

Prevalence of antibiotic resistance genes within indoor environments: athletic facility case study

Institute for Health in the Built Environment - <https://buildhealth.uoregon.edu/>

Biology in the Built Environment Center (BioBE Center) -

Prof. Kevin Van Den Wymelenberg, PhD

With Gwynne Mhuireach, PhD

Background

The spread of antibiotic resistance genes is exacerbated by the widespread use of antimicrobial chemicals, which are prevalent in building materials and personal care products. Unlike antibiotic drugs, antimicrobials leave long-lasting residues and can accumulate in the environment. Triclosan, a commonly used antimicrobial, can promote the development of resistance itself. In the environment, triclosan resistance increases in microbial communities that are exposed to higher concentrations of the chemical. Dust serves as a time-integrated record of organisms in indoor bioaerosols and a repository in which antimicrobial compounds accumulate, thus a potentially selective environment for antibiotic resistance. Prior BioBE Center research has shown that within a building, the dust microbiome is largely shaped by its space type and usage pattern (Kembel et al. 2014). We aim to determine the generalization of this pattern within a mixed-used athletic facility and evaluate the relationship between antimicrobial compounds and the associated microbial communities in dust samples. We expect that the usage of antimicrobial compounds, and thus the resulting concentrations in dust, will vary significantly with space type (e.g. office vs. locker room) and will be affected by building envelope tightness and ventilation. We expect that increased abundance of antimicrobial compounds in dust will correlate with increased expression of antibiotic resistant genes in bacteria.

Experimental Design / Data Overview:

We collected 44 dust samples from a mixed-use athletic and educational facility. Dust samples were subdivided for chemical and DNA extraction and examined using liquid chromatography tandem mass spectrometry (LC- MS/MS) and next-generation nucleic acid sequencing. Specifically, we amplified and sequenced genomic DNA using the Earth Microbiome Project barcoded primer set, adapted for Illumina HiSeq2000 and MiSeq, and we performed shotgun metagenomic sequencing on Illumina NextSeq 500 in high output, paired-end 150 mode. We aim to integrate metagenomic profiles with architectural metadata and chemical data using multivariate linear modeling to determine if and how architectural attributes such as ventilation system, relates to indoor antibiotic resistance profiles and whether the types and quantities of antibacterial compounds present in dust are correlated with the dust resistome.

Research Questions / Hypotheses

- 1) the composition of the resistome and/or the microbiome correlate with the concentration of antimicrobial chemicals
- 2) the abundance of specific antibiotic resistance genes correlates with the concentration of antimicrobial chemicals
- 3) architectural infiltration and mechanical ventilation rates correlate with concentration of antimicrobial chemicals

Goals for the project:

Explore the dataset, test the hypotheses by integrating chemical, biological, and architectural data, determine a storyline worthy of publication, share the story with university athletic facility leadership, publish the results in a deidentified manner, impact the emerging field of healthy building design and operations.

Suggested Reading:

- Fahimipour, A.K., Ben Mamar, S., McFarland, A.G., Blaustein, R.A., Chen, J., Glawe, A.J., Kline, J., Green, J.L., Halden, R.U., Van Den Wymelenberg, K., Huttenhower, C., Hartmann, E.M., 2018. Antimicrobial Chemicals Associate with Microbial Function and Antibiotic Resistance Indoors. *mSystems* 3. <https://doi.org/10.1128/mSystems.00200-18>
- Hartmann, E.M., Hickey, R., Hsu, T., Betancourt Román, C.M., Chen, J., Schwager, R., Kline, J., Brown, G.Z., Halden, R.U., Huttenhower, C., Green, J.L., 2016. Antimicrobial Chemicals Are Associated with Elevated Antibiotic Resistance Genes in the Indoor Dust Microbiome. *Environmental Science & Technology* 50, 9807–9815. <https://doi.org/10.1021/acs.est.6b00262>
- Kembel, S.W., Meadow, J.F., O'Connor, T.K., Mhuireach, G., Northcutt, D., Kline, J., Moriyama, M., Brown, G.Z., Bohannon, B.J.M., Green, J.L., 2014. Architectural Design Drives the Biogeography of Indoor Bacterial Communities. *PLoS ONE* 9, e87093. <https://doi.org/10.1371/journal.pone.0087093>