The microbiome, what it is and why we need to study it

Betsy Foxman
University of Michigan SPH
GOOD CITIZENS
WASH RIGHT!

1. Take soap - rub, rinse
2. Take your share...I towel
3. Take time to wipe dry
4. Take care of your towel

GERMS HATE SOAP and WATER...KEEP CLEAN!

CENTRAL HEALTH COUNCIL of the MERRIAM PUBLIC HOSPITALS in the Merrimack County Federation Association

It's an Old American Custom
KEEP CLEAN

Take a bath every day you can
Parents' Saliva On Pacifiers Could Ward Off Baby's Allergies

by ROB STEIN May 06, 2013 3:43 AM ET
Thousands of species live in and on us

- **Oral Cavity**: 3,000–11,500 bacterial species, 1–7 viral genera, 1–4 fungal phylotypes
- **Nares**: 2,000 bacterial species, 2–5 viral genera
- **Skin**: 2,000–3,000 bacterial species, 3–5 viral genera, 1–6 fungal genera
- **Vagina**: 2,000 bacterial species, 1–5 viral genera, 4–15 fungal OTUs
- **Stool**: 30,000–40,000 bacterial species, 0–2 viral genera, 1–3 fungal genera

We co-evolved for mutual benefit
Including regulating immune function

Short chain fatty acids (SCFA)
- Enhance barrier function
- Immune tolerance
- Enhance mucus production
- Activate inflammasomes
- Increase secretion IgA
- Reduce T cell-activating molecules
- Increase number and function of colonic regulatory T cells
- Decrease inflammatory responses in multiple organs

Rooks and Garrett, Nat Rev Immunology 2016
How to determine effects of the microbiome on human health?
Human microbiome is a dynamic ecologic community
Taxonomy

Do you know what **KPCOFGS** means?

Kingdom Phylum Class
Order Family Genus Species
King Philip Can Only Find Green Socks

![Diagram of the taxonomic hierarchy from Kingdom to Species]

- **Domain**: Eukarya
  - **Kingdom**: Animalia
    - **Phylum**: Chordata
      - **Class**: Mammalia
        - **Order**: Carnivora
          - **Family**: Felidae
            - **Genus**: Panthera
              - **Species**: Panthera pardus

Copyright © Pearson Education, Inc., publishing as Benjamin Cummings.
**Fig. 1.** Phylogeny of intestinal microbiota profiles by sex. Hierarchical clustering identified three distinct clusters in (A) healthy family members of patients with enteric infections, and five clusters in (B) the patients. The Neighbor-Joining tree was constructed based on the Bray–Curtis dissimilarity index with 1000 bootstrap replications. Communities from males are labeled in black outside the phylogeny, whereas female communities are labeled in gray.
Figure 3. Functional Maturation of the Fecal Microbiota in Vaginally Born Infants during the First Year of Life

Bäckhed et al., 2015, Cell Host & Microbe 17, 690–703
Ecologic characteristics

Environmental selection

Species pool

γ-diversity

Invasion sequence

α-diversity

Local community

Habitat type

β-diversity

Science 336, 1255 (2012);
‘omics results in lots of data

Healthcare Workers’ Hand Microbiome May Mediate Carriage of Hospital Pathogens

Mariana Rosenthal¹, Allison Aiello¹, Elaine Larson², Carol Chenoweth¹ and Betsy Foxman¹,*

Pathogens 2014, 3(1), 1-13; doi:10.3390/pathogens3010001
Relative Abundance of Top 12 Genera at 2 months by Milktype

Breast & Formula Fed  
Breast Fed  
Formula Fed

- Streptococcus
- Prevotella
- Haemophilus
- Veillonella
- Rothia
- Neisseria
- NA (Phylum: Proteobacteria)
- Gemella
- Granulicatella
- Actinomyces
- Alloprevotella
- Porphyromonas
- Other
The effects of family, dentition, and dental caries on the salivary microbiome

Betsy Foxman PhD\textsuperscript{a,\,*}, Ting Luo MPH\textsuperscript{a}, Usha Srinivasan PhD\textsuperscript{a}, Kirtana Ramadugu BS\textsuperscript{a}, Ai Wen PhD\textsuperscript{b}, Deborah Goldberg PhD\textsuperscript{c}, Kerby Shedden PhD\textsuperscript{d}, Richard Crout DMD, PhD\textsuperscript{e,f}, Daniel W. McNeil PhD\textsuperscript{f,g}, Robert Weyant DMD, DrPh\textsuperscript{f}, Mary L. Marazita PhD\textsuperscript{f}
Family Effects > Decay Effects
In untargeted metabolomic screen, family > decay

Group pp_ss (n=5)

Group pp_dd (n=4)

Group pp_sd (n=6)

Sib1: primary-sound    Sib2: primary-sound

Sib1: primary-decayed    Sib2: primary-decayed

Sib2: primary-decayed

Sound

Decayed
Transmission of Oral microbiome and Sequencing

Kyu Han Lee
Aubree Gordon
Guillermina Kuan
Angel Balmaseda
Betsy Foxman
Enroll household contacts of influenza cases

Monitor for influenza infection

Examine change in bacterial community structure

- Sociodemographic & clinical factors
- Microbiome
- Bacterial density

Microbiome
Bacterial density
Microbial community types varies by age, and is associated with influenza risk

<table>
<thead>
<tr>
<th>Age</th>
<th>CT Participants</th>
<th>Pr(Influenza)</th>
</tr>
</thead>
<tbody>
<tr>
<td>All</td>
<td>131</td>
<td>14.5%</td>
</tr>
<tr>
<td>2</td>
<td>122</td>
<td>15.6%</td>
</tr>
<tr>
<td>3</td>
<td>121</td>
<td>12.4%</td>
</tr>
<tr>
<td>&lt;6 Yrs</td>
<td>9</td>
<td>33.3%</td>
</tr>
<tr>
<td>2</td>
<td>14</td>
<td>35.7%</td>
</tr>
<tr>
<td>3</td>
<td>3</td>
<td>33.3%</td>
</tr>
<tr>
<td>4</td>
<td>3</td>
<td>0.0%</td>
</tr>
<tr>
<td>5</td>
<td>26</td>
<td>15.4%</td>
</tr>
<tr>
<td>6-17 Yrs</td>
<td>51</td>
<td>17.6%</td>
</tr>
<tr>
<td>2</td>
<td>40</td>
<td>20.0%</td>
</tr>
<tr>
<td>3</td>
<td>38</td>
<td>18.4%</td>
</tr>
<tr>
<td>4</td>
<td>18</td>
<td>16.7%</td>
</tr>
<tr>
<td>5</td>
<td>9</td>
<td>11.1%</td>
</tr>
<tr>
<td>&gt;17 Yrs</td>
<td>71</td>
<td>9.9%</td>
</tr>
<tr>
<td>2</td>
<td>68</td>
<td>8.8%</td>
</tr>
<tr>
<td>3</td>
<td>80</td>
<td>8.8%</td>
</tr>
<tr>
<td>4</td>
<td>62</td>
<td>3.2%</td>
</tr>
<tr>
<td>5</td>
<td>23</td>
<td>4.3%</td>
</tr>
</tbody>
</table>
YOU ARE MAINLY MICROBE

http://i.ytimg.com/vi/4BZME8H7-KU/0.jpg