Integrated Healthy Homes Assessment and Intervention for Children in Memphis

Presented by:

Pratik Banerjee

Assistant Professor

Division of Epidemiology, Biostatistics, and Environmental Health

School of Public Health

University of Memphis

The Problem

- Two pediatric health issues
  - Allergic asthma and Lead poisoning

Poor housing

The Problem

- Memphis has one of the highest percentages of substandard housing in the nation
- Memphis was named as the nation's top 3 "Asthma Capital" for five consecutive years (2011 to 2015)

Mold exposure causes asthmatic and respiratory reactions in children and infants

Why bother about molds?

http://www.mobileoneservices.net/images/Water_Damage_Images/mold400_cartoon_edit.jpg

- Uniquely adaptable to temperature variances, and environmental terrains
- Does cause respiratory diseases and certain species can have toxic effects in humans, especially the vulnerable population
- Respiratory diseases/illnesses include but not limited to…Asthma, Allergies/ Allergic Rhinitis, Idiopathic Pulmonary Haemosiderosis, Chronic Obstructive Pulmonary Disease, Eye irritation, Cancer, Sudden Infant Death Syndrome, etc…
- Some pathogenic species include: *Alternaria alternate*, *Aspergillus fumigatus*, *Cladosporium herbarum*, *Penicillium spp.*, *Stachybotrys chartarum*

Justification

- 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 (Reponen *et al*., 2010)
- Developing a quantitative method to assess the burden of indoor mold and bacteria exposure

Specific Objective

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

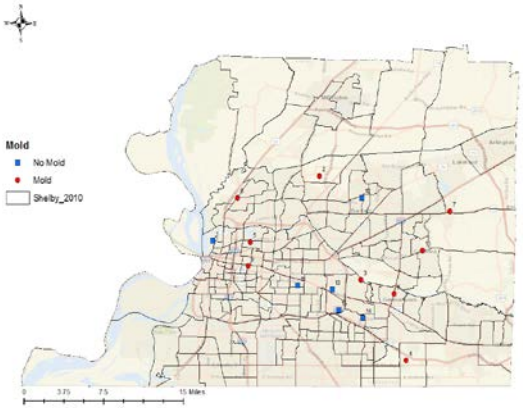
Technological Innovation

We have developed a “one stop” Environmental Monitoring Platform

- Rapid detection of multiple Indoor Environmental Quality (IEQ) parameters simultaneously

Methods - *Field Sampling*

- Dust samples from total 20 households
  - 10 homes with visible mold
  - 10 homes with NO visible mold
  - 1 week sampling period in each home
- Home walkthrough questionnaire survey was administered



SECTION I. DEMOGRAPHICS

1. What is your relationship to the child? (Check ONE)
2. ☐ Father
3. ☐ Mother
4. ☐ Grandfather
5. ☐ Grandmother

99. ☐ Other (please specify) _____

1. How old is your child? _____ years
   _____months

99. ☐ Don't Know
88. ☐ Refused to answer

Including yourself, how many adults 18 years or older live in this residence? Count anyone who spent at least 3 nights per week here for the last month or longer:
Number of adults_____
99. ☐ Don't Know

Do you have any kind of health care coverage, including health insurance, prepaid plans such as HMOs, or government plans such as Medicare?
☐ Yes
☐ No
99. ☐ Don't Know
☐ Refuse to answer

2.1 General respiratory symptoms

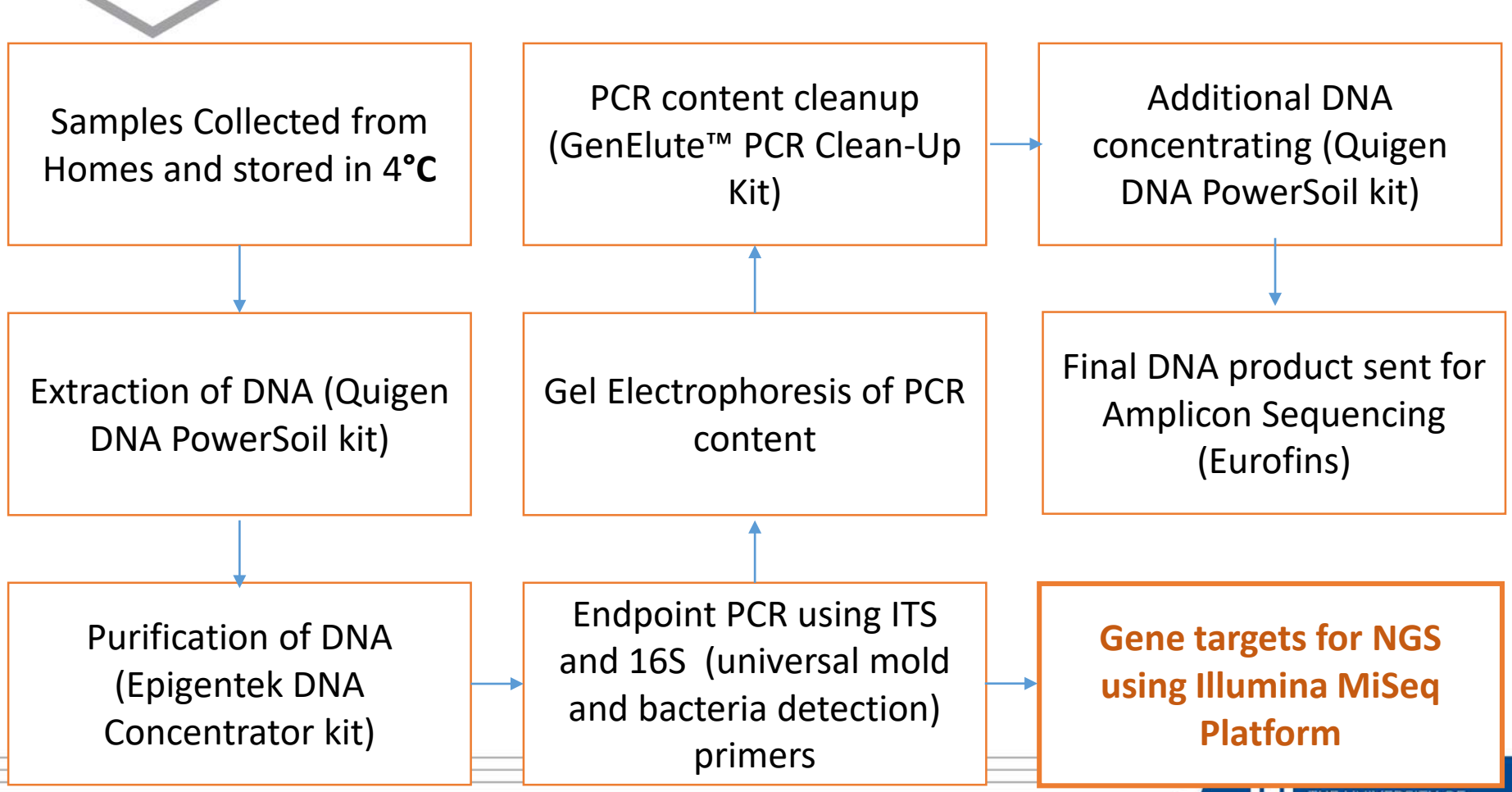
Has your child been diagnosed with asthma?
☐ Yes
☐ No
☐ Don't know

Has he/she ever experienced the following during the past 30 days while living in this home?
☐ Rashes
☐ Headaches
☐ Coughing
☐ Sneezing
☐ Sinus infections
☐ Eye irritation
☐ Don't know

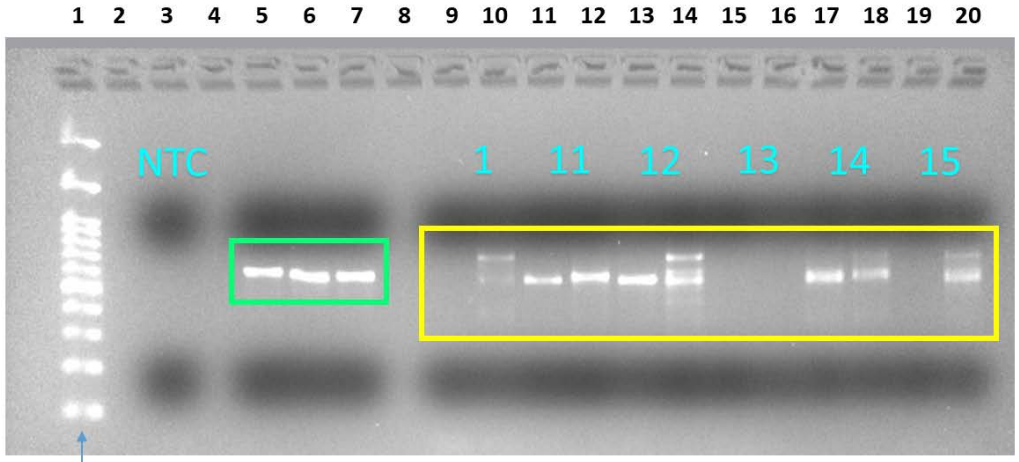
Does he/she have any of the following allergies in the past 30 days?
☐ Pollen (hay fever)
☐ Dust mite
☐ Mold
☐ Food allergies
☐ Don't know

Methods - *Post Field Sampling*

Molecular Detection and Next-Generation Sequencing (NGS)

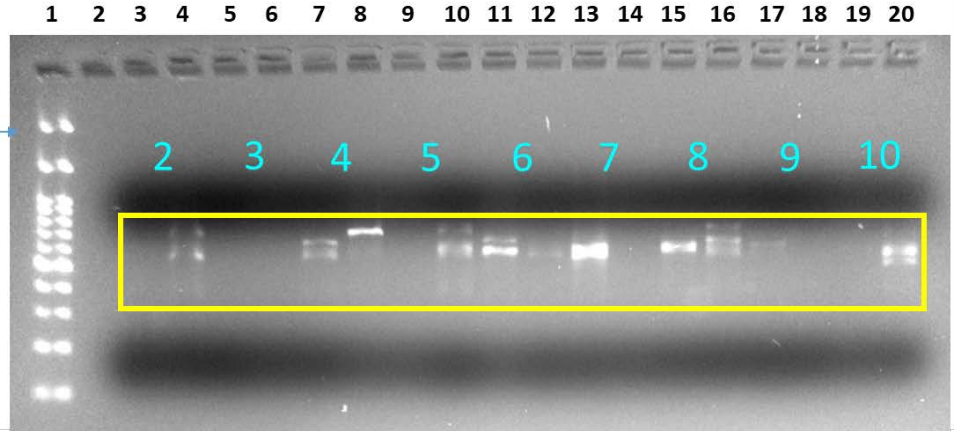


Results - *PCR ITS (molds)*



Homes with NO visible mold

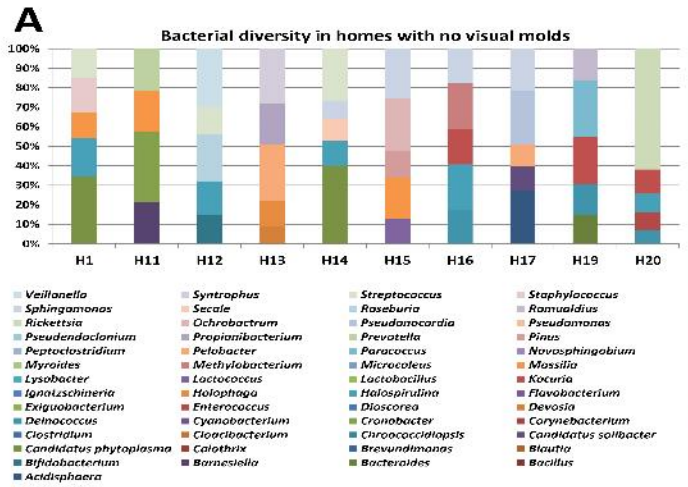
DNA ladder

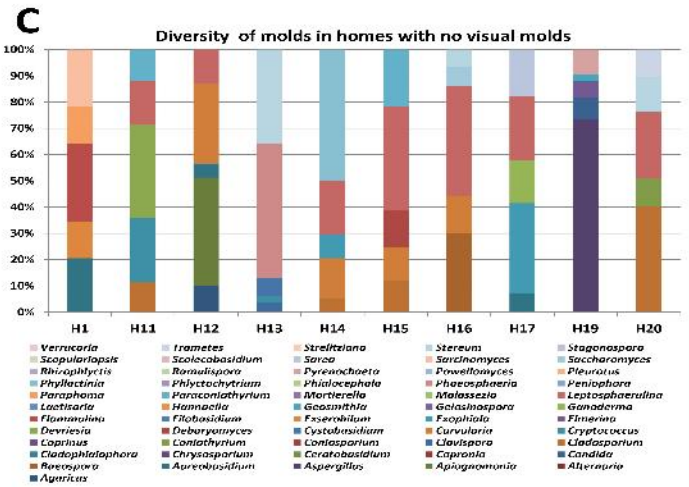


Homes with visible mold

Results - *NGS*

Diversity of major bacteria and mold genera in indoor dust

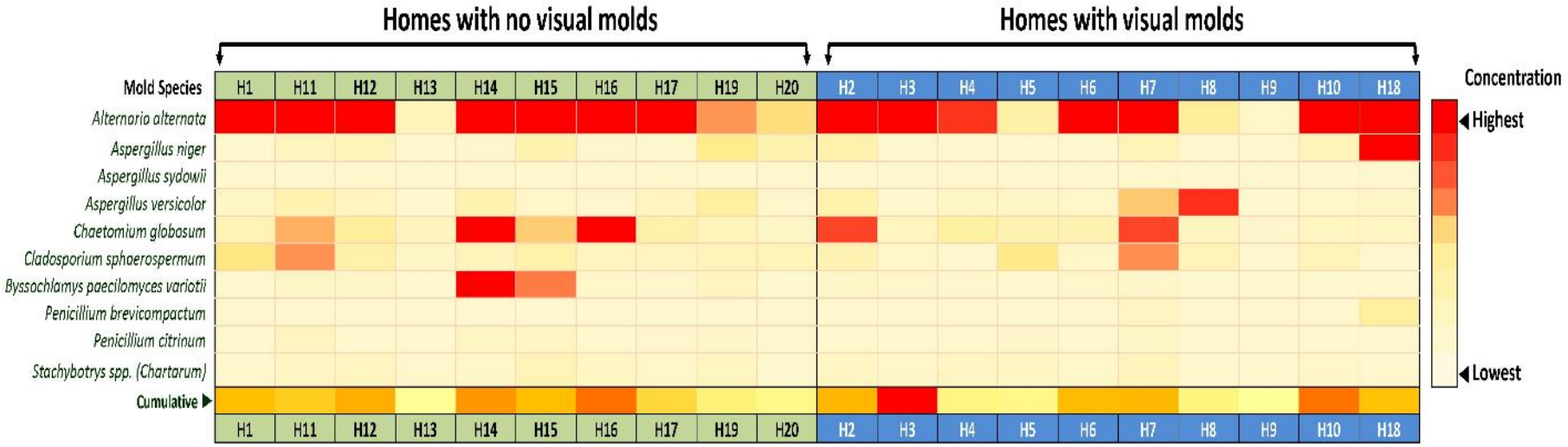




Panels **A** and **B** show relative abundance of most common bacterial genera. While panels **C** and **D** represent the relative abundance of major mold genera. Microbial diversity was estimated by high throughput genetic sequencing techniques targeting bacteria and mold-specific genes from DNA samples extracted directly from dust.

Results - *NGS*

Concentration of mold species known to cause respiratory diseases



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

Summary and Conclusions

- Pathogenic molds such as *Stachybotrys spp*. (black mold), *Alternaria alternate*, *Aspergillus niger*, *Chaetomium globosum*, *Cladosporium sphaerospermum* were detected in both types of homes.
- Molecular techniques can reveal mold contamination in homes which the conventional visual inspections can not detect.
- 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

Acknowledgements

- The study was conducted by University of Memphis MPH student **Bhavin Chauhan** under the supervision of UofM School of Public Health faculty members, Drs. **Pratik Banerjee** and **Chunrong Jia.**
- **Tavita Conway,** MBA (Collaborator) - LIP team. Ms. Conway is the Program Manager, and Lead Based Paint Inspector/ Risk Assessor working for the City Government.

- **FedEx Institute of Technology provided partial financial support for the study.**