

EXECUTIVE SUMMARY

Memphis was named as the nation's top 3 "Asthma Capital" for five consecutive years (2011 to 2015). Moreover, Memphis has one of the highest percentages of substandard housing in the nation. Home environmental factors such as mold, allergens, dust mites, etc. are known to have a causal relationship with asthma and other respiratory illnesses. Indoor mold exposure has been studied extensively, and the results of scientific studies indicate that exposure can lead to increased severity of respiratory symptoms including asthma. Mold exposure does not necessarily have to be from the visible mold; exposure can also come from the invisible mold such as microscopic mold spores. The results of previous studies indicated that high-risk homes with exposure to high levels of molds would have a significant impact in developing respiratory illnesses.

In this project, we evaluated the burden of visible and invisible molds in residences in Memphis. Dust samples from participating homes (with or without visible mold issues) were collected using a specialized vacuum filter collector. To estimate the concentration and diversity of the molds, we extracted DNA from dust samples and performed metagenomic analysis by high-throughput sequencing of mold-specific internal transcribed spacer (ITS) genes, real-time PCR, followed by robust bioinformatics analysis.

Our metagenomic analysis has detected more than fifty different genera of molds which were predominant in house dust samples from both types of residences (with or without visible mold). We also analyzed samples for prominent mold species known to cause respiratory health effects. Pathogenic molds such as *Stachybotrys* spp. (black mold), *Alternaria alternate*, *Aspergillus niger*, *Chaetomium globosum*, *Cladosporium sphaerospermum* were detected in both types of homes.

This study underscores the need for continuous mold monitoring using sensitive and accurate methods (such as sequencing or PCR) that can detect potential mold contamination in homes regardless of the visual inspections.

Overall Objective

To evaluate the diversity and burden of major bacteria and mold genera in indoor dust samples collected from homes with or without visible molds in Memphis metropolitan.

Methods

- Microbial diversity was estimated by high throughput genetic sequencing techniques targeting bacteria and mold-specific genes from DNA samples extracted directly from dust.
- Gene targets for Next-Generation Sequencing (NGS) using Illumina MiSeq Platform:** For bacteria 16S rRNA, and for mold internal transcribed spacer (ITS)

Results

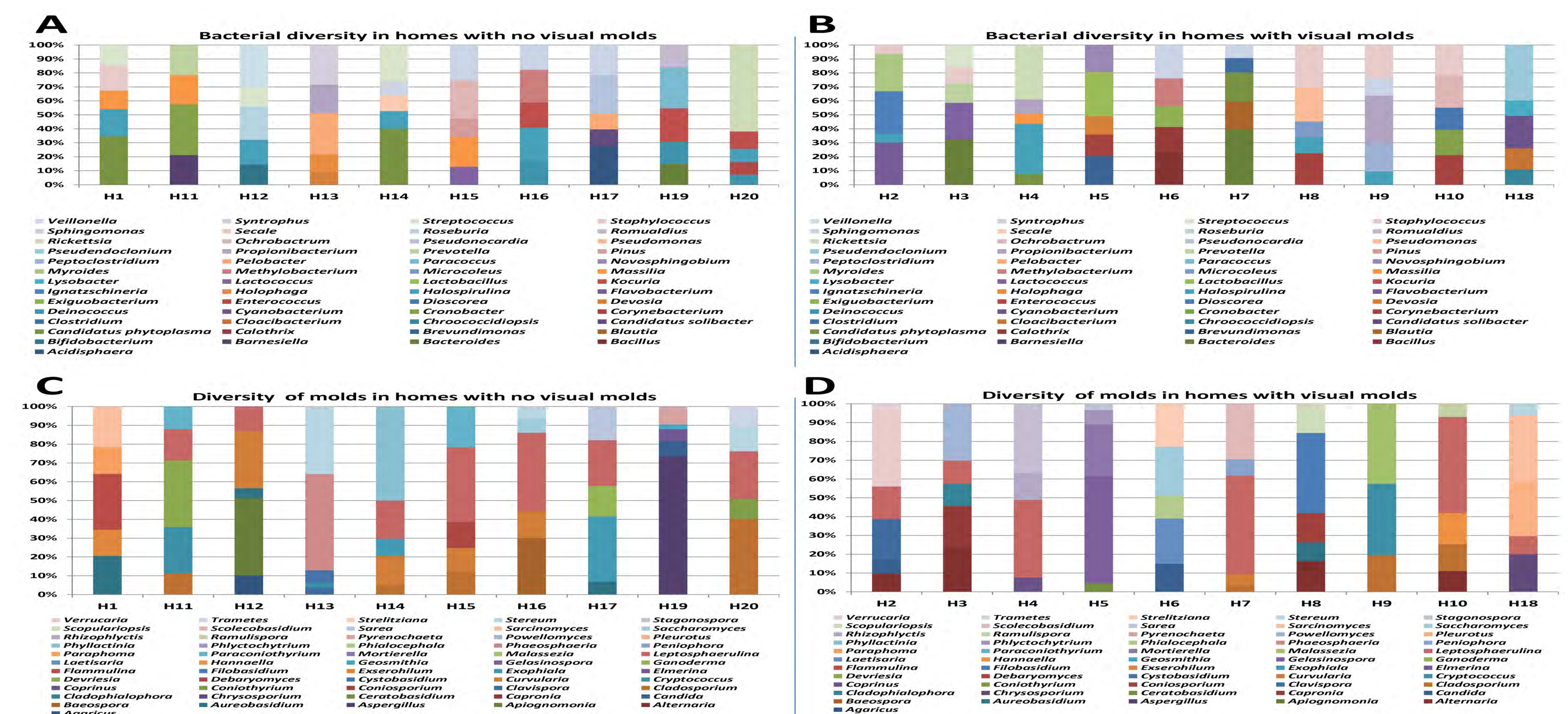


Figure 1. Diversity of major bacteria and mold genera in indoor dust samples collected from homes with or without visual molds in Memphis metropolitan. Panels A and B show relative abundance of most common bacterial genera. While panels C and D represent the relative abundance of major mold genera. Microbial diversity was estimated by high throughput genetic sequencing techniques targeting bacteria and mold-specific genes from DNA samples extracted directly from dust.

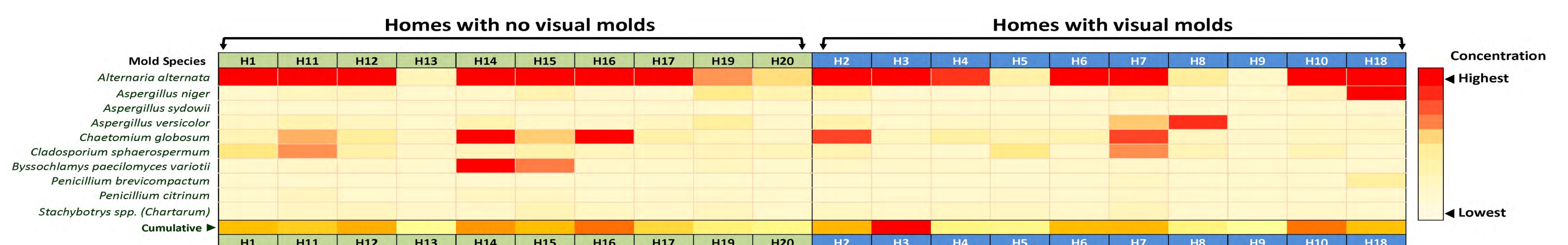


Figure 2. Concentration of mold species known to cause respiratory diseases in indoor dust samples collected from homes with or without visual molds in Memphis metropolitan. The heatmap shows concentrations of major respiratory disease causing molds found in dust samples. Mold concentration was estimated by high throughput genetic sequencing techniques targeting mold-specific internal transcribed spacer (ITS) genes from DNA samples extracted directly from dust.

Conclusions

Molecular techniques can reveal mold contamination in homes which the conventional visual inspections can not detect.

Acknowledgements: FedEx Institute of Technology provided partial financial support for the study