

Impact of household characteristics on the indoor microbiome

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Project Description

Over the past several decades we have seen an alarming increase in asthma and allergies in the United States and around the world. The “hygiene hypotheses” is one of the most intriguing suggestions for the cause of this rapid increase. This hypothesis suggests that our environment has become ‘too clean’ which could prevent our immune system from appropriately targeting and responding to allergens (pollens, pets, etc.) in our environment. We are now seeing new data that indicates that it may be the mix of early environmental exposures, such as microbes in our homes, that influences later allergy and asthma development.

With support from the National Institutes of Health, Rho, Inc., in Chapel Hill NC, is collaborating with the University of California at San Francisco, Johns Hopkins Medical School, Boston University Medical Center, Columbia University Medical School, Washington University at St Louis, and Second Genome in California to explore the importance of early home exposures in determining allergic diseases and asthma. To this end, beginning in 2005, 660 mothers during their third trimester of pregnancy were enrolled in a longitudinal birth cohort study to monitor the development of their children’s allergic disease status. Each of these families had a prior history of allergy that put their children at risk for developing allergies and/or asthma. Extensive data have been collected from these families and homes over the past 10 years, including repeated measures of home allergens and microbial exposures. During their first year of life, for a subset of more than 300 participants, home dust samples were collected. The bacterial 16S rRNA gene from the dust samples was sequenced and revealed more than 50,000 distinct microbial exposures. Our initial studies show the mix (diversity and richness) of microbial exposures in the home may be an important determining factor in allergy and asthma development.

In this project we hope to examine a key underlying question regarding this relationship, namely, ***what are the factors and characteristics of these families and their homes that determine the microbial exposure mix we have found in their homes?***

We are hoping that statistical and mathematical methods can be employed to help us understand whether specific bacterial communities, or discrete taxa within these communities, are associated with the characteristics of the household and its occupants. A better understanding of these relationships may ultimately result in adapting the design of buildings and control of exposures to promote healthier environments and reduce allergy and asthma among children at risk.

Citation

Lynch, Susan V., et al. "Effects of early-life exposure to allergens and bacteria on recurrent wheeze and atopy in urban children. *Journal of Allergy and Clinical Immunology* 134.3 (2014): 593-601.

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