

Indoor microbiome in homes of asthmatic children

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Respiratory health outcomes including asthma and allergy can be influenced by indoor microbiome which is ultimately shaped by home characteristics. Our studies on the effects of mold exposure on asthma development in the birth cohort of Cincinnati Childhood Allergy and Air Pollution Study (CCAAPS) showed that home moldiness (measured using the qPCR-based environmental relative moldiness index or ERMI), was associated with children's asthma development. Further, exposure to *Aspergillus ochraceus*, *A. unguis*, and *Penicillium variable* was significantly associated with asthma. We are currently investigating the levels of bacteria commonly found in indoor water-damaged environments in an effort to better understand the indoor bacterial contamination.

Forty-two homes from CCAAPS cohort were selected based on ERMI. Floor dust was vacuumed. Air samples were collected using a NIOSH 2-stage cyclone sampler for 24 hours. Bacterial DNA was extracted and measured with qPCR assays using bacteria-specific primers and TaqMan probes. Endotoxin was assayed by the *Limulus* amoebocyte lysate method.

Dust loading (cells/mg) of *Stenotrophomonas maltophilia*, a Gram negative bacterium, correlated with ERMI values ($r = 0.36$, $p < 0.05$), as well as with endotoxin ($r = 0.34$, $p < 0.05$), *Streptomyces* (genus) ($r = 0.56$, $p < 0.01$), and *Mycobacterium* (genus) ($r = 0.59$, $p < 0.01$) levels. A strong correlation was observed between *Streptomyces* and *Mycobacterium* ($r = 0.90$, $p < 0.01$), and their levels were significantly higher in homes with dogs. Airborne *S. maltophilia* levels were correlated with dust-borne concentrations ($r = 0.658$, $p = 0.015$).

S. maltophilia is the first bacterial species associated with higher ERMI values in homes. It presumably shares a similar nutrient source with the ERMI fungi, accounting for their communal existence in moisture-damaged areas. *Streptomyces* and *Mycobacterium* are found in varying degrees in soil. Ground trafficking by pets could transport outdoor sources indoors, and might explain the observed association between dog ownership and these particular bacterial species.