofilters showed the phylum *ProteoBacteria* as dominants, which account for 64.3, 63.2, 72.4 and 65.2% of domain *Bacteria* in biofilter A, B, C, D, respectively. In particular, phyla *Bacteroidetes*, *Acidobacteriales*, and *Firmicutes* in biofilter D were classified as orders *Sphingobacteriales*, *Acidobacteriales*, and *Bacillale* with relatively high diversity. The methanogenic archaea classified as phylum *Euryarchaeota* and class *Methanomicrobia* was only found in biofilter D. Moreover, the nitrogen fixation bacterium affiliated to family *Rhizobiales* and genus *Pseudolabrys* and the ammonia oxidizing bacterium affiliated to family *Nitrosomonadales* and genus *Nitrosospora* were also found in biofilter D. Those microorganisms might participate in the nitrogen cycles occurred in the biofilter and help to remove the ammonia produced from the composting process. In summary, D biofilter will be the better choice for odor removal application.

Key words: Odor Removal, Biofilter, Microorganism.

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