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# EXPLORING INTERACTION NETWORKS OF INDOOR ENVIRONMENTAL MICROBIOME AND MYCOBIOME IN ASTHMATIC AND HEALTHY SUBJECTS: INSIGHTS FROM THE COBRA-ENV 2 STUDY

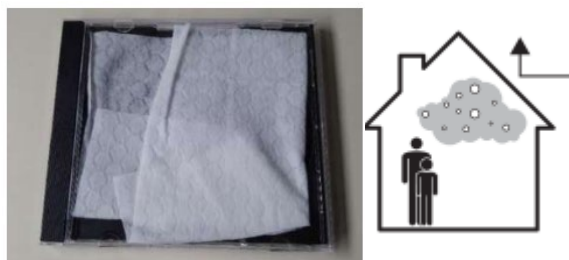
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## Methods:

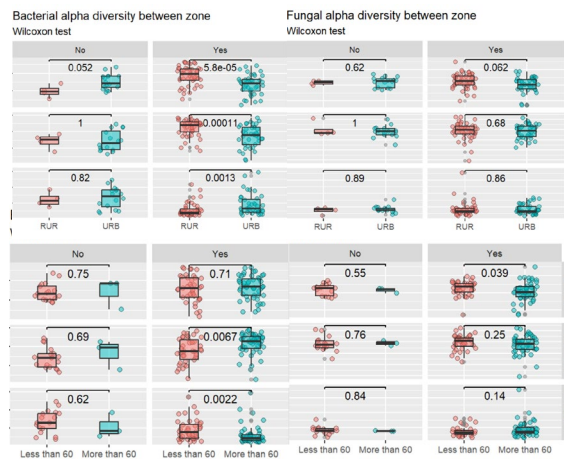
We enrolled 43 asthma patients from the national Cohort of Bronchial Obstruction and Asthma (COBRA) cohort and 20 controls (healthy individuals living in non-asthmatic, non-respiratory allergic households). We analyzed indoor microbial flora using electrostatic dust collectors (EDCs) under standardized conditions. Amplicon targeted metagenomics was employed to compare microbial communities from EDC samples.



Demographic (sex, age, municipality), environmental (rural/urban residence, humidity, coastal wetland proximity, pollen index, air quality) & indoor environmental characteristics (mold) were collected. Interaction networks were inferred for bacterial and fungal relative abundances in cases and controls, while considering significant demographic and environmental factors.

## Results:

The abundances of bacterial genera and fungal species were studied for both cases and controls. Age and rural/urban residence showed significant associations with alpha-diversity. Patients with asthma demonstrated reduced interactions both within and between kingdoms compared to controls.



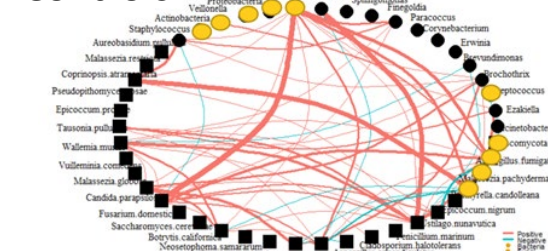
## Conclusions:

Our findings underscore the importance of understanding the interactions between indoor microbiome, mycobiome, and host in asthma pathogenesis.

## Cases



## Controls



## References:

- Chiquet et al. Variational inference for sparse network reconstruction from count data. ICML 2019.
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