Seasonal variation of airborne bacterial and fungal communities in different size fractions in an urban and a semi-urban residential environment using molecular techniques

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Seasonal variation of indoor bioaerosols using molecular biology approaches has been poorly explored, whereas very few culture-independent studies on enclosed spaces have monitored the airborne microbial load and diversity during a long period of time (Gaüzère et al., 2014; Robertson et al., 2013). Moreover, there is still little knowledge concerning the distribution of airborne micro-organisms in different particle size fractions by applying molecular methods (Quian et al., 2012; Yamamoto et al., 2012).

The purpose of this project is to examine the seasonal effect on the size-distributed abundance and diversity of the airborne bacterial and fungal load in indoor air, in relation with the indoor and outdoor sources. Two residential flats with similar characteristics, located in two different types of environments; urban and semi-urban, were monitored over different seasons using active and passive collection methods.

The sampling campaign took place during 2016 in two one-bedroom apartments situated in riverside residential blocks, in Colchester (Essex, UK) and Stratford (London, UK). Both residences were occupied by two people. Sampling was carried out for three days per each site and season, indoors and outdoors, using impaction for whole-day (12 h) collection of size-distributed samples, and filter-based collection (1 h, three times per day) for diurnal variation monitoring. A liquid impinger was also utilised for daily sampling (1 h). Besides active samplers, passive collection method using empty petri dishes suspended from the ceiling (Adams et al., 2013) was implemented for a whole month sampling per each season. Swab samples were also collected from representative house dust reservoirs, expected to be sources. A detailed list of sampling methods is shown on Table 1. Size distributed particle number and mass concentration, as well as temperature, relative humidity and carbon dioxide were monitored continuously during sampling.

Samples will be processed for high-throughput sequencing of 16S rRNA and ITS1 region on Illumina Miseq platform and results are expected to give a complete assessment of the air microbial content in the built environment, based on time-resolved data on both bacterial and fungal diversity within a 1-year time period. Moreover, the indoor air quality will be evaluated not only based on the seasonality, but also according to the site location, comparing an urban and a semi-urban environment. Results on longitudinal variation of bioaerosols' concentration and composition could contribute to development of effective methods for prevention and mitigation of the impacts of bioaerosols on human exposure.

Table 1. Sampling schedule for each site per season.

Sampling method	Collection substrate	Flow rate	Sampling environment	Duration	Replication
6-stage modified Andersen impactor	85 mm mixed cellulose ester filters (0.4 μm pore size)	28.3 l/min	indoors	whole day (12 hours)	3 days
7-stage May impactor	glass slides	20 l/min	indoors and outdoors	whole day (12 hours)	3 days
Filter holders	47 mm mixed cellulose ester filters (0.4 μm pore size)	28.3 l/min	indoors and outdoors	1 hour, 3 times per day	3 replicates for 3 days
Biosampler impinger	Phosphate-buffered saline solution	12.5 l/min	indoors	1 hour	3 days
Suspended passive collectors	empty petri dishes	n/a	indoors	1 month	3 replicates
Settled dust sampling	nylon swabs	n/a	indoors (six points)	n/a	3 replicates

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