Science of the Total Environment 601–602 (2017) 940–945

Contents lists available at ScienceDirect

Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

Floor dust bacteria and fungi and their coexistence with PAHs in Jordanian indoor environments

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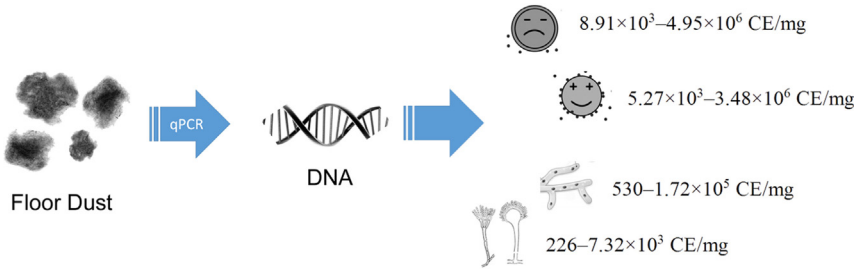
HIGHLIGHTS

- Floor dust bacterial and fungal concentrations vary significantly within the city.
- Newly built dwelling and least occupied has the lowest biocontamination.
- Educational buildings have higher Gram-negative bacteria concentration than dwellings.
- Gram −/+ bacteria and total fungal concentrations are positively correlated.

GRAPHICAL ABSTRACT



ARTICLE INFO

Article history:
Received 3 December 2016
Received in revised form 9 May 2017
Accepted 23 May 2017
Available online xxxx

Keywords:
Gram-positive
Gram-negative
Penicillium/Aspergillus spp.
Total fungi
Dwellings
Educational building

ABSTRACT

Floor dust samples were collected from Jordanian indoor environments (eight dwellings and an educational building) in Amman. Quantitative PCR (qPCR) analyses of selected fungal and bacterial groups were performed. The bacterial and fungal concentrations were also correlated with PAHs concentrations, which were previously measured in the same samples by using GC–MS. The bacterial and fungal concentrations varied significantly among and within the tested indoor environments. Based on the collected samples in the entrance area of the dwellings, the largest variation was found in Gram-negative bacteria and total fungi concentration. The lowest bacterial and fungal concentrations were found in the dwelling that was least occupied and the most recently built. At the educational building, the Gram-positive bacteria concentrations were lower than those observed in the dwellings. Unlike for bacteria, we observed significant negative correlation with some polycyclic aromatic hydrocarbons (PAHs). This calls for further studies investigating biodegradation of PAHs in house dust and presence of potentially health hazardous PAH metabolites. Since biocontamination in floor dust has been given relatively little to no attention in the MENA region we recommend that more extensive measurements be conducted in the future with chemical and biological analysis of floor dust contaminants and their exposure indoors.

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http://dx.doi.org/10.1016/j.scitotenv.2017.05.211
0048-9697/

1. Introduction

Pollution has been a general and common problem for a long time (e.g. Morawska et al., 2013). Exposure to pollution can occur via three main routes: dermal, inhalation, and ingestion causing health problems (e.g. Alam et al., 2014; Grimsley et al., 2012; Günther et al., 1998).

Particularly, household dust accommodates a vast range of biological contamination, which includes microbes (i.e. microorganisms such as fungi, bacteria, and viruses) and non-microbes (such as insects and their dry parts, dust-mites, and cells from humans, plants, and animals). In general, biological contamination have limited direct toxicity on humans but they are often involved in the etiology of building related illness that is either infective or allergic as well as resulting in decreased lung function, respiratory symptoms, asthma and rhinitis, and sick-building syndrome (e.g. Morawska et al., 2013; Mandal and Brandl, 2011; Ross et al., 2000).

The dynamic behavior of biological contamination in the indoor air and floor dust can be described mathematically by means of a material-balance equation (e.g. Bhangar et al., 2014; Nazaroff, 2016; Meadow et al., 2014; Nazaroff and Cass, 1989), which includes several terms to describe the controlling factors (sources and sinks) of the concentration change rate in both the air and the floor dust. The outdoor air concentration of any contaminant drives its concentration indoors via the indoor-outdoor air exchange (i.e. ventilation rate) and the penetration factor (filtration and infiltration), which are the main building characteristics defining the indoor-to-outdoor relationship of air pollutants (e.g. Hussein et al., 2015; Hussein and Kulmala, 2008; Nazaroff, 2004). The production, survival, and decay of bacteria and fungi inside floor dust is affected by many factors: (1) their airborne concentrations, (2) building characteristics (e.g. ventilation, penetration, type of interior surfaces, etc.), (3) occupants and their activities, (4) environmental conditions, and (5) coexistence with chemical pollution (such as polycyclic aromatic hydrocarbons (PAHs) and volatile organic compounds (VOCs)).

It was reported that the fate of PAHs in soil is affected by various factors including biological diversity and abundance (Gupte et al., 2016; Semple et al., 2003; Reid et al., 2000; Heitkamp et al., 1988). Wood-decaying fungi can detoxify, oxidize, and transform PAH (e.g. Günther et al., 1998). A long time ago, it was also confirmed that some microbial metabolites of naphthalene occur in microcosms containing natural freshwater and estuarine sediments (Heitkamp et al., 1987). As an advantage, PAHs can be removed by using microbial and fungal degradation, which is a natural technique (e.g. Leitão, 2009; Johnsen et al., 2006; Muñoz et al., 2003).

In this study, the aim was to quantify fungal and bacterial concentrations inside floor dust samples collected from dwellings and an educational building in Amman, Jordan. We also applied simple statistical tests between the tested microbe concentrations and the PAHs concentrations.

2. Materials and methods

2.1. Floor dust samples

Floor dust samples were collected during April 3–9, 2015 from eight dwellings and an education building located in Amman, Jordan (Fig. 1). These indoor environments were naturally ventilated. The weather condition (T, RH, and precipitation) during this period is presented in Fig. S1. The collection procedure of floor dust samples and detailed description about the dwellings and the education building can be found in our previous studies Maragkidou et al. (2016) and Maragkidou et al. (2017). Here, we provide this information in brief.

Two samples were taken from each dwelling (living room and main entrance). In order to collect a reasonable amount of floor dust samples, the dwellings were not vacuum cleaned for 3–4 days before samples were collected. The type and age of each dwelling as well as the type and area of the floor are given in Table S1. The educational building was the Department of Physics of the University of Jordan (Table S2 and Fig. S2). All samples were collected on the same day. The cleaning staff executed their routine daily cleaning activities normally. Although smoking was prohibited inside the university buildings, sometimes this was violated.

As described by Maragkidou et al. (2016) and Maragkidou et al. (2017). The floor dust samples were collected by using a regular vacuum cleaner. We placed the vacuum dust bags made of nylon (25 μm, 155 mm × 73/38 mm, Allied Filter Fabrics Pty. Ltd) inside the tube of the vacuum cleaner. Each sample was collected from 3 min of vacuum cleaning and a floor surface area as listed in Tables S1 and S2. Immediately after dust collection, the dust bags were closed and put inside a zipped plastic bag. Each dust sample was then put in a glass vial, wrapped with aluminum foil and stored in the freezer (−20 °C). Shipment to the laboratory was undertaken at room temperature and samples were stored in the laboratory at −20 °C until analyses were completed.

2.2. Biological analysis

DNA was extracted from weighted samples of dusts of approximately 20 mg using Chemagic DNA Plant kit (PerkinElmer Chemagen Technologie GmbH, Germany) on KingFisher mL magnetic bead based DNA extraction robot (Thermo Scientific, Finland). In an initial step, microbial cells were disrupted with bead-beating as described in (Kärkkäinen et al., 2010), using MiniBeadBeater-16 (Biospec Products Inc). Salmon tests DNA (Sigma Aldrich, USA) was added as an internal standard to the samples prior to DNA extraction (Haugland et al., 2012) to account for PCR inhibitors and variability in DNA extraction efficiency.

Quantiative PCR (qPCR) analyses of selected fungal and bacterial groups and calculations of cell equivalents per mg of dust were performed as described by Kaarakainen et al. (2009). qPCR assays used in this study have been published previously as follows: total fungal DNA (Haugland & Vesper, US pat. 2002; 6 387 652), group of *Aspergillus* spp./*Penicillium* spp./*Paecilomyces variotii* (Haugland et al., 2004), and Gram-positive and Gram-negative bacteria (Kärkkäinen et al., 2010). QPCR reactions were performed as written in the original publications with minor modifications. In the bacterial duplex assay 20 μl reaction mix included 10 μl of Environmental Master Mix (Applied Biosystems Inc., Foster City, CA), 1.5 μl Bovine serum albumin (2 mg/ml), 1 μl of forward and reverse primers, 0.4 μl of a both TaqMan probes, 3.7 μl of nuclease free water (HyClone Laboratories Inc., Utah, USA) and 2 μl of template DNA. The analysis was performed on Stratagene Mx3005P QPCR System (Agilent Technologies Inc., USA) equipment.

2.3. Polycyclic aromatic hydrocarbons (PAHs)

The polycyclic aromatic hydrocarbons (PAHs) concentrations were previously investigated by Maragkidou et al. (2016) for the dwellings and by Maragkidou et al. (2017) for the educational building (Tables S3 and S4). The PAHs concentrations were quantified via GC-EI/MS.

3. Results and discussion

3.1. Bacterial and fungal contamination

The bacterial and fungal concentrations in the dwellings varied significantly in both the entrance and living room (Table S5 and Fig. 2). The Gram-positive bacteria concentrations in the entrance were 17,700–95,800 CE/mg (excluding the extreme value at A3, ~348,300 CE/mg) and the Gram-negative bacteria were 8900–2,254,300 CE/mg. As for *Penicillium*/*Aspergillus* spp., it was in the range 200–7300 CE/mg and total fungi concentrations were