CORSI – WHITE PAPER

SYMPOSIUM ON MICROBIOMES OF BUILT ENVIRONMENTS

Held in Austin, Texas, on June 8th and 9th, 2011
In conjunction with Indoor Air 2011

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OVERVIEW

On average, Americans spend 18 hour indoors for every hour spent outdoors.[1] As such, our inhalation exposure to most air pollutants, whether of indoor or outdoor origin, is dominated by the air we breathe inside of buildings. The same is true for our exposure to microorganisms.[2] Over the past three decades much has been learned about chemicals (gas and particle phase) in building air, including typical levels, sources, fate, and control. Far less has been learned about the types, sources, and fate of microorganisms in buildings, and how building design, operation and maintenance affect microorganisms in buildings. Expansion of this knowledge base has been limited by historical reliance on culture-based methods that often yield biased assessments of microbial community structure, sometimes dramatically underestimating cultivable fungi.[3] However, advances in culture-independent methods provide a great opportunity for rapidly advancing knowledge related to microorganisms in buildings.

In just the past 3-4 years, advancements in molecular methods have led to significant improvements in the knowledge base related to microbial communities and their diversity in buildings.[4] The usefulness of molecular methods has been demonstrated for identifying bacteria in homes and water damaged buildings, as well as seasonal variations in the community composition of fungal species in office buildings.[3,5,6] Total fungal DNA in daycare centers has been associated with specific flooring materials, dampness, and even pet allergens.[7] Biofilms in

shower heads have been reported to contain high levels of opportunistic human pathogens.[8] Microorganisms in indoor air appear to largely originate from indoor niches and are distinct from the outdoor environment.[2,9] However, the high diversity of indoor fungi has been observed to have little sensitivity to building function, at least for settled dust samples.[2] These recent findings suggest great potential for rapidly advancing knowledge related to microbial communities in buildings. Such advancements should be driven by microbiologists working with building scientists and with the knowledge of policymakers who will ultimately use new information to make important decisions related to future funding and guidelines.

The Alfred P. Sloan Foundation recognized an opportunity for improvement in existing knowledge related to microbiomes of indoor environments and has established a major research initiative through its Indoor Environment program to seize on this opportunity. The stated goal of the program is to "grow a new field of scientific inquiry, focused on the indoor microbial environments where people live, work, and play." A major objective of the program is "to build a national, multi-disciplinary community by establishing a network of scientists, engineers, and architects working on these issues." To continue to build that community the Sloan Foundation sponsored a two-day symposium entitled *Microbiomes of Built Environments* on June 8th and 9th during Indoor Air 2011 in Austin, Texas. Indoor Air is a triennial conference series that started in 1978 and is the signature conference of the International Society of Indoor Air Quality and Climate. It is a research-focused conference that brings together building scientists, health scientists, chemists, biologists, physicists and others from around the world; Indoor Air 2011 had nearly 1,000 attendees from 47 countries.

The goal of the symposium was to bring together some of the best and brightest microbiologists and building scientists from North America and beyond, and to foster cross-

pollination of ideas related to how modern microbiological techniques can be employed to better understand the inter-relationships between building-related variables and the microorganisms that exist in buildings. A summary of the Symposium on *Microbiomes of Built Environments* is provided in this paper. The major structure of the symposium is presented followed by highlights of podium presentations and workgroup findings.

SYMPOSIUM STRUCTURE

The Symposium on *Microbiomes of Built Environments* was designed to include four major components as shown in Figure 1. Although a group of microbiologists, building scientists, and policymakers were specifically invited to attend and participate in the symposium (see Table 1), all components of the symposium were open to general attendees of Indoor Air 2011. The goal of inclusiveness was intended to inform as large a base of scientists as possible about potential advances related to knowledge of microbial dynamics in buildings, and also to gain from the experiences and knowledge of those who have worked in this area but who were not invited to participate directly in the symposium.

The symposium opened on June 8th with a keynote address delivered by Dr. J. Craig Venter (J. Craig Venter Institute) and entitled "From Reading to Writing the Genetic Code." Venter informed conference attendees of the great potential that genomic methods and related research holds for better understanding microbial dynamics in various environmental systems, including building environments. He described recent observations made by him and his colleagues that the major sources of DNA in the air inside New York City buildings are humans, followed by rodents. In contrast, in outdoor air in New York City most DNA was from rodents.

Two technical sessions on Microbiomes of Built Environments were held in series following Venter's keynote address. These sessions consisted of fifteen podium presentations of fifteen minutes each, eight of which were solicited and seven of which were unsolicited submissions to the general conference but fit the theme of the symposium. A list of session speakers and titles of presentations is provided in Table 2. Approximately 200 conference delegates attended the technical sessions.

On June 9th the Symposium involved a workshop with three major components. The workshop was opened by Jesse Ausubel (Alfred P. Sloan Foundation and The Rockefeller University) who described the scope of the Sloan Foundation's initiative related to Microbiomes of Built Environments. He also suggested that workshop participants keep in mind that it is the unknowns that set research agendas for fields, and challenged participants to consider "macroprojects" that necessitate collaboration. Ausubel was followed by two invited workshop opening presenters. Aino Nevalainen (National Institute for Health and Welfare, Kuopio, Finland) spoke on "Microbiology and the Indoor Environment – What Did We Learn with Culturing?" She focused on what we know from several decades of conventional, e.g., primarily culture-based, air and surface sampling for microbes in buildings. Jonathan Eisen (University of California, Davis) then spoke on "Indoor Microbial Ecology (DNA Sequencing Focus)," focusing on advances and challenges related to DNA sequencing methods.

Following the workshop's opening presentations, invited participants and general conference attendees were invited to join two work groups to discuss research needs related to improving the existing knowledge base on microbiomes of built environments. Each workgroup included microbiologists, building scientists, policymakers, and graduate students. Following ninety minute meetings the facilitators of each workgroup provided a summary of their group's

discussion and suggestions, with follow-up opportunities for input from other group members and the general audience.

HIGHLIGHTS

The symposium touched on far ranging issues, from analytical developments to the effects of humans on indoor microbial communities. But most of the presentations and discussions fell into four major categories: (1) historical perspective, (2) influencing building-related factors, (3) effects of humans on indoor microorganisms, and (4) microorganisms associated with flooding and water-challenged building materials. A summary of discussions within these four categories is provided below, followed by a summary of the major recommendations from two breakout groups.

Historical Perspective

Aino Nevalainen (National Institute for Health and Welfare, Finland) provided an overview of what the indoor air quality community has learned about microorganisms in buildings over the past century. In the early 20th century, research focused on the prevention of infectious disease transmission, principally on bacteria of human origin. By the 1940s and 1950s, concerns related to allergy spurred more research on indoor fungi, and indoor culturable plate counts were observed to be greater in complaint homes than non-complaint homes. By the 1970s and 1980s there was much greater interest related to the role of ventilation systems and air conditioning on indoor fungi.

Over the past several decades the general sources of indoor microorganisms have become clearer. Outdoor air is known to be a major source of certain molds, such as *cladosporium*, users

of buildings (humans, pets, and pests) are major sources of bacteria, and wetted areas, including plumbing, are important indoor microbial habitats. Humans constantly shed skin scales that contain both bacterial and yeast cells, with an estimate of 10^4 viable aerobic bacteria shed/minute, including both pathogens and normal protective flora (as measured by culture-based methods). Factors that affect variations in the normal flora shed by humans include climate, location on the human body, age, sex, occupation, and use of soaps and medicines.

Dampness and moisture inside of building envelopes, HVAC systems, or occupied spaces can lead to the growth of mold, bacteria, yeasts, and amoebae. These in turn become sources of spores, cells, microbial fragments, volatile metabolites, and toxic metabolites on bioaerosols. Importantly, culture-based methods are now known to typically capture only 1 to 10% of microbial material present in buildings. This raises two important questions:

- Are culturable microorganisms good surrogates for non-culturable microorganisms?
- What important microorganisms have been missed by those who have studied or sampled for microorganisms in built environments?

Jonathan Eisen (University of California, Davis) followed Nevalainen with a presentation of molecular methods that have emerged over the past three decades and that will likely play an important role in better understanding indoor microbial community and community dynamics in the future. He described four major eras associated with DNA sequencing.

Era 1 took place in the late 1970s and involved the use of analysis of ribosomal RNA (rRNA) sequences to develop the first true evolutionary tree of life that includes all organisms on the planet. This led to a fundamental reshaping of our understanding of the diversity of life on the planet. In addition, it allowed for the first time microbes that could be grown in the lab to be accurately classified as to their "type".

Era 2 spanned the mid-to-late 1980s and early 1990s when symposium participant Norm Pace (University of Colorado Boulder) took rRNA methods from the laboratory and began applying them to analyze environmental samples collected in the field. This work was accelerated greatly in the late 1980s by the development of the polymerase chain reaction (PCR). In turn, the use of PCR amplification of rRNA genes allowed one to rapidly assess the diversity of microbes present in any particular sample. Subsequent "culture-independent" surveys of environmental samples allowed for the first time the sampling of the "hidden majority" of microbes around the globe, including the identification of individual organisms and even entire phyla that had never been cultured. By the early 1990s, these new tools allowed microbiologists to quantify ecological "richness" as the number of species in environmental samples. However, the microbial richness of buildings was a potential research area that was largely ignored compared with other environments.

Era 3 began in the mid-1990s and involved advances in DNA sequencing and computational biology that allowed for the first time the determination of the complete genome sequence of various organisms. Genome sequencing revolutionized many aspects of microbiology, such as making it possible to predict the entire repertoire of functions possessed by diverse organisms.

Era 4 began in the early 21st century and involved the application of genomic techniques to environmental samples. This era can be considered as the genomic analog of the rRNA culture independent surveys. And just as rRNA environmental surveys revealed information about the hidden diversity of kinds of organisms, metagenomic surveys have begun to reveal details about the genetic content of those hidden microbes. This is critical in allowing one to

predict functions for uncultured microbes and even whole communities, and also has allowed the first broad sampling of viruses, which do not have rRNA genes.

While far fewer studies that utilize advanced culture-independent methods have been completed in built environments than natural environments, results for the latter suggest great potential for applications to buildings. For example, genome sequencing has led to knowledge that functional properties of microorganisms evolve much more rapidly than in plants or animals. Could this possibly mean that microorganisms in buildings rapidly evolve to changes in building parameters, e.g., the use of new cleaning agents (including bactericides and fungicides), changes in surface acidity, or seasonal changes in temperature or relative humidity? Do microbial communities respond (change) as new occupants, with different habits from old occupants, take over a building? Building scientists should be aware of the potential that new tools offer to seek answers to important questions related to microbiomes of built environments, and should seek microbiologists as partners in the quest to answer these and other questions.

Influencing Building-Related Factors

It seems intuitive that the ways that buildings are constructed, maintained, and operated affect microbial communities in building envelopes, HVAC systems, and the occupied space of buildings. But knowledge of, and agreement on, the most important building-related factors is critical if the right metadata are to be consistently collected during studies of microbial communities in buildings.

The complexity of linking building-related factors with the presence and dynamics of microorganisms in buildings is far from trivial. This point was underscored in a presentation by symposium participant Bill Nazaroff (University of California Berkeley) who noted that the

world's human population now inhabits more than one billion buildings, that these buildings are characterized by broad variability in factors that affect indoor microbiomes, and that this variability is not just across average conditions between the world's buildings but also across spatial and temporal patterns within individual buildings. Given this large spectrum of differences, the problem of linking building-related factors to indoor microbiology is certainly one of intellectual merit and warrants the attention of the world's best microbiologists and building scientists.

Based on a detailed review of the published literature and interviews with experts in both the building and microbial sciences, Hal Levin (Building Ecology Research Group) identified several important building-related factors that should affect indoor microbial ecology. These factors include the temperature of indoor air and surfaces, relative and absolute humidity, outdoor air exchange rate, air distribution in rooms and between zones in buildings, and building materials located within both the occupied indoor space and in the structure, e.g., building envelope, wall cavities, and HVAC system. These factors can be reasonably measured or otherwise determined, and in many cases controlled. But other factors such as chemicals found primarily on surfaces, such as nutrients and biocides, as well as the pH of moisture on surfaces may also affect microbial growth on materials. Levin noted that airborne carbon dioxide, e.g., from building occupants and combustion sources, might also play an important role in affecting the pH of surfaces.

Lewis Harriman III (Mason-Grant Consulting) noted that growth rates of microorganisms in buildings are highly dependent on the availability of water. As such, it is important to focus on locations in buildings where moisture accumulates for extended periods of time, and to better understand why moisture accumulates in some areas within buildings and not others. To this

end, improvements in three-dimensional moisture mapping and determination of material moisture contents would benefit explorations of microbiomes of buildings. Future information on material moisture contents should be coupled with analyses of both dampness and drying time scales.

Brendan Bohannan (University of Oregon) described a field study involving sample collection and sequencing of 16s rRNA genes to assess airborne bacterial communities in a hospital, and factors that affect airborne bacteria. Bohannan and his colleagues found that the composition and diversity of airborne bacterial communities differed between the outdoor and indoor hospital environments. The diversity and composition of indoor bacterial communities were strongly influenced by the source of ventilation air (natural versus mechanically ventilated), air flow rates, relative humidity and temperature. The factors that led to the highest abundance of potentially pathogenic bacteria were low flow rates, mechanical ventilation, higher temperatures, and lower relative humidity.

The effects of sporulation air temperature on the IgE-binding capacity (an important parameter in defining "allergenicity") of *Aspergillus fumigatus* was described by Jordan Peccia (Yale University). Peccia and his research team used functional gene expression analysis of spores using mRNA expression microarrays and observed that a greater number of genes that encode known major allergens are more highly expressed at lower sporulation temperatures. A 12 x increase in *A. fumigatus* allergenicity per spore was observed when temperature was reduced from 32 ^{o}C to 17 ^{o}C, well within the range of temperatures found in the occupied space of buildings.

While not a specific building-related factor, seasons affect building environmental conditions and operating parameters. Mika Frankel (National Working Centre for the Indoor

Environment, Denmark) presented results of a study involving collection of microorganisms in five Danish homes using airborne particle filters, furniture vacuuming onto filters, liquid impingers, dust fall collectors (DFCs), and electrostatic dust cloths (EDCs). Samples were analyzed for cultivable microorganisms, endotoxins, and enzymes. Substantial differences in the concentrations of cultivable microorganisms were observed between spring and summer. Airborne bacteria concentrations decreased by a factor of eight from spring to summer while airborne fungal spores increased by a factor of five from spring to summer. For dust samples, EDCs showed greater diversity for fungal groups and greater fungal spore concentrations than did DFCs. Based on samples collected with EDCs and furniture vacuuming, fungal spores in surface dusts increased from spring to summer, consistent with air samples.

Effects of Humans on Indoor Microorganisms

Following on the presentation of Nevalainen (see Historical Perspective above), an important outcome of the symposium was general agreement and consistency in recent research findings related to the importance of humans as sources of bacteria in the occupied space of buildings. The results of several recent studies by symposium participants were presented on this issue. Each dealt with a different type of building (residential, hospital, school).

Martin Täubel (National Institute for Health and Welfare, Finland) presented results involving culture-independent analyses that produced over 4,000 full-length 16S rRNA gene sequences to characterize bacteria in mattress and dust samples, as well as surface swab samples of home occupants. He and his colleagues observed high diversity in bacterial flora of residential dust samples, dominated by gram-positive bacteria. While seasonal variations were observed to the species level, differences were far more pronounced between buildings.

Differences in bacterial groups were attributed largely to human sources; in mattress dust samples between 69 and 88% of bacterial sequences were associated with humans. Täubel and colleagues argued that the importance of humans as sources of residential bacterial content requires careful interpretation of bacterial marker data used to assess human environmental exposures to microorganisms.

As described above, Brendan Bohannan and colleagues at the University of Oregon studied airborne bacterial communities in a hospital. They observed that bacterial groups commonly associated with humans, including *betaproteobacteria*, *burkoholderiaceae*, and *pseudomonales*, were more abundant in mechanically-ventilated rooms than in rooms that were ventilated directly with outdoor air. This suggests the recirculation of human-shed bacteria in HVAC systems or colonization of human-shed bacteria on HVAC components.

Denina Hospodsky (Yale University) and colleagues studied size-resolved concentrations and population structure of total bacteria and fungi in the air and floor dust of occupied and unoccupied school classrooms. Ventilation and outdoor air samples were also collected. Multistage cascade impactors were used to collect samples, which were analyzed using real-time qPCR and phylogenetic library production. They observed that airborne fungi concentrations in occupied classrooms were not elevated in comparison to unoccupied classrooms or outdoor air; outdoor sources appeared to dominate indoor fungi concentrations. In contrast, airborne bacterial concentrations in all size ranges were at least one order of magnitude greater in occupied classrooms than in unoccupied classrooms or outdoor air. Source emission rates for airborne bacteria were calculated to be 5 to 55 x 10^6 gene copies/hr/Δlog(diameter), with a peak emission rate in the 3 to 5 μm diameter range. Source allocation analysis and quantitative population comparison for microorganisms revealed that for occupied classrooms the dominant

source of airborne bacteria was resuspension of floor dust, presumably containing an accumulation of bacteria from human room occupants.

Microorganisms Associated with Flooding and Water-Challenged Building Materials

It has long been recognized that rapid microbial growth can occur on water-challenged materials, e.g., from plumbing leaks or floods, but past attempts to ascertain growth and population dynamics have been hindered by the use of culture-dependent methods that require time and do not capture the presence of many microorganisms. Three symposium participants presented the results of studies involving culture-independent sample analysis that expands the knowledge base related to microbial growth on water-challenged buildings and related materials.

Alina Handorean (University of Colorado Boulder) presented the results of a study aimed at characterizing the identity, distribution, and abundance of airborne microorganisms present in the air of flood impacted office buildings. Samples were collected at various stages of remediation and compared with outdoor air samples using direct microscopy, rDNA PCR, and associated DNA sequencing analysis. Phylogenetic analyses were used to assess variations in populations of airborne microorganisms during different remediation stages. Post-flooding airborne microorganism concentrations were an order-of-magnitude greater than pre-flood or simultaneous outdoor airborne microorganism concentrations. Total microbial bioaerosol concentrations peaked three weeks after the flooding event. Levels declined to outdoor concentrations at approximately 60 days after building remediation. This result has potential implications with respect to recommended building re-entry times following remediation after a flood event. Importantly, Handorean and colleagues also observed that airborne fungal populations were different than those often recovered using culture-based methods in water-

challenged buildings. Specifically, genes for the commonly-reported fungi *Alternaria* spp, *Cladosporium* spp, *Penicillium* spp, and *Aspergillus* spp were nearly absent from DNA recovered during the study.

Gunilla Bok (SP Technical Research Institute of Sweden and Gothenburg University, Sweden) presented results from an investigation of fungal biodiversity on water-damaged building materials using the ITS-region of rDNA. The flora was dominated by *Penicillium* and *Aspergillus* species, with further resolution of species made possible with computer-based phylogenetic analysis. Using this approach, the number of species exceeded those identified in previous studies.

Miia Pitkäranta (University of Helsinki) and colleagues studied microorganisms in samples of settled dust collected in healthy, water-damaged, and renovated buildings. Samples were also collected from water-damaged building materials. Both fungal and bacterial communities were studied using DNA barcode sequencing in parallel with culture-based methods, and qPCR for fungi. Total fungal communities in dust were observed to be consistent with both spatial and seasonal variations in outdoor air. However, fungal diversity increased in dust following building water damage. The majority of bacteria in indoor dust were observed to be of human origin, consistent with findings described above (see previous section on Effects of Humans on Indoor Microorganisms). Both fungal and bacterial communities that grew on water-challenged building materials were significantly different than those observed in dust, with viable bacteria accounting for approximately 40% of total microbial diversity on water-damaged materials. Pitkäranta and colleagues suggest that more attention should be paid to determining the diversity of microorganisms capable of growing on water-challenged materials.

Workgroup Recommendations

The final activity of the symposium involved two workgroups, each charged with making recommendations for future research relevant to microbiomes of built environments. Each workgroup consisted of approximately 20-25 participants. One group was facilitated by Hal Levin (Building Ecology Research Group) and Dr. Norm Pace (University of Colorado, Boulder), and the other was facilitated by Drs. Jonathan Eisen (University of California, Davis) and Kerry Kinney (University of Texas at Austin). A combined summary of major recommendations stemming from workgroup discussions is provided below.

1. The interaction between microbial communities and building materials needs far greater attention. Specifically, building materials in the occupied space and building envelope are generally poorly characterized in terms of both physical structure and chemical composition, factors that may greatly influence the nature of microorganisms and their growth rates on the materials.
2. More attention should be given to longitudinal studies of microbial ecology in buildings. How do microbial communities change over various time scales, particularly in response to changes in building environmental conditions, interior materials, and operating and maintenance conditions?
3. A valuable community resource could be the sequencing of "reference genomes" of cultured isolates of different kinds of microbes from the built environment. Such genome sequences would be of value both for predicting functions of importance but also for interpreting PCR and metagenomic sequence data.
4. Future research should focus not just on the identification of microorganisms in buildings, but also on their functioning, i.e., "what are they doing?"

5. Shared building sites for doing research at several locations around the world would be highly beneficial for researchers. This would allow interdisciplinary researchers from around the world to conduct studies in a more controlled and systematic manner than is currently possible in field studies where many of the building factors are uncontrolled (and/or not measured). These building test sites would enable building scientists and microbiologists to work together to verify sampling methodologies and assess how the indoor microbial communities respond to building factors such as ventilation rates as well as human factors such as occupancy loads. Ideally these sites would be located in different climatic zones and in locations dispersed throughout the world to more accurately capture the diversity of built environments.
6. Given the importance of humans as sources of indoor bacteria, additional research is warranted to study the effects of human behavior and activity patterns on indoor bacterial communities. Such studies could focus not only on humans as sources, but also on how human activities, e.g., cleaning, affect bacterial communities.
7. Pets are also an important source of indoor bacteria and more research is needed to better understand their importance. For example, how does the diet or cleaning frequency of an indoor pet affect it as a source of bacteria? Do indoor bacterial communities vary for outdoor/indoor pets in comparison to pets that are largely indoor pets?
8. How are the microbiomes of built environments likely to change as a result of outdoor climate change? Such research should focus not only on direct impacts of climate change, e.g., heat waves or southwestern U.S. dust storms, but also on changes in buildings to mitigate or adapt to climate change. The latter two should include the effects of

weatherization of existing buildings and "tight" envelope design of new buildings, rapid implementation of new green building materials, increased and new insulations, and more.

9. Researchers should have a checklist of metadata that are collected during investigations of microbiomes in buildings. This list should include sampling methodologies employed, environmental conditions, information on ventilation methods and HVAC systems, building materials, building operation, building maintenance (including cleaning procedures, etc.), previous water challenges, and more. A consistent list used across research efforts will allow greater comparison between studies.
10. Research is needed to ascertain interactions between indoor microbial communities and chemicals and pollutants. For example, can the accumulation of carbon dioxide emitted by building occupants lead to changes in the pH of water films on materials in such a way that influences microbial growth or diversity? Do the products of indoor air or surface chemistry do the same?
11. Consideration should be given to "citizen science" projects for which the general population becomes more involved in collecting samples that elucidate the nature of microbial communities in homes, classrooms, and more. Such an effort would require centralized analysis sites. Metadata could be collected via questionnaire. For example, one possibility is to use HVAC filters as common "sampling" devices that are donated to science instead of being thrown away by homeowners.
12. The development and verification of new technologies for routine surveillance of indoor microorganisms would facilitate field studies and, depending on cost and complexity, could be used for citizen science projects.

SUMMARY

A two-day symposium on *Microbiomes of Built Environments* was held at Indoor Air 2011 in Austin, Texas. The symposium included a keynote address by J. Craig Venter followed by fifteen podium presentations in two technical sessions on the first day. A workshop was held on the second day and included initial presentations by Aino Nevalainen and Jonathan Eisen to define the state of knowledge related to microorganisms in buildings and possible advancements of such knowledge in the future. The remainder of the workshop involved two workgroups charged with developing a list of recommendations to expand the existing knowledge base related to microbial communities in buildings.

The symposium on *Microbiomes of Built Environments* was successful on several fronts. It succeeded in bringing together and catalyzing discussions between exceptional researchers in the fields of microbiology and building science. It provided a professional development experience for the six invited graduate students and others who attended the symposium. The symposium helped to define the current state of knowledge related to microbial communities in buildings, and the potential for filling major knowledge gaps. Finally, it led to a list of important recommendations for research that will advance the existing knowledge base related to microbiomes of built environments. This list should serve as a benchmark to assess continued advancements in knowledge relevant to microbial communities in built environments over the next several years, and to bring together microbiologists and building scientists in a collaborative effort to forge those advancements.

ACKNOWLEDGEMENTS

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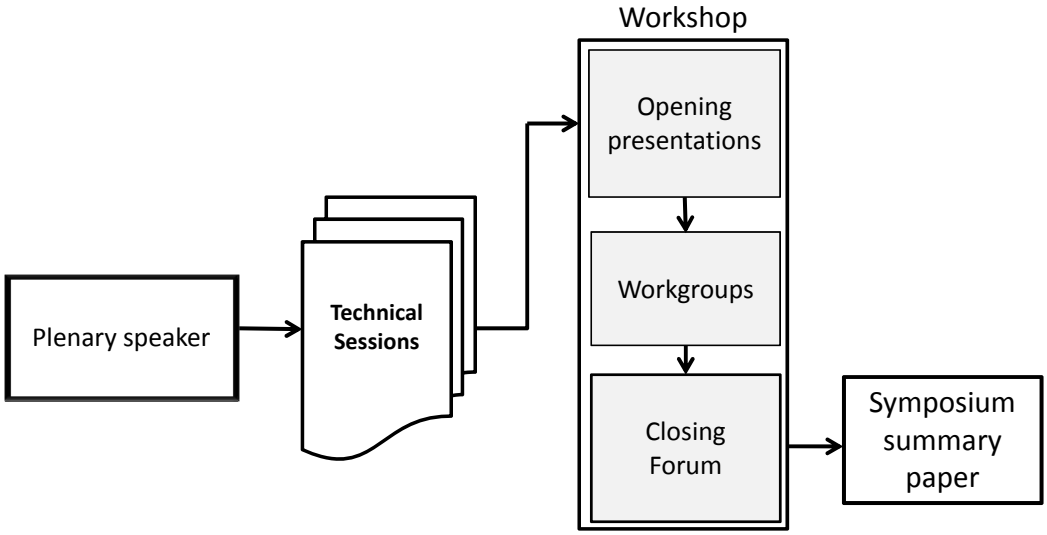

Figure 1. Major components of the Symposium on Microbiomes of Built Environments.

Table 1. Invited Participants

Participant	**Affiliation**
Rachel Adams*	University of California, Berkeley
Steven Ahrendt*	University of California, Riverside
Gary Anderson	Lawrence Berkeley National Lab (LBNL)
Peter Ashley	U.S. Department of Housing and Urban Development
Jesse Ausubel	Sloan Foundation and The Rockefeller University
William Bahnfleth	Penn State University
Brendan Bohannan	University of Oregon
Terry Brennan	Camroden Associates, Inc.
Charlie Brown	University of Oregon
Thomas Bruns	University of California, Berkeley
David Coil	University of California, Davis
Richard Corsi	University of Texas at Austin
Jonathan Eisen	University of California, Davis
Bill Fisk	Lawrence Berkeley National Lab
Lewis Harriman III	Mason-Grant Consulting
Mark Hernandez	University of Colorado Boulder
Andrew Hoisington*	University of Texas at Austin
Peggy Jenkins	California Air Resources Board
Kerry Kinney	University of Texas at Austin
Mary Jo Kirisits	University of Texas at Austin
Laura Kolb	U.S. Environmental Protection Agency
Hal Levin	Building Ecology Research Group
Ming-Ching Liang*	University of Texas at Austin
Janet Macher	California Department of Public Health
Mark Mendell	California Department of Public Health & LBNL
William Nazaroff	University of California, Berkeley
Russell Neches*	University of California, Davis
Aino Nevalainen	National Institute for Health and Welfare (Finland)
Atila Novoselac	University of Texas at Austin
Norm Pace	University of Colorado Boulder
Jordan Peccia	Yale University
Tom Phillips	Retired
Kim Ross*	University of Colorado Boulder
Jeffrey Siegel	University of Texas at Austin
Jason Stajich	University of California, Riverside
J. Craig Venter	J. Craig Venter Institute
Shannon Williamson	J. Craig Venter Institute

* = Graduate student.

Table 2. Presenters and Presentation Titles in Symposium Technical Sessions

Presenter	**Affiliation**	**Title of Presentation**	**Paper #**
William Nazaroff	UC Berkeley	*Newton Meets Darwin in the Indoor Biome*	1588
Norman Pace	U of Colorado	*Ribosomal RNA Surveys of Human-Occupied Indoor Environments*	1802
Martin Täubel	National Institute for Health and Welfare, Finland	*Diversity, Seasonal Dynamics and Sources of Bacteria in House Dust*	333
Denina Hospodsky	Yale University	*Size-Fractionated Emissions and Microbial Population Characterization to Reveal Sources of Bacteria in Indoor Air*	216
Lewis Harriman III	Mason-Grant Consulting	*Spatial and Temporal Variations of Moisture in Buildings: Factors Which Influence Microbial Growth Rates and the Ecology of Indoor Environments*	1587
Miia Pitkäranta	U of Helsinki	*Sources and Characteristics of Cultivable and Uncultivable Microbial Diversity in Indoor Environments*	901
Gunilla G.V. Bok	SP Technical Research Institute of Sweden	*Identification of Mould Fungi by Combining Blast-Based Similarity Searches and Phylogenetic Analysis*	932
Alina M. Handorean	U of Colorado	*Phylogenetic Analysis of Bioaerosols Recovered from Commercial Office Environments Reclaimed from Flood Damage*	1095
Hal Levin	Building Ecology Research Group	*Building Ecology: Linking Microbial Ecology with Indoor Environment and Building Science*	1092
Mika Frankel	National Working Centre for the Indoor Environment, Denmark	*Influence of Season and Sampling Methods on the Measured Exposure to Indoor Microorganisms and Their Inflammatory Potential*	382
Brendan Bohannan	U of Oregon	*Architectural Design Shapes the Built Environment Microbiome*	1586
Jordan Peccia	Yale University	*Growth Temperature Strongly Influences the Allergenicity of Aspergillus Fumigatus Spores*	846
Sophie Barral	Mairie de Paris	*Measurement of Indoor Mould Exposure: Development of a Global Approach Associating Quantitative and Qualitative Tools from Long Duration Air Samplings*	855
Mark Mendell	California Department of Public Health & LBNL	*Using the Environmental Relative Moldiness Index (ERMI) with Fungal PCR to Evaluate Damp Houses – a Review of the Epidemiologic Evidence for its Use*	934
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