

Home microbiome study

DANIEL SMITH ARGONNE NATIONAL LABORATORY

YOUR MICROBIOTA

- 10 bacterial cells for every human cell.
- Human health is dependent on microbiota



YOUR MICROBIOTA

o Science, 2009

Topographical and Temporal Diversity of the Human Skin Microbiome

Elizabeth A. Grice,¹ Heidi H. Kong,² Sean Conlan,¹ Clayton B. Deming,¹ Joie Davis,³ Alice C. Young,⁴ NISC Comparative Sequencing Program,⁴* Gerard G. Bouffard,^{4,5} Robert W. Blakesley,^{4,5} Patrick R. Murray,⁶ Eric D. Green,^{4,5} Maria L. Turner,² Julia A. Segre¹†

Human skin is a large, heterogeneous organ that protects the body from pathogens while sustaining microorganisms that influence human health and disease. Our analysis of 165 ribosomal RNA gene sequences obtained from 20 distinct skin sites of healthy humans revealed that physiologically comparable sites harbor similar bacterial communities. The complexity and stability of the microbial community are dependent on the specific characteristics of the skin site. This topographical and temporal survey provides a baseline for studies that examine the role of bacterial communities in disease states and the microbial interdependencies required to maintain healthy skin.

YOUR MICROBIOTA

Nature Reviews Microbiology, 2011

The skin microbiome

Elizabeth A. Grice and Julia A. Segre

Abstract | The skin is the human body's largest organ, colonized by a diverse milieu of microorganisms, most of which are harmless or even beneficial to their host. Colonization is driven by the ecology of the skin surface, which is highly variable depending on topographical location, endogenous host factors and exogenous environmental factors. The cutaneous innate and adaptive immune responses can modulate the skin microbiota, but the microbiota also functions in educating the immune system. The development of molecular methods to identify microorganisms has led to an emerging view of the resident skin bacteria as highly diverse and variable. An enhanced understanding of the skin microbiome is necessary to gain insight into microbial involvement in human skin disorders and to enable novel promicrobial and antimicrobial therapeutic approaches for their treatment.

YOUR HOME'S MICROBIOME

OPEN OACCESS Freely available online



The Airborne Metagenome in an Indoor Urban Environment

Susannah G. Tringe^{1,2®}, Tao Zhang^{3®}, Xuguo Liu³, Yiting Yu³, Wah Heng Lee³, Jennifer Yap⁴, Fei Yao³, Sim Tiow Suan⁵, Seah Keng Ing⁵, Matthew Haynes⁶, Forest Rohwer⁶, Chia Lin Wei³, Patrick Tan³, James Bristow^{1,2}, Edward M. Rubin^{1,2*}, Yijun Ruan^{3*}

1 Department of Energy (DOE) Joint Genome Institute, Walnut Creek, California, United States of America, 2 Genomics Division, Lawrence Berkeley National Laboratory, Berkeley, California, United States of America, 3 Genome Institute of Singapore, Singapore, Republic of Singapore, 4 Environmental Health Institute, National Environment Agency, Singapore, Republic of Singapore, 5 Department of Microbiology, National University of Singapore, Singapore, Republic of Singapore, 6 Biology Department and Center for Microbial Science, San Diego State University, North Life Sciences, San Diego, California, United States of America

Abstract

The indoor atmosphere is an ecological unit that impacts on public health. To investigate the composition of organisms in this space, we applied culture-independent approaches to microbes harvested from the air of two densely populated urban buildings, from which we analyzed 80 megabases genomic DNA sequence and 6000 16S rDNA clones. The air microbiota is primarily bacteria, including potential opportunistic pathogens commonly isolated from human-inhabited environments such as hospitals, but none of the data contain matches to virulent pathogens or bioterror agents. 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. Sequence annotation by gene function revealed specific adaptive capabilities enriched in the air environment, including genes potentially involved in resistance to desiccation and oxidative damage. This baseline index of air microbiota will be valuable for improving designs of surveillance for natural or man-made release of virulent pathogens.

YOUR HOME'S MICROBIOME

- Building-specific seasonal patterns in bacteria found on dust.
- In-progress research is exploring the microbial communities of several locations in houses: kitchen surfaces (including inside the refrigerator), tv screens, pillows, the water inside of water heaters, etc, etc.





INTERACTION OF MICROBIOMES

 Human shed about 1.5 millions cells per hour, along with their associated 15 million bacteria cells.

 Direct contact can transfer millions of cells in each event.

Journal of Applied Microbiology ISSN 1364-5072

ORIGINAL ARTICLE

Residence time and food contact time effects on transfer of *Salmonella* Typhimurium from tile, wood and carpet: testing the five-second rule

P. Dawson¹, I. Han¹, M. Cox¹, C. Black² and L. Simmons¹

Department of Food Science and Human Nutrition, Clemson University, Clemson, SC, USA
South Carolina Governor's School for Science and Mathematics summer research internship at Clemson University

Keywords

bacterial transfer, cross-contamination, fivesecond rule, food contact surface, residence time, *Salmonella*.

Abstract

Aims: Three experiments were conducted to determine the survival and transfer of *Salmonella* Typhimurium from wood, tile or carpet to bologna (sausage) and bread.



INTERACTION OF MICROBIOMES

 There is a lack of evidence regarding how rapidly the human skin microbiota is transferred to the surfaces of the homes in which we live.

• Hypotheses:

- Microbes from the occupant are transferred rapidly to the home and replace existing communities.
- The occupant's microbiome is reflected by the home's microbiome.
- Bacteria on surfaces will be most similar to the bacteria on the body parts that come into contact with it.

WHEN BIOMES COLLIDE



FIELD STUDY

Monitoring the home and human microbiota of relocating "citizen scientists".



SAMPLING

o <u>Human:</u>

- Palm of hand
- Heel of foot
- Inside of nose





- Kitchen countertop
- Kitchen floor
- Kitchen light switch
- Bedroom floor
- Front door knob
- Bathroom door knob

HOME METADATA

- Type of paint on walls
- Countertop material
- Type of flooring
- Light intensity
- o HVAC system
- Pets in household
- o Square footage

DAILY METADATA

 Placed five-minute interval data loggers in the bathroom, kitchen, and bedroom to track:

- Relative Humidity
- Temperature
- Dew Point
- Participants also fill out the form at right each time they collect samples.

House:	Day:	Date:
Sampling Time		



....

ANALYSIS PCR-Amplify 16S rDNA V4-V5 Region Sequence 150bp x2 (paired end) **QIIME** Phylogenetic Assignment **Principle Coordinate Analysis**

ALPHA DIVERSITY





ALPHA DIVERSITY

 Most Diverse: Nose, hand, and handcontact surfaces in house #1.

Most Diverse House: House 1, followed by 2, then 3.



HOUSE 1 RESULTS



HOUSE 2 RESULTS



- -Corynebacteriaceae
- -Streptococcaceae
- -Actinomycetales

-Streptophyta

- ---Moraxellaceae (A)
- ---Pseudomonadaceae

HOUSE 3 RESULTS



3D PRINCIPLE COORDINATE PLOTS

HAND MICROBIAL COMMUNITIES

Individuals from different houses



Individuals from the same



BEDROOM FLOORS



KITCHEN COUNTERS



KITCHEN FLOORS



LIVE UPDATES

o HomeMicrobiome.com

o Facebook.com/HomeMicrobiome

- o Twitter.com/HomeMicrobiome
- All data publicly available



ACKNOWLEDGEMENTS

- o Jack Gilbert P.I.
- Jarrad Hampton-Marcell Sample Preps
- Sarah Owens Sequencing Manager
- Alfred P. Sloan Foundation Funding

