The effect of filter-based sampling parameters on abundance and diversity of indoor bioaerosols

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Despite the public health importance of bioaerosols in the context of human exposure (Douwes et al. 2003), the microbial content of indoor air has been poorly explored. Molecular biology methods demonstrate a great potential for exploring the diversity and abundance of indoor bioaerosols. However, owing to the low biomass of the air, it is challenging to obtain a representative microbiological sample in order to recover sufficient DNA for molecular analysis (Peccia and Hernandez, 2006). Although numerous studies have utilized membrane filters in bioaerosol monitoring, no standardized methods and protocols are currently available, making difficult the cross-comparison of molecular results between studies.

The objective of this research was to investigate the effect of sampling parameters, i.e. sampling time, filter collection material, diameter, pore size, type of filter sampler, on DNA recovery and PCR detection of airborne bacteria and fungi in indoor air.

Direct comparison sampling tests were carried out in an unoccupied room, investigating the efficiency of commercially available filters. Samples were collected simultaneously in triplicate at a flow rate of 28 L/min (Fig. 1). Total genomic DNA of each sample was extracted and analysed by quantitative PCR (qPCR) of bacterial 16S rRNA gene and PCR of the fungal internal transcribed spacer (ITS) 2 region and will be further processed for Miseq sequencing of 16S rRNA and ITS1 region.

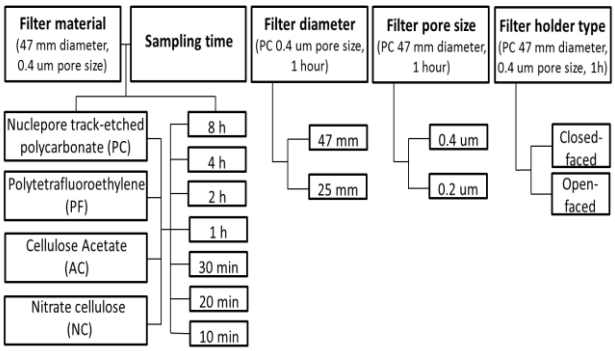

Figure 1. Workflow diagram of the sampling parameter comparisons.

Results showed that the applied extraction protocol was suitable for all four types of filters for both bacterial and fungal recovery from aerosol filter samples. In terms of sampling time, one hour at 28 L/min seemed to be a good compromise for both bacterial and fungal detection, considering that shorter sampling times might result in insufficient collected biomass, while prolonged sampling is not preferred for practical reasons of sampling facilitation (Fig. 2). Results could contribute to the establishment of an appropriate sampling protocol for bioaerosol molecular analysis under optimum conditions.

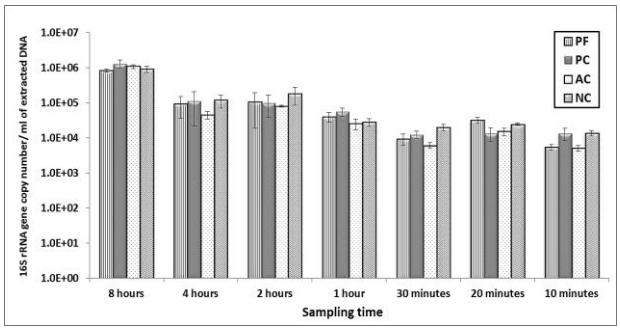

Figure 2. Quantitative PCR data of 16S rRNA gene copy number in indoor air collected at 28 L/min for different sampling periods using PF, PC, AC and NC filters simultaneously. Results are presented as an average over three repetitions. Axis y is on log scale and error bars represent standard error.

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Douwes, J., Thorne, P., Pearce, N., Heederik, D., (2003). Bioaerosol health effects and exposure assessment: progress and prospects. *Annals of Occupational Hygiene*, 47, 187-200.

Peccia, J. and Hernandez, M., (2006). Incorporating polymerase chain reaction-based identification, population characterization, and quantification of micro-organisms into aerosol science: A review. *Atmospheric Environment*, 40, 3941-3961.