Microbes in the house

Fungal and bacterial growth in floor dust at elevated relative humidity levels — Karen C. Dannemiller — Indoor Air ($6 to rent, $38 to own)

Under sustained, elevated building moisture conditions, bacterial and fungal growth occurs. The goal of this study was to characterize microbial growth in floor dust at variable equilibrium relative humidity (ERH) levels. (...) Quantitative PCR and DNA sequencing of ribosomal DNA for bacteria and fungi were used to quantify growth and community shifts. Over a one week period, fungal growth occurred above 80% ERH. (...) Comparisons between fungal taxa incubated at different ERH levels revealed more than 100 fungal and bacterial species that were attributable to elevated ERH. Resuspension modeling indicated that more than 50% of airborne microbes could originate from the resuspension of fungi grown at ERH levels of 85% and above.

Molecular investigation of bacterial communities: Data from two frequently used surfaces in the SÃ£o Paulo Institute of Tropical Medicine – Tairacan Augusto Pereira da Fonseca – Data in Brief (OA)

This article contains data on the bacterial population of two frequently used surfaces in the SÃ£o Paulo Institute of Tropical Medicine (ITM) using the Illumina sequencing for massive parallel investigation of the bacterial 16S ribosomal RNA gene. Surface samples were obtained from restroom surfaces and the fingerprint door clock system. Mothur package and Shannon-ace-table.pl software programs (Chunlab Inc.: Seoul, Korea) were used to compute the diversity indices of bacterial community. The sequencing data from both surfaces have been uploaded to Zenodo: http://dx.doi.org/10.5281/zenodo.47709
The prevalence of foodborne pathogenic bacteria on cutting boards and their ecological correlation with background biota – Noor-Azira Abdul-Mutalib – AIMS Microbiology (OA)

This study implemented the pyrosequencing technique and real-time quantitative PCR to determine the prevalence of foodborne pathogenic bacteria (FPB) and as well as the ecological correlations of background biota and FPB present on restaurant cutting boards (CBs) collected in Seri Kembangan, Malaysia. The prevalence of FPB in high background biota (HBB) was lower (0.24%) compared to that of low background biota (LBB) (0.54%). In addition, a multiple linear regression analysis indicated that only HBB had a significant ecological correlation with FPB. Furthermore, statistical analysis revealed that the combinations of Clostridiales, Flavobacteriales, and Lactobacillales orders in HBB had significant negative associations with FPB, suggesting that these bacteria may interact to ensure survivability and impair the growth of pathogenic bacteria.

Microbes on buildings

Profile of microbial communities on carbonate stones of the medieval church of San Leonardo di Siponto (Italy) by Illumina-based deep sequencing – Guglielmina Chimienti – Applied Microbiology and Biotechnology ($39.95)

Comprehensive studies of the biodiversity of the microbial epilithic community on monuments may provide critical insights for clarifying factors involved in the colonization processes. We carried out a high-throughput investigation of the communities colonizing the medieval church of San Leonardo di Siponto (Italy) by Illumina-based deep sequencing. The metagenomic analysis of sequences revealed the presence of Archaea, Bacteria, and Eukarya. Bacteria were Actinobacteria, Proteobacteria, Bacteroidetes, Cyanobacteria, Chloroflexi, Firmicutes and Candidatus Saccharibacteria. (...) The results highlighted a structured community, showing low diversity, made up of extremophile organisms adapted to desiccation and UV radiation. Notably, the microbiome appeared to be composed not only of microorganisms possibly involved in biodeterioration but also of carbonatogenic bacteria, such as those belonging to the genus Arthrobacter, which could be useful in bioconservation. Our investigation demonstrated that molecular tools, and in particular the easy-to-run next-generation sequencing, are powerful to perform a microbiological diagnosis in order to plan restoration and protection strategies.

Microbes and stormwater ponds

Site-specific environmental factors control bacterial and viral diversity in stormwater retention ponds – Matthew A. Saxton – Inter-Research in Aquatic Microbial Ecology (subscription required, no price listed)
Stormwater retention ponds are ubiquitous in urban and suburban landscapes of the United States. Most studies of the microbiology of these ponds have focused on the abundance and removal efficiency of fecal indicator bacteria. Here we provide the first comprehensive study of microbial community diversity and activity in these ponds, and assess how different environmental and engineering factors influence these communities. (…) Collectively, our results indicate that the environmental conditions and microbial communities of these ponds vary greatly, even among ponds in close spatial proximity, and that pond microbial communities appear to be shaped by site-specific environmental factors.

Microbes on the farm

A buried Neolithic paddy soil reveals loss of microbial functional diversity after modern rice cultivation – Yong-Guan Zhu – Science Bulletin ($39.95)

It has been documented that human activities are causing the rapid loss of taxonomic, phylogenetic, genetic and functional diversity in soils. However, it remains unclear how modern intensive rice cultivation impacts the soil microbiome and its functionality. Here we examined the microbial composition and function differences between a buried Neolithic paddy soil and an adjacent, currently-cultivated paddy soil using high throughput metagenomics technologies. Our results showed that the currently cultivated soil contained about 10-fold more microbial biomass than the buried one. Analyses based on both 16S rRNA genes and functional gene array showed that the currently cultivated soil had significantly higher phylogenetic diversity, but less functional diversity than the buried Neolithic one. (…) This study implies that, modern intensive rice cultivation has substantially altered soil microbial functional structure, leading to functional homogenization and the promotion of soil ecological functions related to the acceleration of nutrient cycling which is necessary for high crop yields.

Microbes and pollution

reduced inorganic or organic compounds, including soluble ferrous ion, reduced inorganic sulfur compounds (RISC) and acid-stable organic compounds. By-products of these oxidative processes, such as soluble ferric ion and sulfuric acid create favourable chemical conditions for leaching. This review is focused on the behaviour of common bioleaching microorganisms, their responses to changing pH in an industrial setting, and how both changes and microbial responses can impact the micro and macro environment.

Bacterial community composition and structure in an Urban River impacted by different pollutant sources – A. Mark Ibekwe – Science of The Total Environment ($41.95)

Microbial communities in terrestrial fresh water are diverse and dynamic in composition due to different environmental factors. The goal of this study was to undertake a comprehensive analysis of bacterial composition along different rivers and creeks and correlate these to land-use practices and pollutant sources. Here we used 454 pyrosequencing to determine the total bacterial community composition, and bacterial communities that are potentially of fecal origin, and of relevance to water quality assessment. (…) Our results suggest that microbial community compositions were influenced by several environmental factors, and pH, NO₂, and NH₄ were the major environmental factors driving FIB in surface water based on CCA analysis, while NO₃ was the only factor in sediment.

Chronic exposure to triclosan sustains microbial community shifts and alters antibiotic resistance gene levels in anaerobic digesters — Daniel Carey — Environ Science: Processes Impacts (subscription required, no price listed)

(…) In this study, the impacts of chronic triclosan (TCS) exposure on antibiotic resistance genes (ARGs) and microbial community structure were assessed in lab-scale anaerobic digesters. TCS concentrations from below detection to 2500 mg/kg dry solids were amended into anaerobic digesters over 110 days and acclimated for >3 solid retention time values. (…) Little to no impact of TCS was observed on intI1 relative abundance. Microbial communities were also surveyed by high-throughput 16S rRNA gene sequencing. Compared to the control digesters, significant shifts in community structure towards clades containing commensal and pathogenic bacteria were observed in digesters containing TCS. Based on these results, TCS should be included in studies and risk assessments that attempt to elucidate relationships between chemical stressors (e.g. antibiotics), antibiotic resistance genes, and public health.

Pyrosequencing analysis of bacterial diversity in soils contaminated long-term with PAHs and heavy metals: Implications to bioremediation — Saranya Kuppusamy — Journal of Hazardous Materials ($41.95)
Diversity, distribution and composition of bacterial community of soils contaminated long-term with both polycyclic aromatic hydrocarbons (PAHs) and heavy metals were explored for the first time following 454 pyrosequencing. Strikingly, the complete picture of the Gram positive (+ve) and Gram negative (−ve) bacterial profile obtained in our study illustrates novel postulates that include: (1) Metal-tolerant and PAH-degrading Gram −ves belonging to the class Alphaproteobacteria persist relatively more in the real contaminated sites compared to Gram +ves, (2) Gram +ves are not always resistant to heavy metal toxicity, (…) Thus, the most promising indigenous Gram +/-ve strains from the long-term contaminated sites with increased catabolic potential, enzymatic activity and metal tolerance need to be harnessed for mixed contaminant cleanups.