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Integrity of DNA-Based Analysis of HVAC Filters from a Tropical Building

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SUMMARY

Ventilation system filter offers a practical alternative for indoor bioaerosol sampling due to its high flow rate and long operational duration. However, as it samples the air, the filter is also regularly exposed to air flow stresses and elevated temperature for a long duration (months). This study utilized DNA-based methods (fluorometry, qPCR and sequencing) to investigate the effect of exposure to such conditions to the integrity of DNA that is analysed at the end of the filter's service (3 months of operations). Current results indicated that microbial diversity was only mildly affected by the exposure but quantitative analysis must be performed with cautions as biomass loss was detected from total, bacterial and fungal DNA.

KEYWORDS

HVAC filters, bioaerosol, DNA conservation, tropical buildings, DNA-based analysis

1 INTRODUCTION

Heating, ventilation and air conditioning (HVAC) filters have recently been applied as an indoor air sampler (Luhung et al., 2017; Haaland and Siegel, 2016). Such a sampling approach can be especially beneficial for bioaerosol studies that target low biomass concentrations owing to its relatively higher sampling flow rate and duration (up to several months). Notwithstanding these advantages, published studies investigating factors that could affect the accuracy of such a sampling approach are relatively scarce.

One potential factor limiting accuracy could be whether DNA is fully conserved during the filter's deployment period. Past work (Luhung et al., 2015) indicated that prolonged exposure to air flow stresses and elevated temperatures could degrade DNA that accumulates on filters. In Singapore, it is typical to house HVAC filters in an air handling unit (AHU) room as it operates in unison with other ventilation system equipment such as a cooling coil or dehumidifier. AHUs serving typical offices, libraries or classrooms in Singapore could operate for 10-14 hours a day, which translates to 840 h per 3 months of high air flow exposure on the filter media. Furthermore, during the AHU's off time, when the indoor space is closed, the temperature could rise to above 30 °C owing to heat sources from outdoor or a heater that recharges a dessicant-based dehumidifier. This study explores how well biomass is conserved on a used HVAC filter, particularly considering the possible effects of high air flow rates and elevated temperatures. DNA-based analysis is used for both quantitative and microbial community assessment before and after exposure to controlled environmental conditions.

2 METHODS

Pieces of in-use HVAC filter (MERV-7) were collected from an AHU in a library at a Singapore university at the end of month 1, month 2 and month 3 of operation. Each filter set was then exposed to two different conditions in a laboratory test of one-week duration. One set was put in a chamber and maintained at 35 °C, while the other set was put into an air flow test rig and exposed to a velocity of 1.5 m/s of clean air. These temperature and air speed conditions were

chosen based on actual temperature and air flow speed measurements in the AHU room from which the filters were acquired. DNA was extracted from the filter pieces before and after treatment using the MOBIO Power Water kit with some modifications to improve DNA yield. The extracted DNA was analysed with fluorometry for total DNA concentration, with qPCR for partial quantification, and with non-amplicon, metagenomic sequencing (Illumina HiSeq).

3 RESULTS AND DISCUSSION

Figure 1a displays a reduction in DNA concentration of all three measured biological entities on the first month filter after each treatment. The reduction was seen to be the highest in total and fungal DNA with 47% and 30% overall loss, respectively. Bacterial DNA showed a more modest reduction at 11%. Figure 1b suggests no significant difference in biomass diversity before and after the treatments. Broadly agreeing with the quantitative results, an average reduction of 26% was only observed on the top two fungal phyla but not on the bacterial phyla.

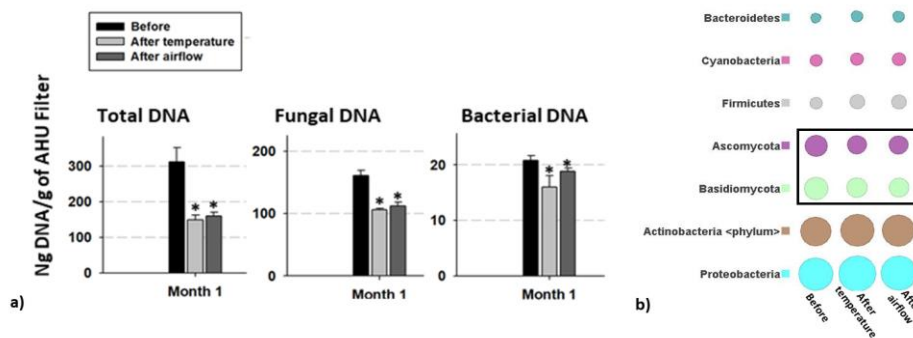


Figure 1. DNA measurements for a) total, bacterial and fungal DNA, b) shotgun sequencing analysis (phylum level) before and after the temperature and airflow treatment on the HVAC filter (one month of operation). * indicates a significant difference at $p < 0.05$, paired t test.

Based on current results, continuous exposure to such conditions during AHU operation would only mildly affect the composition of the microbes on the filter. However, one should be more cautious with quantitative analysis from such sampling as it tends to underestimate the actual concentration due to potential biomass loss. Ongoing investigations on older filters (month 2 and month 3) and the effect of fluctuating occupancy in the served indoor space are warranted to gain more understanding on interpreting results from HVAC filter sampling and analysis.

4 CONCLUSION

In the context of indoor bioaerosols studies, the current results indicate that HVAC filter sampling and analysis broadly maintains the integrity of microbial communities on the filter but there may be a tendency to underestimate the actual airborne biomass concentration owing to biomass loss. It is important to understand the mechanisms of such loss as it could also influence indoor occupants and the downstream equipment protected by the filter.

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