Human Migration and Resuspension: The Microbial Community Dynamics of the Indoor Built Environment

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Abstract: The interplay between humans and built environments is a new frontier for microbial ecology. Approximately 90% of human activities are performed indoors, and the diversity of the inanimate microbiome has been estimated at the level of trillions of microorganisms. Human migration and other anthropogenic activities contribute to spatial and temporal variation of indoor microbial communities. One source of diversity for air samples is microbial resuspension (i.e., the surface to air release of biotic and abiotic particulate matter) following a disturbance event, such as anthropogenic traffic. Previous studies have investigated resuspension during human occupancy and with different flooring materials. However, prior research has not sufficiently integrated flooring structure, human-mediated resuspension, and phylogenetic analysis. Our study examined the effect of surface composition and human traffic intensity on the taxonomic composition of airborne microbial communities. We hypothesized that the greatest quantity and diversity of microorganisms would be present in the carpeting and high human activity samples. More broadly, we anticipate that our data will help to elucidate the role of building design in modulating microbial resuspension dynamics induced by human traffic patterns between indoor and outdoor environments. In a college academic building, 24 air samples were collected over carpeting during high (n=6) and low (n=6) human activity periods and over linoleum during high (n=6) and low (n=6) activity. DNA was extracted, amplified using prokaryotic 16S primers, sequenced using the Illumina MiSeq platform, and analyzed with the Qualitative Insights into Microbial Ecology statistical package. While only preliminary data analysis has been completed, 227 sequences were yielded across 15 samples. Sequence richness was found to be statistically greater for high activity samples in comparison to low activity samples ($p<0.05$). All samples yielded much lower microbial diversity than expected, which may be attributed to DNA extraction or sampling protocols.

Introduction:

- Microbial ecology applies ecological principles of diversity to microorganisms interacting within a given area, known as a microbiome[1,2]
- Studies of indoor microbiomes provide insight into pathogen dispersal and building design[2,3]
- Dispersal mechanisms serve as sources of diversity[4]
- Anthropogenic disturbances have been linked to dispersal via microbial resuspension:
  - Human activity correlated to resuspension of particulate matter[5] and human/outdoor-associated taxonomic groups[6,7,8]
  - Particle resuspension rates elevated with carpeting and depressed with metal flooring[9]

Current Study Rationale:

- Most investigations focus solely on abiotic components of air and a single flooring type
- Rise of high-throughput, culture-independent sequencing greatly facilitates taxonomic analysis

Objective:

How is the phylogenetic profile of indoor air influenced by variations in flooring type and human activity?

Materials and Methods:

- Air sample collection in a college academic building
- Two variables and four treatments (N=24):

6 High Activity/Carpeting	**6 High Activity/Linoleum**
6 Low Activity/Carpeting	**6 Low Activity/Linoleum**

- 0.45 μm filter membrane DNA extraction
- 16S rRNA Illumina tag PCR to amplify V4 region
- Sequenced using the Illumina MiSeq Platform
- Analysis via Qualitative Insights into Microbial Ecology statistical package

Results:

- Pre-PCR DNA concentrations: Range of 0.024 – 0.08 ng/μL
- Post-Quality Filtering: 227 sequences across 15 samples, 9 samples yielded no sequences
- Average Q score >30 across 250 base reads (equiv. to 99.9% nucleotide accuracy)

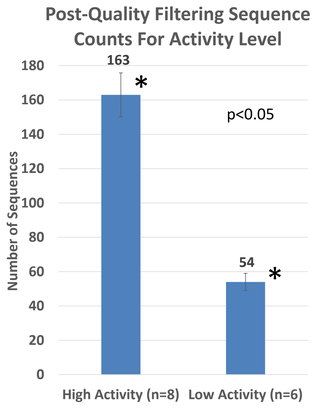

Figure 1: Number of sequences across activity conditions. Quantities significantly different for high activity versus low activity ($p<0.05$).

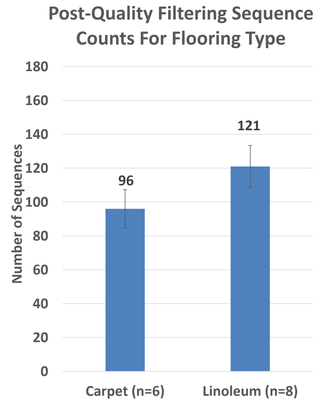

Figure 2: Number of sequences across flooring conditions. No significant difference in sequence quantity when comparing flooring type.

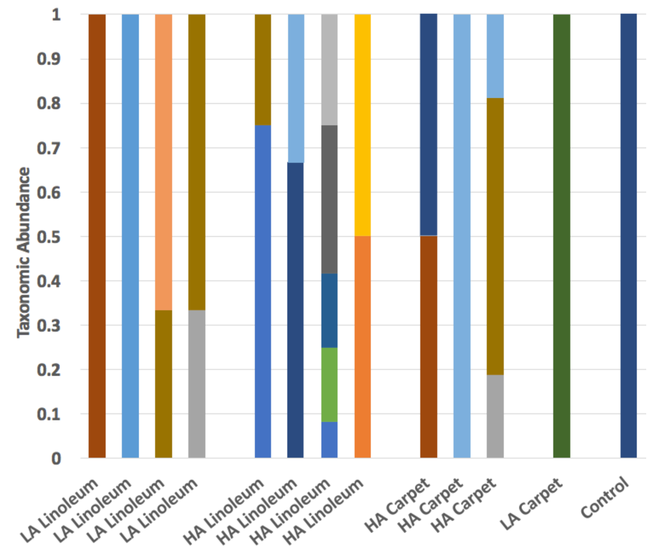

Figure 3: Genera Abundances Across Sampling Conditions, HA = high activity and LA = low activity

Results (Continued):

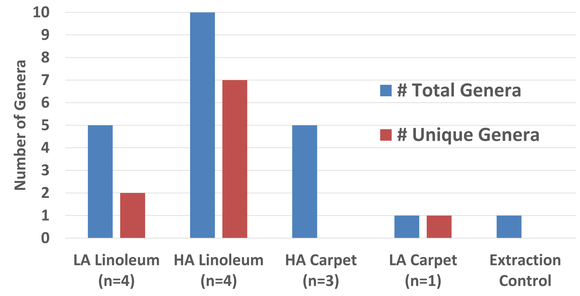

Figure 4: Total Genera/Unique General Across Sampling Conditions

Discussion:

- No substantial conclusions possible from data set
- Significant difference in terms of sequence abundance between activity conditions
- Few sequences yielded suggests errors with DNA extraction or sample collection
  - Statistical power limitations
- Need to optimize duration and flow rate of sample collection in future experiments
- Will continue analysis of alpha and beta diversity indices for samples

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References:

1. Konopka, A. (2009). What is microbial ecology? *The ISME Journal, 3*, 1223-1230.
2. Kembel, S. W., Jones, E., Kline, J., Northcutt, D., Stenson, J., Womack, A. M., Bohannan, B. J., Brown, G. Z., & Green, J. L. (2012). Architectural design influences the diversity and structure of the built environment microbiome. *The ISME Journal, 6*, 1469-1479.
3. Kembel, S. W., Meadow, J. F., O'Connor, T. K., Mhuireach, G., Northcutt, D., Kline, J., Moriyama, M., Brown, G. Z., Bohannan, B. J., & Green, J. L. (2014). Architectural design drives the biogeography of indoor bacterial communities. *PLOS ONE, 9*(1), 1-10.
4. Hughes Martiny, J. B., Bohannan, B. J., Brown, J. H., Colwell, R. K., Fuhrman, J. A., Green, J. L., Horner-Devine, M. C., Kane, M., Krumins, J. A., Kuske, C. R., Morin, P. J., Naeem, S., Ovreas, L., Reysenbach, A., Smith, V. H., & Staley, J. T. (2006). Microbial biogeography: Putting microorganisms on the map. *Nature Reviews Microbiology, 4*, 102-112.
5. Schneider, T. (2008). Dust and fibers as a cause of indoor environmental problems. *Scandinavian Journal of Work, Environment & Health Supplement*, 4, 10-17.
6. Qian, J., Hospodsky, D., Yamamoto, N., Nazaroff, W., & Peccia, J. (2012). Size-resolved emission rates of airborne bacteria and fungi in an occupied classroom. *Indoor Air*, 22, 339-351.
7. Hospodsky, D., Qian, J., Nazaroff, W. W., Yamamoto, N., Bibby, K., Rismani-Yazdi, H., & Peccia, J. (2012). Human occupancy as a source of indoor airborne bacteria. *PLOS ONE, 7*(4), 1-10.
8. Meadow, J. F., Altrichter, A. E., Kembel, S. W., Kline, J., Mhuireach, G., Moriyama, M., Northcutt, D., O'Connor, T. K., Womack, A. M., Brown, G. Z., Green, J. L., & Bohannan, B. J. (2014). Indoor airborne bacterial communities are influenced by ventilation, occupancy, and outdoor air source. *Indoor Air*, 24, 41-48.
9. Mukai, C., Siegel, J. A., & Novoselac, A. (2009). Impact of airflow characteristics on particle resuspension from indoor surfaces. *Aerosol Science and Technology*, 43, 1022-1032.