Building science to advance research in the microbiology of the built environment (MoBE)

Supported by the Alfred P. Sloan Foundation

May 22-23, 2014 | Illinois Institute of Technology | Chicago, IL

ALFRED P. SLOAN FOUNDATION

ILLINOIS INSTITUTE OF TECHNOLOGY

Brent Stephens, Illinois Institute of Technology

Workshop agenda

8:30 am: Kick-off presentations

- Paula Olsiewski, Sloan Foundation: Welcome
- Brent Stephens, IIT: Review of recent MoBE research

9:15 am: MoBE from the perspective of building science (and other related disciplines)

- 20-min invited presentations

11:00 am: Group discussion and facilitated brainstorming session

- Assign individual breakout groups and tasks

12:00 pm: Lunch delivered in main meeting room

1:00 pm: Get outside! IIT campus tour

1:45 pm: Breakout discussion groups (groups of 7-8)

3:00 pm: Synthesize themes from breakout sessions and pitch a series research goals for the MoBE program

- Led by group leaders; participation from all team members
  - 15-min each team

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5:00 pm: End of workshop and departures

Introduction to the Sloan Foundation MoBE Program

The primary goal of the Microbiology of the Built Environment (MoBE) program is to grow a new field of scientific inquiry

- We spend the majority of our time indoors
- We come in contact with trillions of microorganisms
  - Microbes are everywhere (bacteria, fungi, viruses, protozoa)
- Humans are composed of ~10x as many microbial cells as human cells
  - We are constantly shedding, acquiring, and sharing microbes
- Historically, microbial ecology research has focused on natural outdoor environments
- Little is (*was*) known about microbial ecosystems in the indoor environment
- New molecular tools and techniques (and $ reductions) have dramatically increased our ability to detect microbes in indoor environments

2004: Is everything really everywhere?

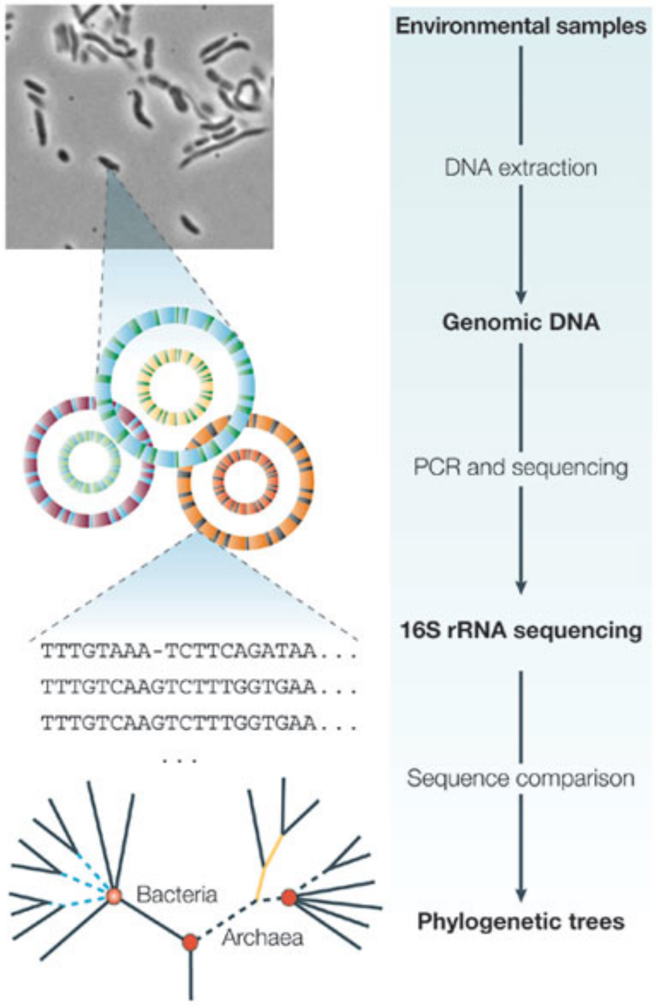
"For about a century, microbiologists have believed that the organisms they study are unhindered by geographic boundaries, traveling the world and thriving wherever they find their preferred environment—be it hot springs, freshwater ponds, or rotting fir trees."

"The ability to sequence DNA samples from the environment has allowed scientists to detect far more than the 1% of microbes that can be cultured in the laboratory. It has also revealed how they vary from place to place."

"We are beginning to see biogeographic patterns in microorganisms… There will be organisms that are global and can get anywhere, and you'll also find ones that don't have those ranges"

Whitfield, J. **2005** *Science* 310:960-961

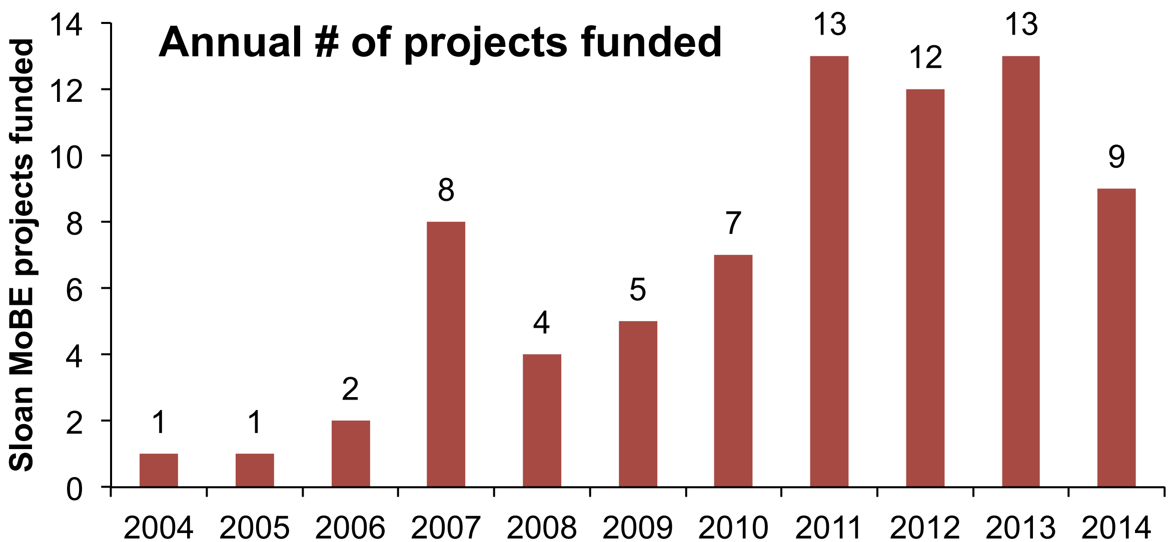
16S rRNA sequencing

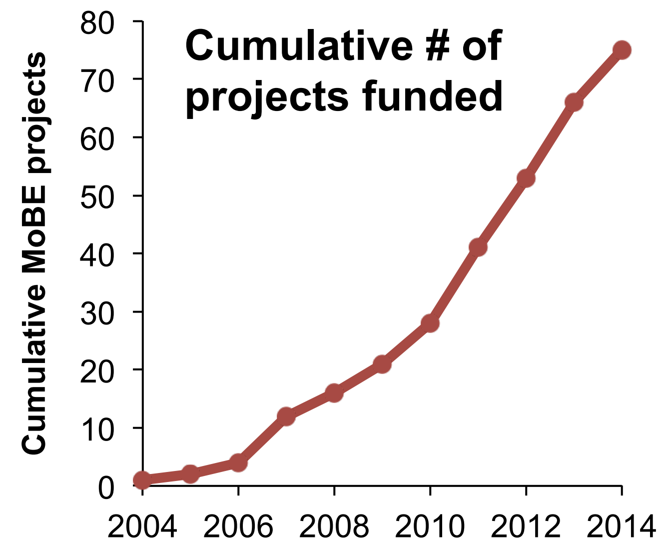


Tringe, S., Rubin, E. **2005** *Nature Rev Gen* 6:805-814

2004-present: Sloan MoBE program

- Microbiologists, armed with new molecular techniques and software tools, focused their trades indoors
  - Early Sloan MoBE program grantees:
    - J. Craig Venter Institute, Norm Pace, Jordan Peccia, and others





~75 projects funded by Sloan MoBE program to date

2004-2008: Initial MoBE studies (16 projects)

- Several early projects demonstrated the utility of new molecular methods for applications in indoor environments
  - Began to elucidate differences in microbial communities among various locations between and within buildings
    - As well as sources of microbes, including potential pathogens
- Sampled environments:
  - Homes
    - Shower curtains — Kelley et al. **2004** *Appl Environ Microbiol* 70:4187-4192
  - Child-care facility — Lee et al. **2007** *BMC Microbiol* 7:27
    - Toys and furniture
  - Hospital — Angenent et al. **2005** *PNAS* 102:4860-4865
    - Therapy pool water and air
  - Retail/office
    - HVAC filter — Tringe et al. **2008** *PLoS ONE* 3:e1862
    - Settled dust — Rintala et al. **2008** *BMC Microbiol* 8:56

2009-2011: 25 Sloan MoBE projects funded

- BioBE (Green)
- microBEnet (Eisen, Levin)
- BIMERC (Bruns, Nazaroff)
- Continued tool/method development (various PIs)
- Viral explorations (Kelley)
- Homes (Fierer, Gilbert)
- NICUs (Banfield, Morowitz)
- Indoor bioaerosols (Peccia, Nazaroff)
- Water delivery systems (Pace)
- Several workshops/symposia (various PIs)
- First annual MoBE conference (Hernandez)

2012-present: Latest phase of Sloan MoBE projects (34+)

- Continued work on homes
  - Homes across global cultures (Dominguez Bello)
  - 1000 homes in the US (Fierer, Miller)
  - Pre and post weatherization (Angenent)
  - Fungi in dust (Lynch)
  - Flood damaged homes (Fierer)
  - Insect infestations (Schal) and arthropods (Madden)
  - Interactions with phthalates (Dannemiller)
- Hospital Microbiome Project (Gilbert)
- Plumbing systems (2) (Pruden, Bibby)
- Office surfaces (Caporaso)
- Building materials
  - Test methods (Scott), moisture (Peccia), pH (Kolter)
- Public transportation (Huttenhower)
- ICUs (Banfield)
- Daycares (Prussin)
- Wine and cheese making facilities (Mills)
- Bioaerosol transport and control (Kunkel)
- Built environment metadata (Schriml)
- Open sensor building science sensors (Stephens)

Motivation for this workshop

- Recent advances in culture-independent molecular techniques and computational tools for analyzing microbial communities, coupled with the recognition that the majority of people in the developed world spend most of their lives indoors, has led to a rapid increase in the number of studies exploring microbial diversity within the built environment

- Many of these recent studies, particularly those funded by the Alfred P. Sloan Foundation's program on the Microbiology of the Built Environment (MoBE), have been driven and led primarily by microbiologists

- However, there remains a need to solicit input from expert building scientists and engineers on the overall effectiveness of these previous studies for advancing knowledge of microbial communities in the indoor environment, to identify existing gaps in these studies, and to inform a research agenda for future studies of the microbiology of the built environment that stems from deep knowledge of how buildings are constructed, operated, and occupied

Goals of this workshop

- This workshop was designed to bring together a group of experts in building science and engineering (including those with expertise in architectural engineering, environmental engineering, architecture, aerosol science, and environmental health) with a smaller number of key microbiologists to ~~keep us honest~~ discuss existing gaps and future opportunities for research on the microbiology of the built environment

- The primary goal of the workshop is to advance the MoBE program's research agenda and ultimately increase efficiency and impact among grantees

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Workshop personnel

- Introductions
- 5 speakers
  - Jeffrey Siegel, University of Toronto
  - Hal Levin, Building Ecology
  - Shelly Miller, University of Colorado
  - Rachel Adams, University of California Berkeley
  - Seema Bhangar, University of California Berkeley
- 3 breakout group leaders
  - Jeffrey Siegel, University of Toronto
  - Bill Fisk, LBNL
  - Paul Francisco, UIUC
- 3 note takers (IIT)
  - Parham Azimi, Tiffanie Ramos, Stephanie Kunkel
- Edoarda Corradi Dell'Acqua, Adjunct Prof., IIT CAEE
  - Architect + Engineer

Summary of MoBE research (2004 – present)

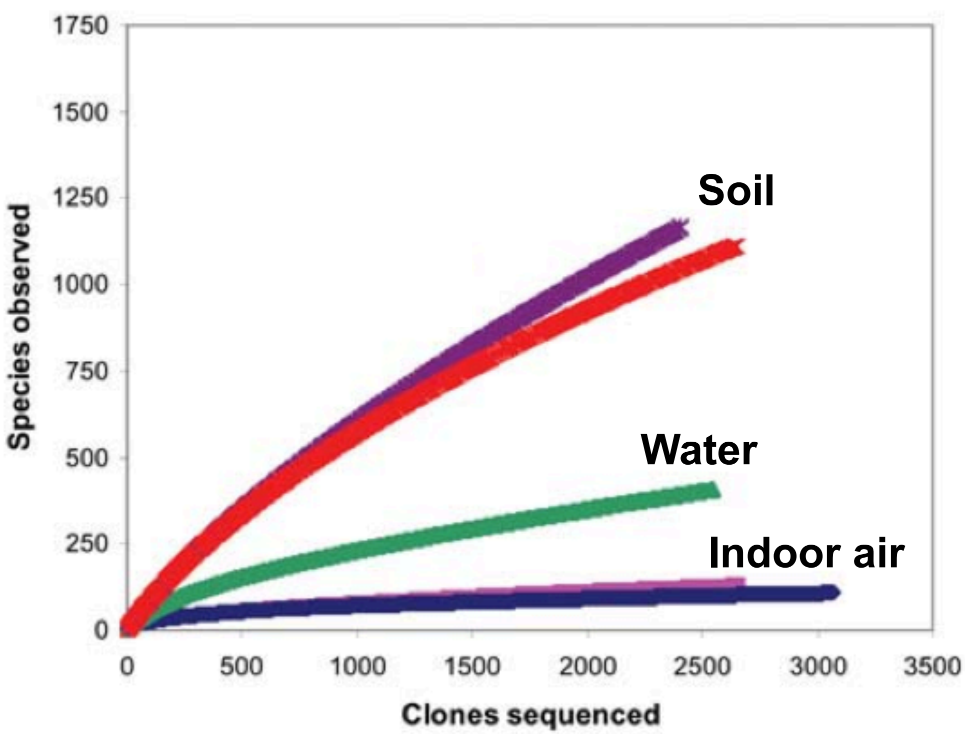
Through the lens of a(n) ____________

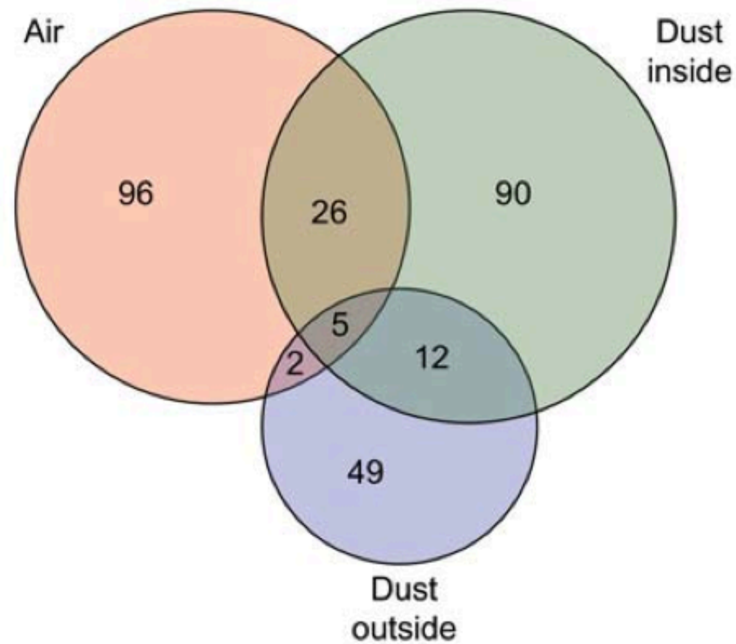
① Building scientist
② Environmental engineer
③ Architectural engineer
④ Architect
⑤ Aerosol scientist
⑥ Health scientist
⑦ Microbiologist
⑧ Objective observer

2004-2008: Initial MoBE studies

Early findings

"Comparison of air samples with each other and nearby environments suggested that the indoor air microbes are not random transients from surrounding outdoor environments, but rather originate from indoor niches."





Two shopping centers in Singapore

Tringe et al. **2008** *PLoS ONE* 3:e1862

2004-2008: Initial MoBE studies

Early findings

"The composition and dynamics of indoor dust bacterial flora were investigated in two buildings over a period of one year. Four samples were taken in each building, corresponding to the four seasons, and 16S rDNA libraries were constructed"

"Bacterial flora of the two buildings differed during all seasons except spring, but differences between seasons within one building were not that clear, indicating that differences between the buildings were greater than the differences between seasons"

"This work demonstrated that the bacterial flora of indoor dust is complex and dominated by Gram-positive species. The dominant phylotypes most probably originated from users of the building"

Offices in two buildings in Finland

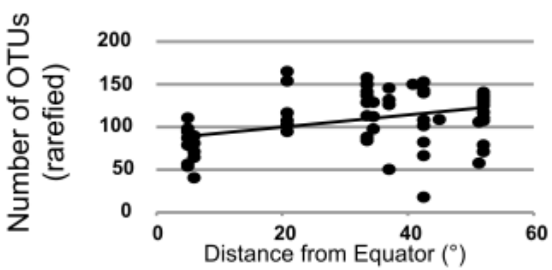
Rintala et al. **2008** *BMC Microbiol* 8:56

2009-present: Indoor fungal communities are largely driven by outdoor fungal communities

Indoor fungal composition is geographically patterned and more diverse in temperate zones than in the tropics

Anthony S. Amend[a,1], Keith A. Seifert[b], Robert Samson[c], and Thomas D. Bruns[a]

"Contrary to common ecological patterns, we show that fungal diversity is significantly higher in temperate zones than in the tropics, with distance from the equator being the best predictor of phylogenetic community similarity"



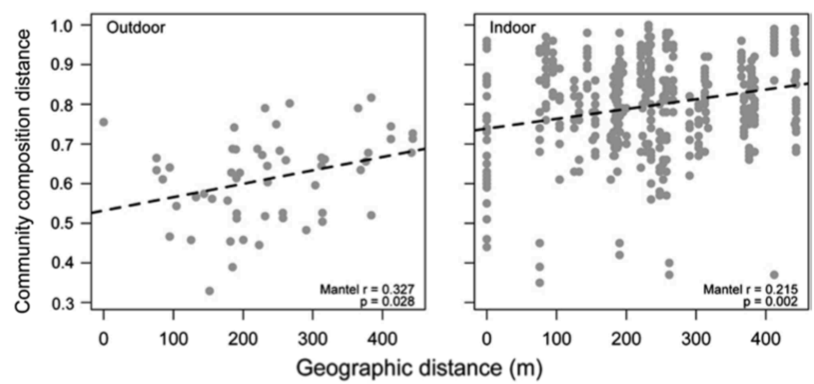
"Remarkably, building function has no significant effect on indoor fungal composition, despite stark contrasts between architecture and materials of some buildings in close proximity"

Amend et al. **2010** *PNAS* 107(31):13748

Dispersal in microbes: fungi in indoor air are dominated by outdoor air and show dispersal limitation at short distances

Rachel I Adams, Marzia Miletto, John W Taylor and Thomas D Bruns
Department of Plant and Microbial Biology, University of California, Berkeley, CA, USA

"Fungal assemblages indoors were diverse and strongly determined by dispersal from outdoors, and no fungal taxa were found as indicators of indoor air"



"More fungal biomass was detected outdoors than indoors"

"Room and occupant behavior had no detectable effect on the fungi found in indoor air"

Adams et al. **2013** *ISME J* 1:1-12

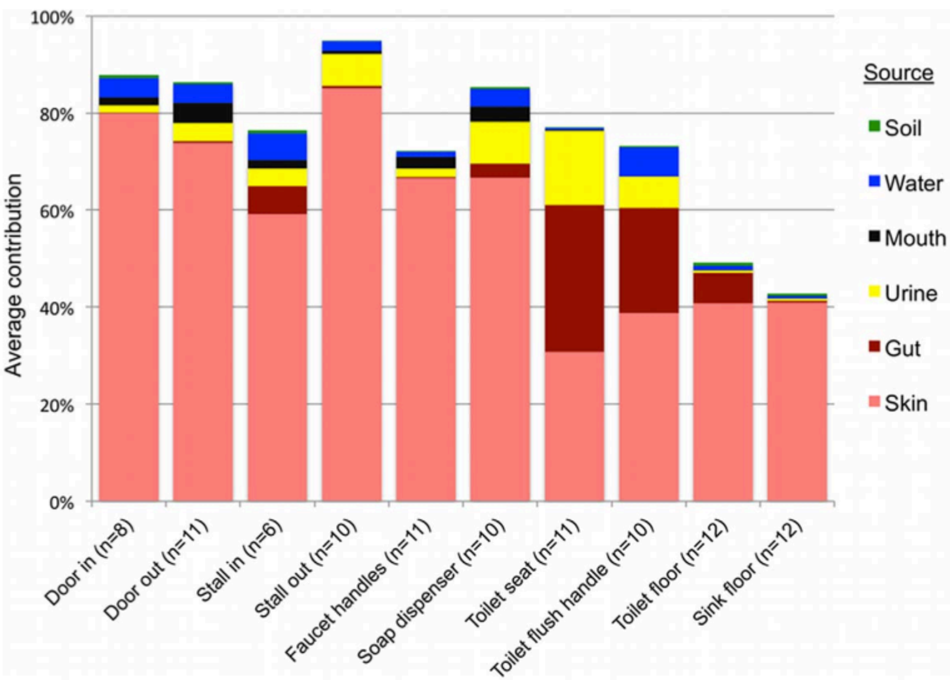
2009-present: Humans often dominate indoor bacterial communities in public spaces

Microbial Biogeography of Public Restroom Surfaces

Gilberto E. Flores[1], Scott T. Bates[1], Dan Knights[2], Christian L. Lauber[1], Jesse Stombaugh[3], Rob Knight[3,4], Noah Fierer[1,5]*

"Human-associated microbes are commonly found on restroom surfaces"

"Bacterial pathogens could readily be transmitted between individuals by the touching of surfaces"



Flores et al. **2011** *PLoS ONE* 6(11):e28132

Human Occupancy as a Source of Indoor Airborne Bacteria

Denina Hospodsky[1], Jing Qian[1¤a], William W. Nazaroff[2], Naomichi Yamamoto[1,3], Kyle Bibby[1], Hamid Rismani-Yazdi[1¤b], Jordan Peccia[1]*

"Occupancy increased the total aerosol mass and bacterial genome concentration in indoor air… with an increase of nearly two orders of magnitude in airborne bacterial genome concentration in PM_{10}"

"Floors are an important reservoir of human-associated bacteria"

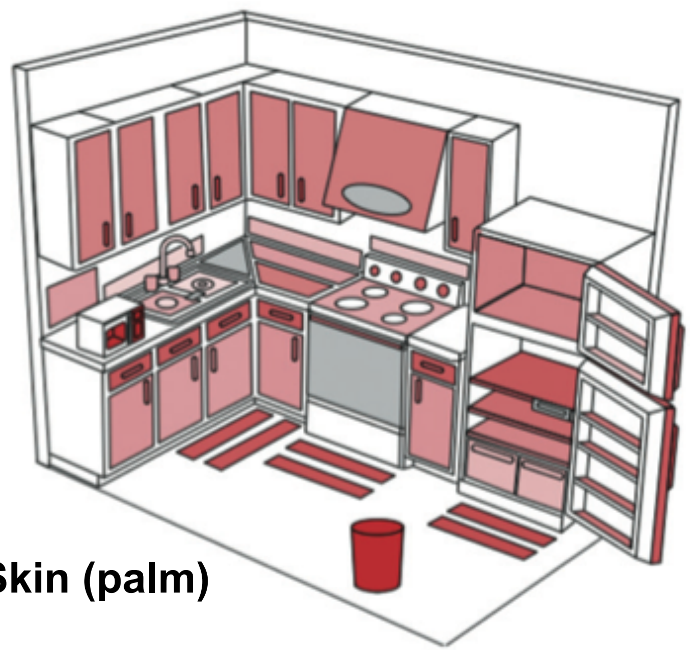
"Direct particle shedding of desquamated skin cells and their subsequent resuspension strongly influenced the airborne bacteria population structure in this human-occupied environment"

Hospodsky et al. **2012** *PLoS ONE* 7(40:e34867

2009-present: Humans often dominate indoor bacterial communities in homes (w/ modifications by other factors)

Diversity, distribution and sources of bacteria in residential kitchens

"Human skin was the primary source of bacteria across all kitchen surfaces, with contributions from food and faucet water dominating in a few specific locations"



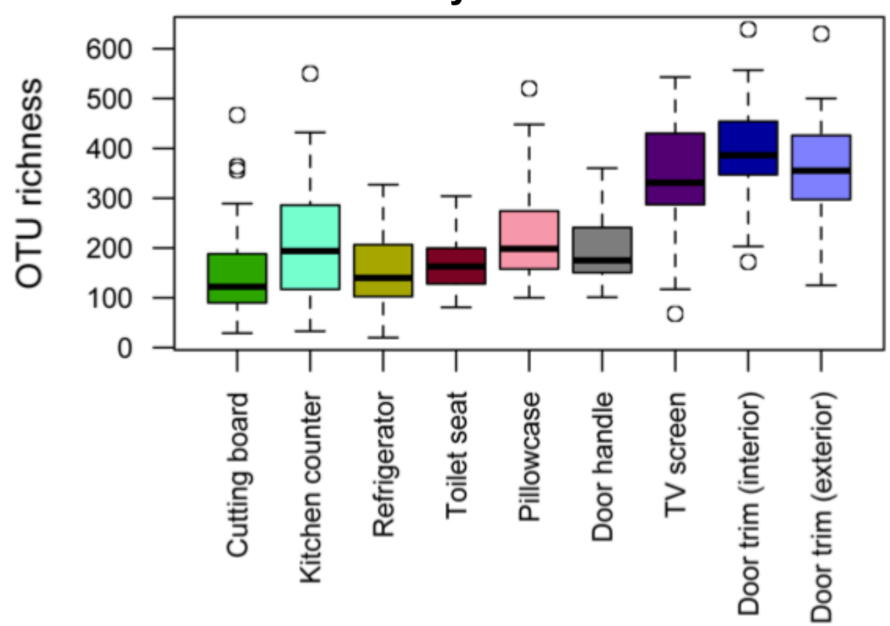
Flores et al. **2013** *Environ Microbio* 15:588-596

Home Life: Factors Structuring the Bacterial Diversity Found within and between Homes

Robert R. Dunn[1*], Noah Fierer[2,3], Jessica B. Henley[2], Jonathan W. Leff[2], Holly L. Menninger[1]

- Specific locations were distinct
- Presence of dogs → more diversity
- Correlations between I and O communities

Bacterial diversity across 40 homes in NC



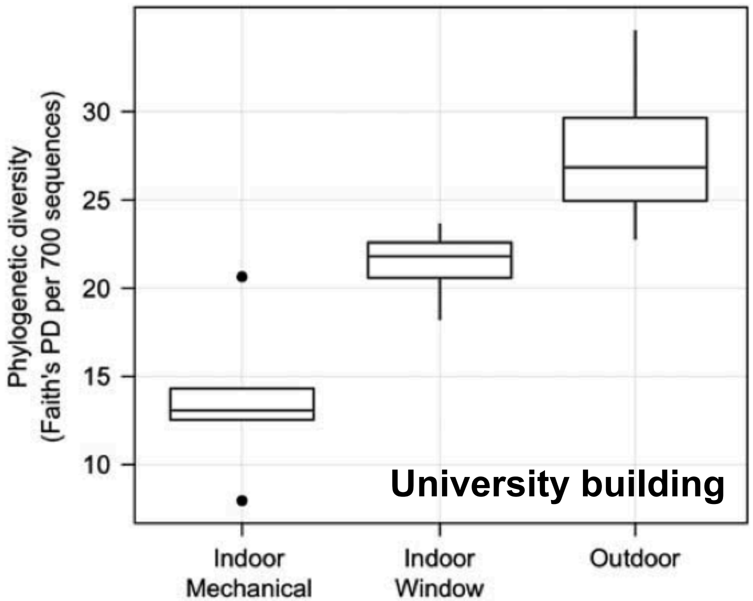
Dunn et al. **2013** *PLoS ONE* 8(5):e64133

2009-present: Building design can influence microbial communities

Architectural design influences the diversity and structure of the built environment microbiome

Steven W Kembel[1], Evan Jones[1], Jeff Kline[1,2], Dale Northcutt[1,2], Jason Stenson[1,2], Ann M Womack[1], Brendan JM Bohannan[1], G Z Brown[1,2] and Jessica L Green[1,3]

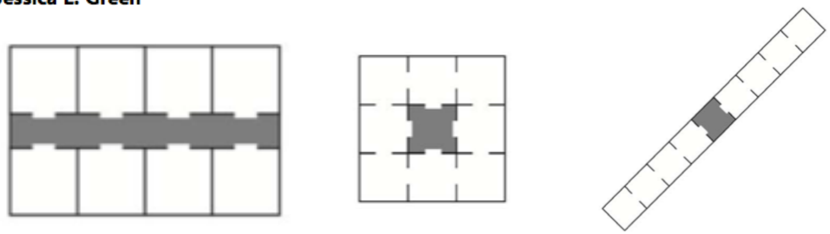
- Bacterial diversity: IA < OA
- Rooms w/ HVAC were less diverse than open window rooms
- Source of ventilation air and T/RH correlated w/ composition of IA bacteria



Kembel et al. **2012** *ISME J* 6:1469-1479

Architectural Design Drives the Biogeography of Indoor Bacterial Communities

Steven W. Kembel[1,2,3], James F. Meadow[2,3*], Timothy K. O'Connor[2,3,4], Gwynne Mhuireach[2,5], Dale Northcutt[2,5], Jeff Kline[2,5], Maxwell Moriyama[2,5], G. Z. Brown[2,5,6], Brendan J. M. Bohannan[2,3], Jessica L. Green[2,3,7]



"Spaces with high human occupant diversity and a high degree of connectedness to other spaces via ventilation or human movement contained a distinct set of bacterial taxa when compared to spaces with low occupant diversity and low connectedness"

"Within offices, the source of ventilation air had the greatest effect on bacterial community structure"

Kembel et al. **2014** *PLoS ONE* 9(1):e87093

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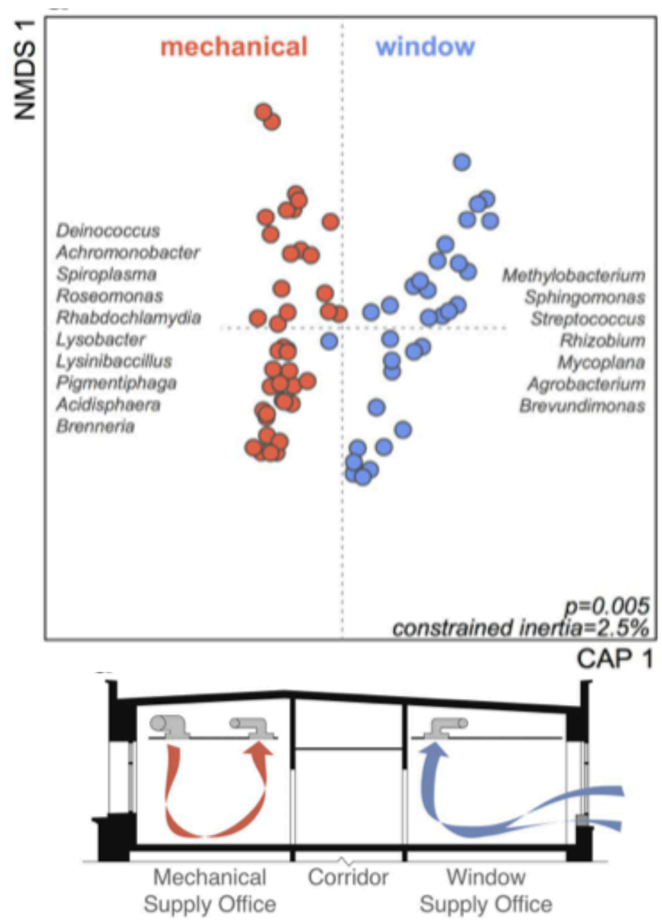
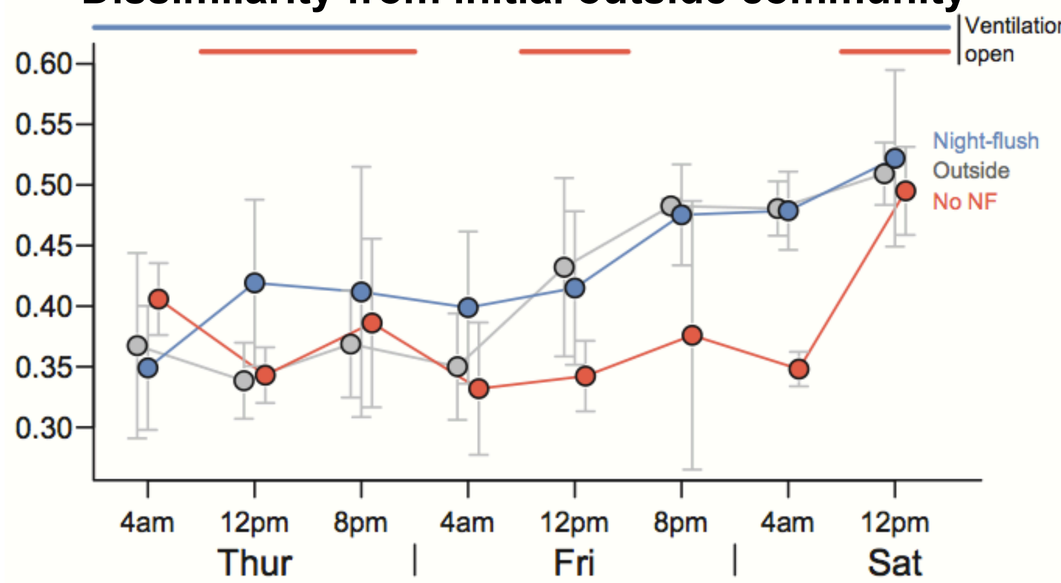


Indoor airborne bacterial communities are influenced by ventilation, occupancy, and outdoor air source

- Indoor air communities closely tracked OA
- Human-associated bacterial genera were more than 2x as abundant in IA vs. OA
- Ventilation had a demonstrated effect on indoor airborne bacterial community composition (following a time lag)

Dissimilarity from initial outside community



Kembel et al. **2014** *PLoS ONE* 9(1):e87093

Meadow et al. **2013** *Indoor Air* 24(1):41-48

Synthesis of MoBE project outcomes

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② Environmental engineer
③ Architectural engineer
④ Architect
⑤ Aerosol scientist
⑥ Health scientist
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Through the lens of a building scientist

- These recent studies have greatly increased our knowledge of microbial ecology of the indoor environment

- BUT the number of studies collecting robust, long-term data using standardized methods to characterize important building operational characteristics, indoor environmental conditions, and human occupancy (i.e., built environment metadata) remains limited

- Insufficiently described built environment metadata limits our ability to compare microbial ecology results from one indoor environment to another or to use the results to assess how best to control indoor microbial communities

Three main categories of investigations

We identified three general categories based on level of detail in documenting built environment metadata:

1. Microbial diversity in the absence of building characteristics

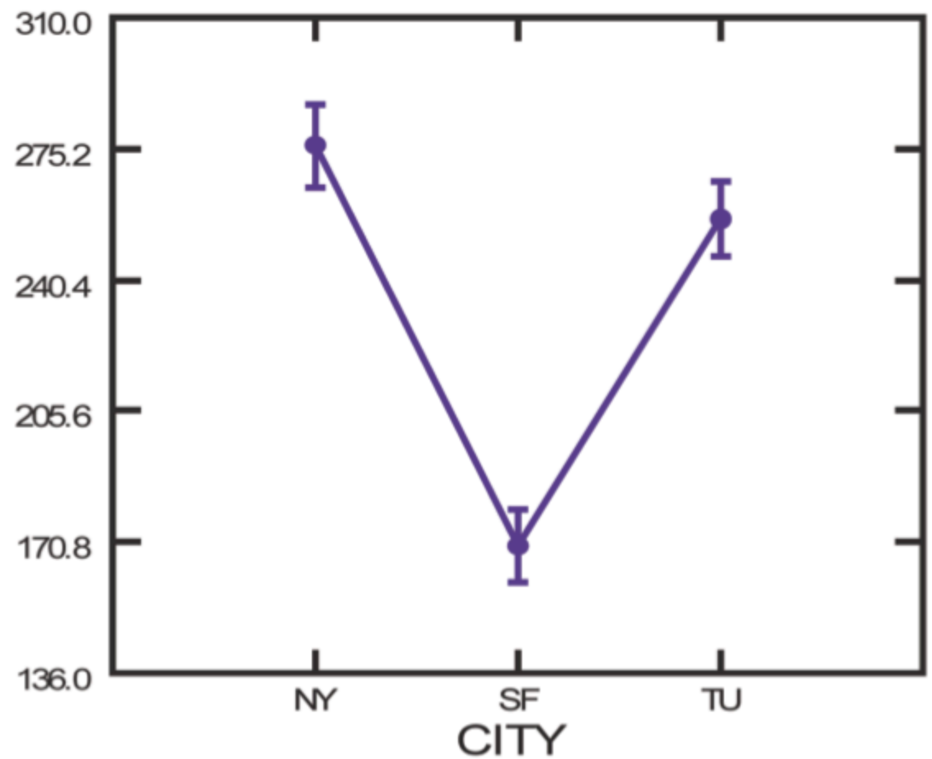
2. Microbial diversity and *basic* building, HVAC, and/or environmental metadata

3. Microbial diversity and *detailed* characterizations of built environment metadata and/or human occupancy/activities

Ramos and Stephens **2014** *under review*

1. Microbial diversity in the absence of building characteristics

Bacterial abundance in offices in 3 US cities

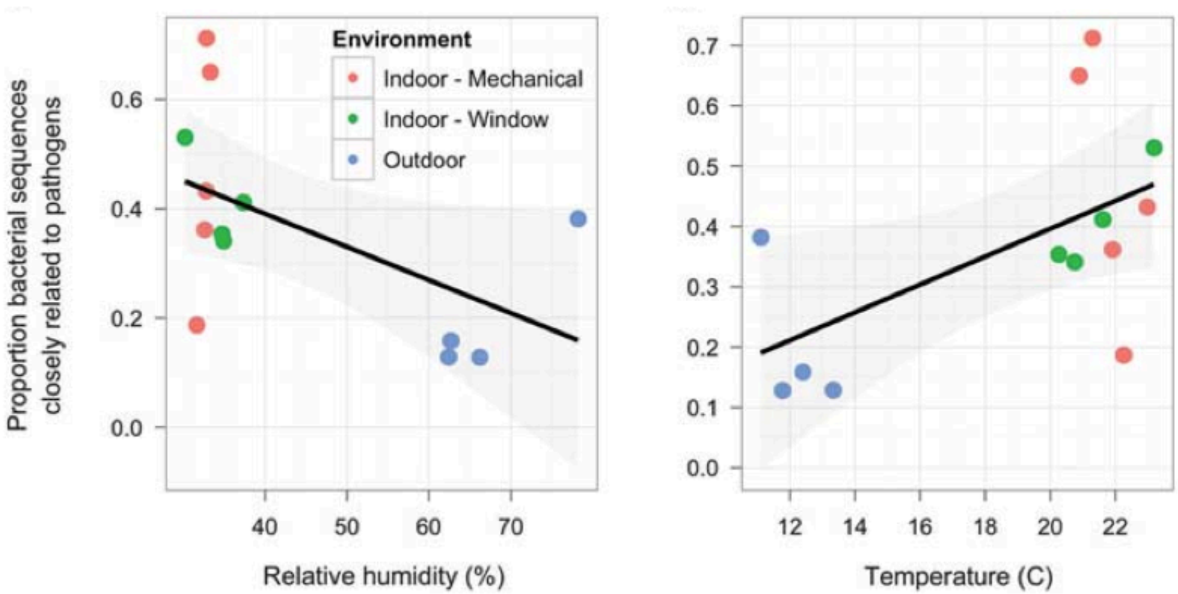


"Bacterial community diversity of the Tucson samples was clearly distinguishable from that of New York and San Francisco, which were indistinguishable"

Interesting, but ***why***?

Hewitt et al. **2012** *PLoS ONE* 7(5):e37849

2. Microbial diversity and *basic* building, HVAC, and/or environmental metadata



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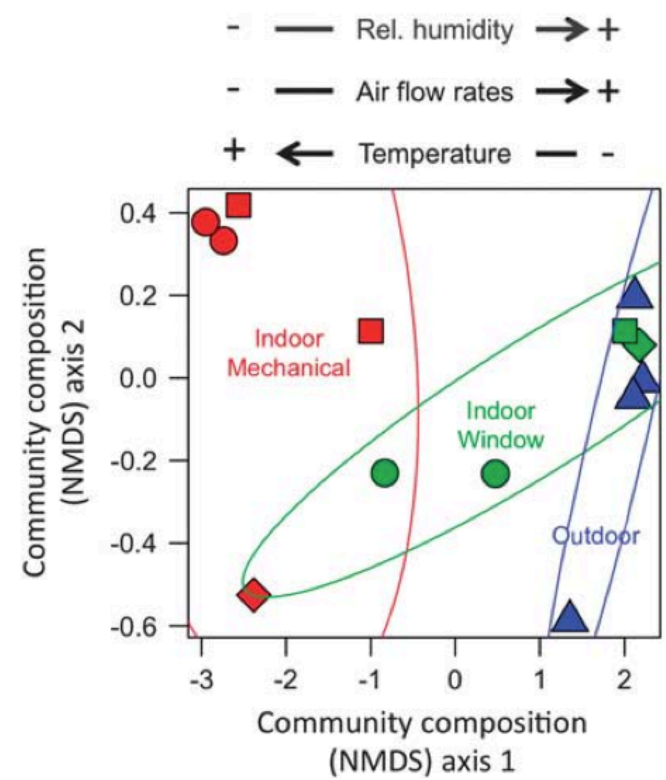


Interesting, but factors are correlated

"Bacterial richness tended to be higher in those four (of 11) units that reported at least occasional humidifier use"

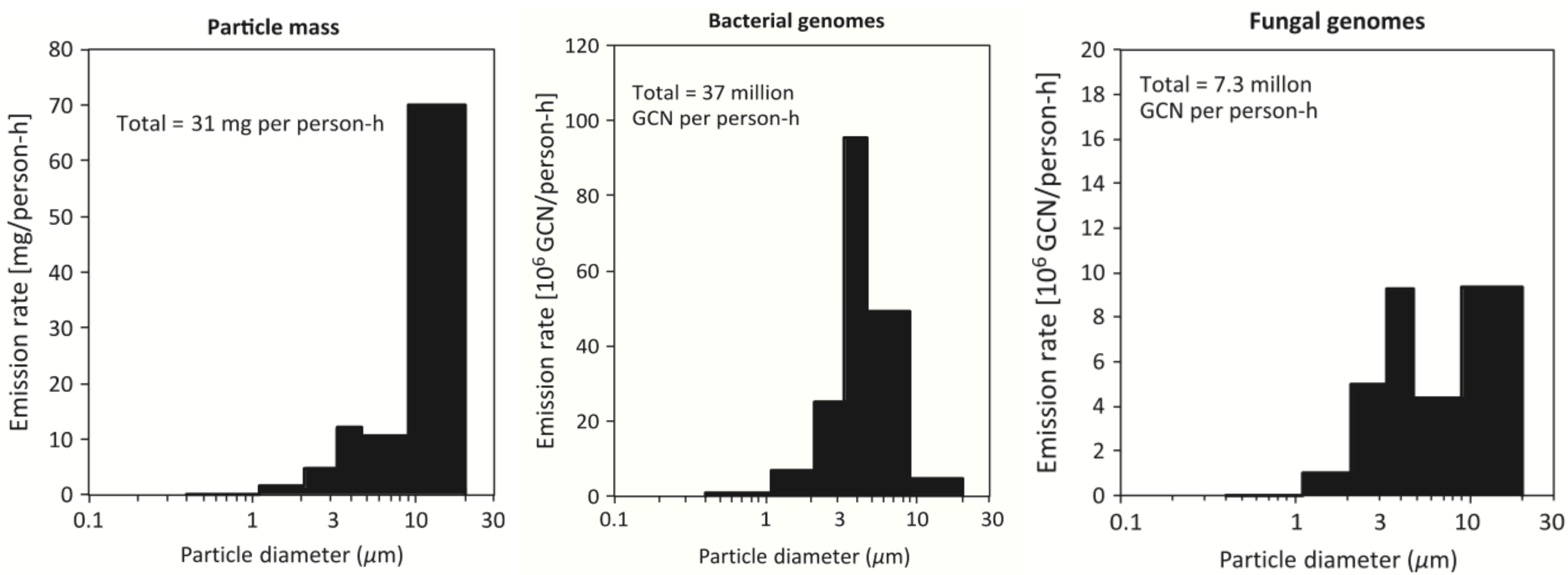
Adams et al. **2014** *PLoS ONE* 9(3):e91283

3. Microbial diversity and *detailed* building metadata and/or human activities

Size-resolved emission rates of airborne bacteria and fungi in an occupied classroom

J. Qian[1,2], D. Hospodsky[1], N. Yamamoto[1,3], W. W. Nazaroff[4], J. Peccia[1]

- Detailed characterization of building operation and occupancy allowed for estimating per-occupant emission rates using a mass-balance model… the power of building characterization



Qian et al. **2012** *Indoor Air* 22:339-351

Built environment metadata recommendations

I think that we should be paying closer attention to:

1. Measuring detailed building characteristics and indoor environmental conditions
   - Temp, RH, W, light
2. Measuring human occupancy and activity
   - Proximity, trip wires, CO_2, RFID, acoustic, Bluetooth, video
3. Characterizing HVAC systems and measuring ventilation rates
4. Standardizing air sampling and quantifying aerosol dynamics
5. Characterizing surfaces
   - Temp, a_w, pH, porosity, qualitative details, frequency of cleaning

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This morning's speakers

Perspectives on the MoBE program & identification of research needs:

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② Environmental engineer
③ Architectural engineer
④ Architect
⑤ Aerosol scientist
⑥ Health scientist
⑦ Microbiologist
⑧ Objective observer

- Jeffrey Siegel, University of Toronto | ①②③⑤
- Hal Levin, Building Ecology | ①④
- Shelly Miller, University of Colorado | ①②③⑤⑥
- Rachel Adams, University of California Berkeley | ⑦
- Seema Bhangar, University of California Berkeley | ②⑤⑥

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Breakout group assignments

Group 1	Group 2	Group 3
Rachel Adams	Seema Bhangar (**notes**)	Paul Francisco (**leader**)
Parham Azimi (**notes**)	Kyle Bibby	Jack Gilbert
Ian Cull	Edoarda Corradi (**notes**)	Denina Hospodsky
Rachael Jones	Bill Fisk (**leader**)	Hal Levin
Stephanie Kunkel (**notes**)	Lew Harriman	Shelly Miller
Bill Rose	Ben Stark	Atila Novoselac
Jeff Siegel (**leader**)	Iain Walker	Tiffanie Ramos (**notes**)
Brett Singer	Michael Waring	Zack Zanzinger (**notes**)

Roving: Brent Stephens, Paula Osliewski

Your tasks:

- Answer starter questions
- Develop list of specific research questions
- Group these into smaller list of thematic/overarching areas
- Work on a parallel list of ‘guiding principles’

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1:00 pm: Get outside! IIT campus tour

1:45 pm: Breakout discussion groups (groups of 7-8)

3:00 pm: Synthesize themes from breakout sessions and pitch a series research goals for the MoBE program

- Led by group leaders; participation from all team members
  - 15-min each team

3:45 pm: Group discussion leading towards consensus on research priorities

5:00 pm: End of workshop and departures

Workshop agenda

8:30 am: Kick-off presentations

- Paula Olsiewski, Sloan Foundation: Welcome
- Brent Stephens, IIT: Review of recent MoBE research

9:15 am: MoBE from the perspective of building science (and other related disciplines)

- 20-min invited presentations

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Consensus **priorities**

- Piggy back on health studies
- Investing in better methods for quantification
- Time for a cross-disciplinary hands-on workshop
  - Building science → microbial ecology
  - Microbial ecology → building science
- Need for a microbial swab-off
- Need for small sample size intervention studies / controlled environment studies
  - Fundamental processes (emission, survival)
  - Transport mechanisms
  - Impacts of BE factors (ventilation…)
    - Issues with recreating communities
- Personal dispersal of microbes within micro environments
  - Responsibility of surface Xfer versus air Xfer
- Think about ASHRAE money

Building science to advance research in the microbiology of the built environment (MoBE)

Supported by the Alfred P. Sloan Foundation

May 22-23, 2014 | Illinois Institute of Technology | Chicago, IL

ALFRED P. SLOAN FOUNDATION

ILLINOIS INSTITUTE OF TECHNOLOGY

- Reimbursements
- Travel back to airports
- Evaluation survey
- Summary report writing

Transit directions to Chicago O'Hare International Airport

3201 S Dearborn St
Chicago, IL 60616

Walk to 35-Bronzeville-IIT
About 13 mins (0.6 mi)

35-Bronzeville-IIT
M Green Line Subway towards Harlem
6:13am - 6:24am (12 mins, 6 stops)

Clark/Lake
M Blue Line Subway towards O'Hare
6:32am - 7:12am (40 mins, 16 stops)

O'Hare
Walk to Chicago O'Hare International Airport
About 4 mins (0.2 mi)

Chicago O'Hare International Airport
10000 West O'Hare Ave
Chicago, IL 60666

Travel time: about **1 hour 14 mins**

Transit directions to Chicago Midway International Airport

3201 S Dearborn St
Chicago, IL 60616

Walk to 35-Bronzeville-IIT
About 13 mins (0.6 mi)

35-Bronzeville-IIT
M Green Line Subway towards Harlem
6:13am - 6:21am (8 mins, 2 stops)

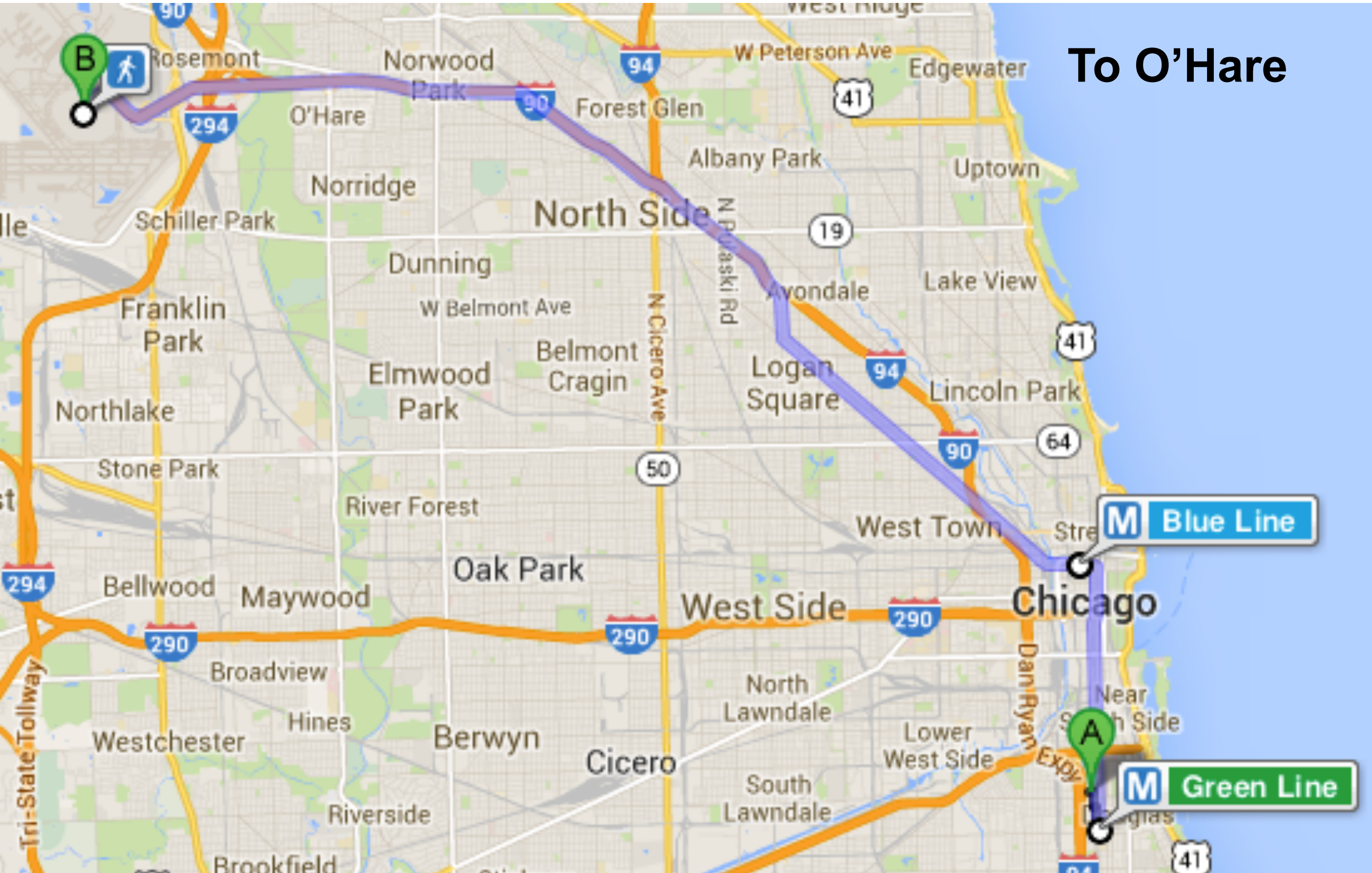
Adams/Wabash
M Orange Line Subway towards Midway
6:26am - 6:48am (22 mins, 8 stops)

Midway
Walk to Chicago Midway International Airport
About 7 mins (0.3 mi)

Chicago Midway International Airport
5700 S Cicero Ave
Chicago, IL 60638

Travel time: about **51 mins**

To O'Hare



To Midway