



# Microbial Ecology Exemplifies Building Ecology

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## SUMMARY

Recent advances in molecular methods have dramatically improved knowledge of the microbial communities and their diversity in indoor environments. We have retrieved over 150 references with results of indoor microbial investigations and environmental factors. Representative papers are summarized here. The results show that buildings are complex, ecosystem-like, and that collaboration between microbial ecologists and indoor environment scientists is an important emerging trend that will help us understand building ecology.

## KEYWORDS

*Indoor environment, microbiology, ventilation, molecular biology, culture-independent methods.*

## INTRODUCTION

Over three decades of molecular-phylogenetic studies, researchers have compiled an increasingly robust map of evolutionary diversification showing that the main diversity of life is microbial, distributed among three primary relatedness groups or domains: Archaea, Bacteria, and Eukarya. The application of molecular-phylogenetic methods to study natural microbial ecosystems without the traditional requirement for cultivation has resulted in the discovery of many unexpected evolutionary lineages; members of some of these lineages are only distantly related to known organisms but are sufficiently abundant that they are likely to have impact on the chemistry of the biosphere. (Pace, 1997)

Recent advances in molecular methods have dramatically improved knowledge of the microbial communities and their diversity in indoor environments. Molecular methods are useful to identify bacteria (and other microbes) in water damaged homes and other buildings and to characterize seasonal variations in community compositions of microbial species. These recent advances suggest great potential for rapidly advancing knowledge related to microbial communities in buildings. Such advances should be driven by microbiologists working with building scientists. (Corsi, 2012)

The inter-relationships between the physical, chemical and biological environments are dynamic and characterized by multiple pathways. Microbial ecology is an often slow but constantly evolving process in a building, as it is in nature. Survival, replication, evolution, and pathogenicity or toxicity of microbial species may be strongly affected by environmental conditions. Temperature, humidity, surface moisture and pH, air movement, ventilation, and nutrient availability may determine what microbes are present and what their state is. When stressed their metabolism changes and they emit different chemicals (e.g., microbial volatile organic compounds - MVOCs) from those emitted by healthy, thriving organisms.

Buildings are complex ecosystems that house trillions of microorganisms interacting with each other, with humans and with their environment. Understanding the ecological and evolutionary processes that determine the diversity and composition of the built environment microbiome—the community of microorganisms that live indoors—is important for understanding the relationship between building design and operation, biodiversity and human health.

Bacteria from the human biome dominate the bacterial species found indoors. There are roughly ten times as many bacteria on our environmentally exposed surfaces (dermal, respiratory, and gastrointestinal) as there are cells in our bodies (Bassler, 2009). Personal characteristics ranging from genetic to environmental, and from diet to hygiene may influence the flora found on/in the human biome.

We are interested in the environmental determinants of the microbial ecology of the indoor environment. In particular, we seek to identify and elucidate the relationships between indoor environmental parameters and the biodiversity and community structure of species present in both the occupied and non-occupied spaces of buildings. We seek information on sources of microbes found indoors, common substrates, and temporal and spatial distributions of microorganisms. The purpose of this investigation is 1) to assist microbial ecologists to prioritize environmental parameter measurements in the planning of environmental sampling and 2) to enhance understanding of environmental factors that influence microbial ecology. The results are expected to lead to more effective control of microbial populations through manipulation of indoor environmental design, construction and control.

Our research has focused on literature reporting indoor microbial ecology together with environmental data. We have accumulated a database of ca. 150 articles. We are organizing the data by organism and the associated environmental characteristics. Here we present a review of representative publications suggesting the range of work recently and currently underway.

## **OVERVIEW**

Remarkably, building function has no significant effect on indoor fungal composition determined in dust samples by culture-independent methods, despite stark contrasts between architecture and materials of some buildings in close proximity (Amend et al, 2010). Since humans dominate the sources of bacteria found indoors, it is theoretically logical that all human-occupied buildings are reasonably similar in bacterial populations. Humans shed their skin cells every two to four weeks (Milstone, 2004) resulting in some similar impacts on indoor environments regardless of building or occupancy type (Weschler, 2011). However, Moschandreas et al (2003) found significant differences in concentrations of culturable airborne bacteria within and between geographically-proximate residences and between seasons.

Distribution of individual fungal taxa is significantly range- and latitude-limited compared with a null model of randomized distribution (Amend et al, 2010). The factors driving fungal composition are primarily global (related to location) rather than mediated by building design or function (Amend et al, 2010). Fungi are found in all indoor human environments where most contact between humans and microbes occurs. While the majority of fungal species apparently play a neutral role, some are detrimental to human lifestyles and health. Recent studies based on culture-independent sampling methods demonstrated a high diversity of indoor fungi distinct from that of outdoor environments. Others have shown temporal

fluctuations of fungal assemblages in human environments and modest correlations with human activity. (Amend et al, 2010)

Moschandreas et al (2003) assessed spatial and temporal variation of indoor gram-positive bacteria and *Staphylococcus* spp. in 10 Chicago area residences. Using data from Andersen samplers, the authors concluded that seasonal variation is residence-dependent with typically higher summer levels, but a clear pattern of variation could not be established. Room-to-room difference was not statistically significant, but basement levels indicate that the basement is a distinct microenvironment. Indoor concentrations exceeded corresponding outdoor concentrations 75% of the time. *Staphylococcus* spp. accounted for approximately 27% of the average indoor bacteria levels, and the highest levels of gram-positive bacteria were found in the kitchen. The presence of multiple indoor sources with variable emission rates in multiple indoor locations results in bacteria levels that varied with time and space.

#### **Human bacterial emission rates**

Qian et al (2012) examined the role of occupancy as a source of indoor biological aerosols in a university classroom to determine size-resolved concentrations of total and biological particles. rDNA gene sequence analysis was used to determine the microbial diversity of indoor and outdoor air during occupancy. Total particle mass and bacterial genome concentrations were observed to be higher during the occupied period compared to the vacant case with particle size dependent increases ranging from 3 to 68 times for total mass, 12 to 2,700 times for bacterial genomes and 1.5 to 5.2 times for fungal genomes. Emission rates per person-h due to occupancy were 31 mg,  $37 \times 10^6$  genome copies, and  $7.3 \times 10^6$  genome copies for total particle mass, bacteria, and fungi, respectively. Approximately 18% of the bacterial emissions were from taxa closely associated with the human skin microbiome. These results show that bacterial exposure indoors depends strongly on bacteria that are associated with previous or current human occupants.

#### **EFFECT OF VENTILATION TYPE AND RATE**

Bartlett et al (2004) reported the results of a survey to determine indoor concentrations of culturable bacteria in 39 elementary schools in British Columbia, Canada. The results for airborne bacteria showed that naturally-ventilated rooms (47% of the total surveyed) had higher bacterial counts than mechanically ventilated rooms (geometric mean 325 vs. 166 CFU/m<sup>3</sup>, respectively,  $p < 0.001$ ). Bacterial counts were negatively correlated with supply and exhaust flow rates, air exchange rates, and the percentage of the day that occupants spent quietly sitting at their desks. Analysis of bacterial groups indicated various sources of the bacterial aerosol, with micrococci and staphylococci closely associated with occupancy variables. They examined the relationships of airborne bacteria with various environmental factors (outdoor temperature, relative humidity, season, weather), ventilation and comfort parameters (indoor relative humidity, temperature, indoor CO<sub>2</sub> concentration, indoor fungal concentration), and occupancy (number of occupants, activity levels, occupancy patterns) variables. *Bacillus* spp. concentrations were associated with site and occupancy, and coryneform bacteria with site variables only. Approximately 60% of the variance in the outcome measurement of total bacteria was accounted for by indoor CO<sub>2</sub>, lower air exchange rate, the age of the building, signs of current or old moisture stains, room volume, indoor relative humidity, and occupant activity level. In a multiple linear regression model, ventilation factors accounted for 40% of the variance.

Kembel et al, (2012) used high-throughput sequencing of the bacterial 16S rRNA gene to quantify relationships between building attributes and airborne bacterial communities in

vacant patient rooms at a health-care facility. They quantified and compared the airborne bacterial community structure and environmental conditions in rooms with ventilation from the mechanical ventilation system or window ventilation, and compared these results with the bacteria found in outdoor air. They found lower phylogenetic diversity of airborne bacterial communities indoors than outdoors. Mechanically ventilated, rooms contained less diverse microbial communities than window-ventilated rooms. Bacterial communities found in indoor air contained many taxa that were absent or rare in outdoor air. They reported that some of the indoor taxa found are closely related to potential human pathogens. The most important correlates of the diversity and composition of indoor bacterial communities were several building-related attributes, specifically the source of ventilation air, airflow rates, relative humidity and temperature.

Bonetta et al (2010) evaluated the level and composition of culturable bacteria and fungi in the indoor air of an Italian office building equipped with a heating, ventilation and air conditioning (HVAC) system during different seasons. *Staphylococcus* and *Micrococcus* were the most commonly found genera. A high fungal concentration was measured due to a flood that occurred during the winter. The indoor seasonal distribution of fungal genera was related to the outdoor fungal distribution. Significant seasonal and daily variation in airborne microorganisms was found, underlining a relationship with the frequency of HVAC system switching on/off. The results highlight the role of the HVAC system on the indoor air quality of an office building.

#### **WATER DAMAGED MATERIALS, DAMP BUILDINGS**

Andersen et al (2011) estimated the qualitative and quantitative diversity of fungi growing on damp or water-damaged building materials and characterized associations between the most commonly found fungal species and different types of materials. More than 5,300 surface samples were collected from materials with visible fungal growth. The results confirmed that *Penicillium chrysogenum* and *Aspergillus versicolor* were the most common fungal species in materials from water-damaged buildings. *Chaetomium* spp., *Acremonium* spp. and *Ulocladium* spp. were commonly found on damp building materials. The analyses revealed associated mycobiota on different building materials: (i) *Acremonium* spp., *Penicillium chrysogenum*, *Stachybotrys* spp., *Ulocladium* spp., and gypsum and wallpaper; (ii) *Arthrinium phaeospermum*, *Aureobasidium pullulans*, *Cladosporium herbarum*, *Trichoderma* spp., yeasts, and different types of wood and plywood; and (iii) *Aspergillus fumigatus*, *Aspergillus melleus*, *Aspergillus niger*, *Aspergillus ochraceus*, *Chaetomium* spp., *Mucor racemosus*, *Mucor spinosus*, and concrete and other floor-related materials.

Schäfer et al (2010) used both culture-based and culture-independent methods to detect Actinobacteria on different wall materials from water damaged buildings. Actinobacteria were detected in all but one of the investigated materials by both methods. The detected concentrations of Actinobacteria spanned a range of  $10^4$  to  $10^7$  CFU  $g^{-1}$  of investigated material. The genera *Streptomyces*, *Amycolatopsis*, *Nocardopsis*, *Saccharopolyspora*, *Promicromonospora*, and *Pseudonocardia* were found most frequently. Both methods indicated a high abundance and variety of Actinobacteria in water damaged buildings.

#### **SUMMARY AND CONCLUSIONS**

Human activities and patterns and building operation seem to have the greatest impact on indoor microbial ecology. Based on our review, a number of issues remain that are not well-researched; clearly there is need for further attention. Prominent among these are (1) the effects of indoor cleaning activities and use of biocides on indoor microbial ecology, and, (2)

the rate at which indoor microbiomes adapt to changes in occupant activities, building operation, and maintenance.

High-throughput genetic sequencing of environmental samples has dramatically expanded the tools available to scientists from microbiology, engineering, and ecology, and should help to address these research needs. What has been learned so far suggests that the indoor environment is far more complex than previously thought, and that dynamic interdependencies among environmental factors and microbes illustrate that the indoor environment is an "ecosystem" susceptible to study using conceptual approaches previously thought to apply only to "natural systems."

#### ACKNOWLEDGEMENTS

The authors gratefully acknowledge the bibliographic assistance of Shela Ray. Funding for the research and preparation of this paper was provided by the Alfred P. Sloan Foundation through a grant to the University of California, Davis for the creation of the Microbiology of the Built Environment Network (microBEnet). More information about the microBEnet project and the Sloan Foundation's "Microbiology of the Built Environment" Program is available at <http://www.microbe.net>.

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