

A picture containing car, microwave, sitting, oven

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**Samuel Cochran**

**September 11, 2020 | 2:00-3:00 PM**

Zoom Meeting ID: 989 2470 8162

<https://osu.zoom.us/j/98924708162?pwd=VFF1WWNwOGFGd2kzZWN3RXQ0Z09uQT09>

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Abstract

Asthma development has been associated with childhood exposure to decreased fungal diversity. However, processes underlying this association are still not fully understood, nor is the impact of fungal diversity on asthma morbidity. The goal of this study is to test whether fungal diversity is inversely associated with neighborhood asthma prevalence and to assess diversity and specific fungal species in association with measures of asthma morbidity. Bedroom floor dust was collected from children aged 7-8 years old (n=349) living in higher (11-18%) and lower (3-9%) asthma prevalence neighborhoods. Fungal communities were analyzed using high-throughput DNA sequencing and quantitative polymerase chain reaction (qPCR). Neighborhood asthma prevalence was inversely associated with both fungal species richness (P=0.005) and Shannon diversity (P=0.01). Shannon diversity was inversely associated with more frequent asthma symptoms at age 7-8 (OR 0.72, P=0.017) and richness was inversely associated with asthma persistence to age 10-11 (OR 0.99, P=0.040). Analyses of individual fungal species did not show significant associations with asthma outcomes when adjusted for false discovery rates. In this New York City Cohort, fungal diversity was inversely associated with asthma prevalence as well as symptom frequency and persistence. No fungal species were associated with asthma outcomes, which is likely explained by a confluence of indoor environmental factors. The effect of these factors on indoor fungal exposures warrants further investigation in order to better characterize a healthy indoor microbiome.

Fungal diversity and individual fungal taxa in association with asthma prevalence and morbidity among school-age children in a New York City cohort

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