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Variability of indoor fungal microbiome of green and non-green low-income homes in Cincinnati, Ohio

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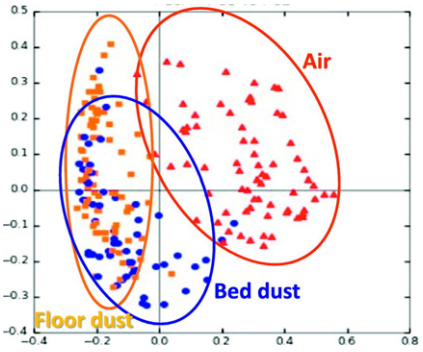
HIGHLIGHTS

- No difference was found in the mycobiome between green and non-green buildings.
- Mycobiomes obtained in each home 12 months apart differed.
- Largest differences were observed in mycobiomes from air, floor, and bed samples.

GRAPHICAL ABSTRACT



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ABSTRACT

"Green" housing is designed to use low-impact materials, increase energy efficiency and improve occupant health. However, little is known about the indoor mycobiome of green homes. The current study is a subset of a multicenter study that aims to investigate the indoor environment of green homes and the respiratory health of asthmatic children. In the current study, the mycobiome in air, bed dust and floor dust was compared between green (study site) and non-green (control site), low-income homes in Cincinnati, Ohio. The samples were collected at baseline (within four months following renovation), and 12 months after the baseline at the study site. Parallel sample collection was conducted in non-green control homes. Air samples were collected by PM2.5 samplers over 5-days. Bed and floor dust samples were vacuumed after the air sampling was completed. The DNA sample extracts were analyzed using ITS amplicon sequencing. Analysis indicated that there was no clear trend in the fungal communities between green and non-green homes. Instead, fungal community differences were greatest between sample types - air, bed, and floor. Microbial communities also changed substantially between sampling intervals in both green and non-green homes for all sample types, potentially indicating that there was very little stability in the mycobiomes. Research gaps remain regarding how indoor mycobiome fluctuates over time. Longer follow-up periods might elucidate the effect of green renovation on microbial load in buildings.

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1. Introduction

The built environment microbiome, coupled with the extensive amount of time spent by individuals indoors, has been known to influence human health (Kanchongkittiphon et al., 2015; Mendell et al., 2011). Exposure to fungi has been linked to a range of detrimental health effects (Douwes et al., 2003) including asthma (Jaakkola et al., 2010; Reponen et al., 2011). However, protective effects of fungi have also been reported. Exposure to increased levels of mold-derived components early in life was found to protect children from allergic diseases and allergic sensitization (Iossifova et al., 2007). Due to these links to human health, it is imperative to better understand the complex microbial habitat of the indoor built environment, especially if immunocompromised or mold-sensitized individuals are present.

With the "green" building movement, more and more homes are opting to be energy efficient. "Green" housing is designed to use low-impact materials, increase energy efficiency and improve occupant health (Kibert, 2016). Previous studies have shown that green and non-green materials support microbial growth similarly (Mensah-Attipoe et al., 2015; Coombs et al., 2016). However, trends in energy efficiency, having led to "tighter" buildings with reduced ventilation could potentially result in increased humidity and lead to altered microbial load (Fabian et al., 2014; Macher et al., 2017).

High-throughput DNA sequencing has recently been used for obtaining a culture-independent and comprehensive picture of the microbial dimension of a variety of ecosystems (Konya and Scott, 2014). Microbial diversity has also been assessed in a variety of indoor environments, ranging from homes and offices to healthcare facilities and transportation environments, as previously reviewed (Ramos and Stephens, 2014). The majority of studies examining residences have focused on the bacterial diversity in the indoor environment (Dunn et al., 2013; Flores et al., 2013; Kelley et al., 2004). One prior study (Kembel et al., 2014) characterized bacterial biomes in dust samples collected in a "green" university building. The few studies of fungal taxa within homes have mostly investigated swabbed surfaces, vacuumed floor dust or indoor air using either gravity settled air samples or portable air samplers (Adams et al., 2013a,b; Dannemiller et al., 2014; Kettleson et al., 2015; Rittenour et al., 2014; Yooseph et al., 2013). No previous studies, however, have compared fungal communities in air, bed dust and floor dust. Furthermore, very limited data are available on the effect of "green" building practices on indoor fungal load. Lower levels of ergosterol (an estimate of fungal biomass) were found after a year of residency in green-renovated homes compared to levels measured in the old home before moving out (Takaro et al., 2011).

This study is a subset of a multicenter study designed by the Centers for Disease Control and Prevention (CDC) and the Department of Housing and Urban Development (HUD). The goal of the multicenter study is to investigate the relationship between the indoor environment of green homes and the respiratory health of children with asthma living in low-income homes. Previously, we reported that no difference was found in the levels of PM2.5, black carbon, sulfur, ultrafine particles, total volatile organic carbons or formaldehyde between green and non-green homes (Coombs et al., 2016). Here we characterize and compare the mycobiomes (fungal microbiomes) of indoor air, bed dust and floor dust between green and non-green homes in Cincinnati, Ohio. The goal of the study was to determine if green renovation altered richness and diversity of the indoor mycobiome.

2. Materials and methods

2.1. Study design

The study included 52 low-income homes (26 green-renovated apartments, and 26 non-green control apartments) (Fig. 1). Green-renovated apartments were drawn from a low-income, 800 apartment complex in Cincinnati. All of the green homes were renovated from previously non-green units. The characteristics of the study homes have been reported previously (Coombs et al., 2016). Briefly, green features that were expected to affect the humidity and thereby, the microbial load included energy efficient windows and doors, whole house insulation, energy efficient central heating/cooling system, and bathroom fans. The first post-renovation (baseline) samples from green-renovated homes were collected within four months of renovation, and another set of samples was collected 12 months later. Parallel sampling, matched by the season, was conducted in non-green homes; 6 non-green homes were located in the same community as the green-renovated homes and 20 were located at the control site about 6 miles from the green-renovated homes. Sampling at a control home was matched with the study home by season. Both apartment complexes receive federal assistance to allow them to provide subsidized housing to low-income families (U.S. Housing Act of 1937). Homes were considered for inclusion if a child who lived in the home was age 7–12 years and the caregiver reported the child had a diagnosis of asthma and current symptoms in past six months.

Temperature and relative humidity were measured using a HOBO® data logger (Onset Computer Corporation, Bourne, MA) and were continuously recorded every 5 min throughout the five-day air sampling duration. The data were downloaded, and a five-day average was used in the data analysis. The mean relative humidity (±standard deviation) was 40.5 ± 13.5% in green homes and 41.8 ± 10.7% in non-green homes. The difference was not significant (*t*-test: $p = 0.323$). The respective values for temperature were 24.5 ± 1.9 °C and 24.6 ± 1.8 °C

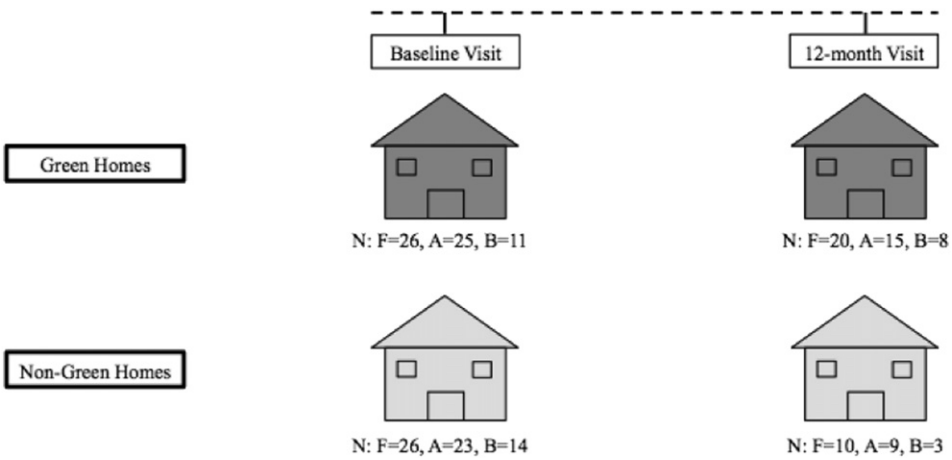

Fig. 1. The Cincinnati Green Housing Mycobiome study design. Homes were assessed at baseline (within four months post-renovation) and 12 months after baseline. The number of samples included in the analysis is indicated as Air (A), Bed (B), and Floor (F).