New papers on microbiology of the built environment, September 6, 2015

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Here are the microbiology of the built environment papers that were already featured on my MicrobiomeDigest blog this week, all in one handy edition. The first paper is about dust, so Siouxsie & The Banshees – Cities In Dust would match perfectly.

The ecology of microscopic life in household dust – Albert Barberán – Proceedings B

Here, we investigated the fungal and bacterial communities found in settled dust collected from inside and outside approximately 1200 homes located across the continental US, homes that represent a broad range of home designs and span many climatic zones. (…) In particular, the female : male ratio and whether a house had pets had a significant influence on the types of bacteria found inside our homes highlighting that who you live with determines what bacteria are found inside your home.

Coexistence of lactic acid bacteria and potential spoilage microbiota in a dairy-processing environment – Giuseppina Stellato – Applied and Environmental Microbiology

In this study, the microbiota in a dairy plant was studied both by 16S rRNA and 26S rRNA – based culture-independent high-throughput amplicon sequencing. Environmental samples from surfaces and tools were studied along with the different types of cheese produced in the same plant. (…) Beta-diversity analyses showed a clear separation of environmental and cheese samples based on both yeast and bacterial community structure.

Microbiological consequences of indoor composting – Alexandre Naegele – Indoor Air

The aim of this study was to evaluate the microbiological contamination around organic waste bins at three distances over a 12-month period. Contamination near the customary trash of control households was evaluated at the beginning to ensure that there is no recruitment bias. Air samples using the MAS 100 impactor were carried out in 38 dwellings that do household waste composting and in 10 dwellings of controls. Collection of particles by CIP 10 rotating cup sampler and dust samples collected by electrostatic dust collector cloths were acquired in dwellings that do household waste composting. Samples were analyzed by culture and by real time quantitative PCR.

A Pilot Study on Integrating Videography and Environmental Microbial Sampling to Model Fecal Bacterial Exposures in Peri-Urban Tanzania – Timothy R. Julian – PLOS ONE

In the present study, we collected activity data and microbiological sampling data to develop a quantitative microbial exposure model for two female caretakers in peri-urban Tanzania. Activity data were combined with microbiological data of contacted surfaces and fomites (e.g. broom handle, soil,
clothing) to develop example exposure profiles describing second-by-second estimates of fecal indicator bacteria (E. coli and enterococci) concentrations on the caretaker’s hands.

**Bacterial Communities and Midgut Microbiota Associated with Mosquito Populations from Waste Tires in East-Central Illinois** – Chang-Hyun Kim – Journal of Medical Entomology

We used culture-dependent and culture-independent techniques to characterize the bacterial composition and abundance in water and midgut samples of larval and adult females of Aedes japonicus (Theobald), Aedes triseriatus (Say), and Culex restuans (Theobald) collected from waste tires at two wooded study sites in Urbana, IL.

**Hospital’s Hidden Environmental Hazards: Probing the Microbiome** – BioScience

(…) researchers have been tackling dangerous superbugs with little fanfare. Among the newest of these efforts is the Hospital Microbiome Project (HMP), funded by the Sloan Foundation. The project aims to make hospitals safer by understanding the basic ecology of microbial communities that live in healthcare settings.

**Pyrosequencing analysis of bacterial communities in biofilms from different pipe materials in a city drinking water distribution system of East China** – Hongxing Ren – Applied Microbiology and Biotechnology

In this study, ten biofilm samples from different pipe materials, including ductile cast iron pipe (DCIP), gray cast iron pipe (GCIP), galvanized steel pipe (GSP), stainless steel clad pipe (SSCP), and polyvinyl chloride (PVC), were collected from an actual DWDS to investigate the effect of pipe material on bacterial community. Real-time quantitative polymerase chain reaction (qPCR) and culture-based method were used to quantify bacteria. 454 pyrosequencing was used for bacterial community analysis.

**Thesis: The building science of office surfaces: implications for microbial community succession** – Mahnaz Zare – University of Toronto

The Surface Project studied the microbial succession on office surfaces in nine offices in three North American cities. Building science parameters including relative humidity (RH), temperature, equilibrium relative humidity (ERH), illumination, and occupancy were measured to investigate their impact on microbial communities.

**Anthropogenic activities drive the microbial community and its function in urban riverine sediment** – Xu Zhang – Journal of Soils and Sediments

We compared the community structure and abundance of C, N and S transformation-related functional microorganisms along two rivers in south-eastern China that flow through three typical anthropogenic zones corresponding to agricultural, residential and industrial areas.