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NHGRI/NIH

for NIH Human Microbiome Project

April 11, 2011

Health Disparities Summit
Today’s talk

What are microbes and why are they important?

What is the human microbiome and why is it important?

Highlights from the NIH Human Microbiome Project

Summary
What are microbes?

- often used to mean bacteria
- broader meaning: microbial lifeforms
- common features: microscopic, communities
- many kinds: bacteria, viruses, fungi, protozoa

Bacteria
- Living cells
  - Ex. Cheese bacteria

Viruses
- Not living, reproduce in cells
  - Ex. Cold virus

Fungi
- Living cells
  - Ex. Bread yeasts

Protozoa
- Living cells, eat bacteria
  - Ex. amoeba
Though many diseases are caused by microbes: cholera, tuberculosis, AIDS, malaria, measles, food-borne disease, etc.

The **MAJORITY** of microbes do not cause disease. Rather, they contribute to:

- Food production (bread, cheese, yogurt, beer, chocolate, coffee, etc.)
- Soil production/regeneration
- Oxygen production
- Pollutant/toxin degradation
- Human health
Human Microbiome:
full complement of microbes and their genes in/on the human body.

- 10x more microbial cells than human cells.
- Human microbiome has ~ 1000 species.
- ~ 3 million microbial genes vs 23,000 human genes.
- ~ 3 lbs of microbes in the human gut; ~ 60% of stool dry matter is microbial mass.
- Each body site (e.g. gut, skin, oral, nasal, urogenital) is home to a unique community.

Source for figure: Costello et al. (2009)
Roles of the human microbiota

*Develop/manage our immune system*

*Protect against opportunistic pathogens*

*Digest food/produce energy*

*Produce beneficial compounds*
Newborns obtain microbes from the mother.

Source of figure: Dominguez-Bello et al. (2010).
Infant microbiome establishes during first year of life.

Bacterial numbers increase ~ 6 orders of magnitude within weeks of life. And becomes more adult-like within the first year of life.

In the adult

Microbiota composition is unique to each body site.

with few differences:
over time between adults by gender

Source of figures: Costello et al. (2009)
But the microbiome continues to change over a lifetime.

Gut microbiome changes from mid-age to elderly adults. Elderly (> 65 y.o.) have unique microbiota.

Source of figure: M. J. Claesson et al. (2010). (ELDERMET project)
NIH HMP Mission:

to characterize the microbes that inhabit the human body and examine whether changes in the microbiome can be related to health and disease.

http://commonfund.nih.gov/hmp

http://www.hmpdacc.org
A. “Normal” cohort study:
   - Five major body sites (GI tract, skin, oral, nasal, urogenital)
   - Adult subjects only

B. Microbiome and disease studies ("Demonstration Projects"):
   - GI tract, skin, urogenital
   - Adults & children
Demonstration Projects:
Diseases associated with the GI tract microbiome.

Esophageal adenocarcinoma

Crohn’s diseases
Irritable bowel syndrome
Necrotizing enterocolitis
Ulcerative colitis
Demonstration Projects:
Diseases associated with the skin microbiome.

Atopic dermatitis (eczema)

Psoriasis

Source of figure: Kong and Segre (2011) Fitzpatrick’s Dermatology in General Medicine
Demonstration Projects: Diseases associated with the urogenital microbiome.

<table>
<thead>
<tr>
<th>Vaginal microbiome</th>
<th>Penis microbiome</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bacterial vaginosis</td>
<td>Circumcision</td>
</tr>
<tr>
<td>Reproductive history</td>
<td>Sexual history</td>
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<tr>
<td>STDs</td>
<td>STDs</td>
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</tbody>
</table>
### Gender/Ethnic/Racial Distribution in NIH Human Microbiome Studies

<table>
<thead>
<tr>
<th></th>
<th>HMP “Normal Cohort” (1)</th>
<th>HMP “Normal Cohort” (1)</th>
<th>HMP “Demo Projs” (15)</th>
<th>HMP “Demo Projs” (15)</th>
<th>NHLBI Lung (10)</th>
<th>NHLBI Lung (10)</th>
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</thead>
<tbody>
<tr>
<td><strong>Total no. of volunteers: M/F</strong></td>
<td>No.</td>
<td>%</td>
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<tr>
<td>150/150 (300)</td>
<td>50/50%</td>
<td>785/2960 (3745)</td>
<td>21/79%</td>
<td>1228/371 (1599)</td>
<td>77/23%</td>
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<tr>
<td><strong>Ethnicity</strong></td>
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<tr>
<td>Hispanic/Latino</td>
<td>123 11%</td>
<td>145 4%</td>
<td>246 15%</td>
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<tr>
<td>Not Hispanic/Latino</td>
<td>267 89%</td>
<td>3600 96%</td>
<td>1353 85%</td>
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<td><strong>Racial</strong></td>
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<tr>
<td>American Indian/Alaska Native</td>
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<td>-  -</td>
<td>14 1%</td>
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<tr>
<td>Asian</td>
<td>30 10%</td>
<td>98 3%</td>
<td>56 3%</td>
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<tr>
<td>Native Hawaiian/other Pacific Islander</td>
<td>-  -</td>
<td>-  -</td>
<td>-  -</td>
<td>11 1%</td>
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</tr>
<tr>
<td>Black or African American</td>
<td>18 6%</td>
<td>1587 42%</td>
<td>777 49%</td>
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</tr>
<tr>
<td>White</td>
<td>231 77%</td>
<td>1872 50%</td>
<td>741 46%</td>
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<tr>
<td>More than one race</td>
<td>12 4%</td>
<td>81 2%</td>
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</table>

Estimates based on data provided by grantees 040111. Some data are missing.
THE PROLIFERATION OF HUMAN MICROBIOME PROJECTS

- Canadian Microbiome Initiative: $10 million
- MetaHIT (EU and China): $31 million
- Human MetaGenome Consortium (Japan): $5 million
- MicroObes (France): $3 million
- Meta-GUT (China): $1.5 million
- Human Gastric Microbiome (Singapore): $750,000
- Australian Urogenital Microbiome Consortium: $600,000

All figures are estimates of cost in US dollars.

Source of figure: Nature 2008
Summary points

1. Microbiome composed of ~ 1000 species and ~3,000,000 microbial genes.


3. Infants acquire microbiota from mother & microbiome changes throughout lifetime.

4. Applications to treating disease and restoring health under intense investigation.
Acknowledgments

- Data Analysis and Coordination Center (DACC)
- 2 Clinical Sampling Centers
- 4 Sequencing Centers
- Data Analysis Working Group (DAWG)
- Demonstration Project Working Group (DPWG)
- 9 Demonstration Projects
- 10 Computational Tools Projects
- 15 Technology Development Projects
- 5 ELSI Projects
- ATCC/BEI

- NCCAM
- NCI
- NHGRI
- NHLBI
- NIA
- NIAAA
- NIAID
- NIAMS
- NIBIB
- NICHD
- NIDA
- NIDCR
- NIDDK
- NIEHS
- NIGMS
- NIMH
- OD
- ORWH
Questions?

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