

Welcome to the  
Symposium  
on

Our Second Genome

**Only about 10% of cells associated  
with a human body are human cells;  
the remaining 90% are cells of  
microorganisms.**

**Human body  
comprises 10  
trillion cells**

**100 trillion non-pathogenic  
bacteria/microorganisms  
reside in or on a human body**

# Microbiome

- Coined by: Joshua Lederberg (2001)
- “the ecological community of commensal, symbiotic, and pathogenic microorganisms that literally share our body space and have been all but ignored as determinants of health and disease.”

**Nose and throat  
(upper respiratory system)**

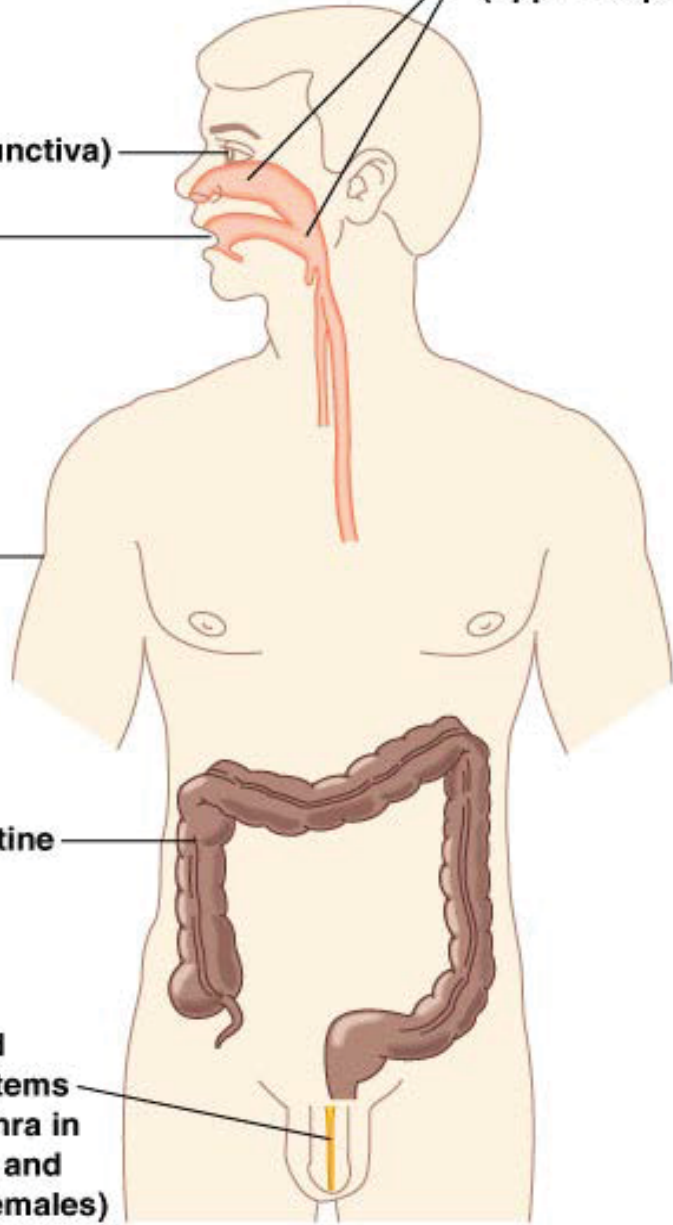
**Eyes (conjunctiva)**

**Mouth**

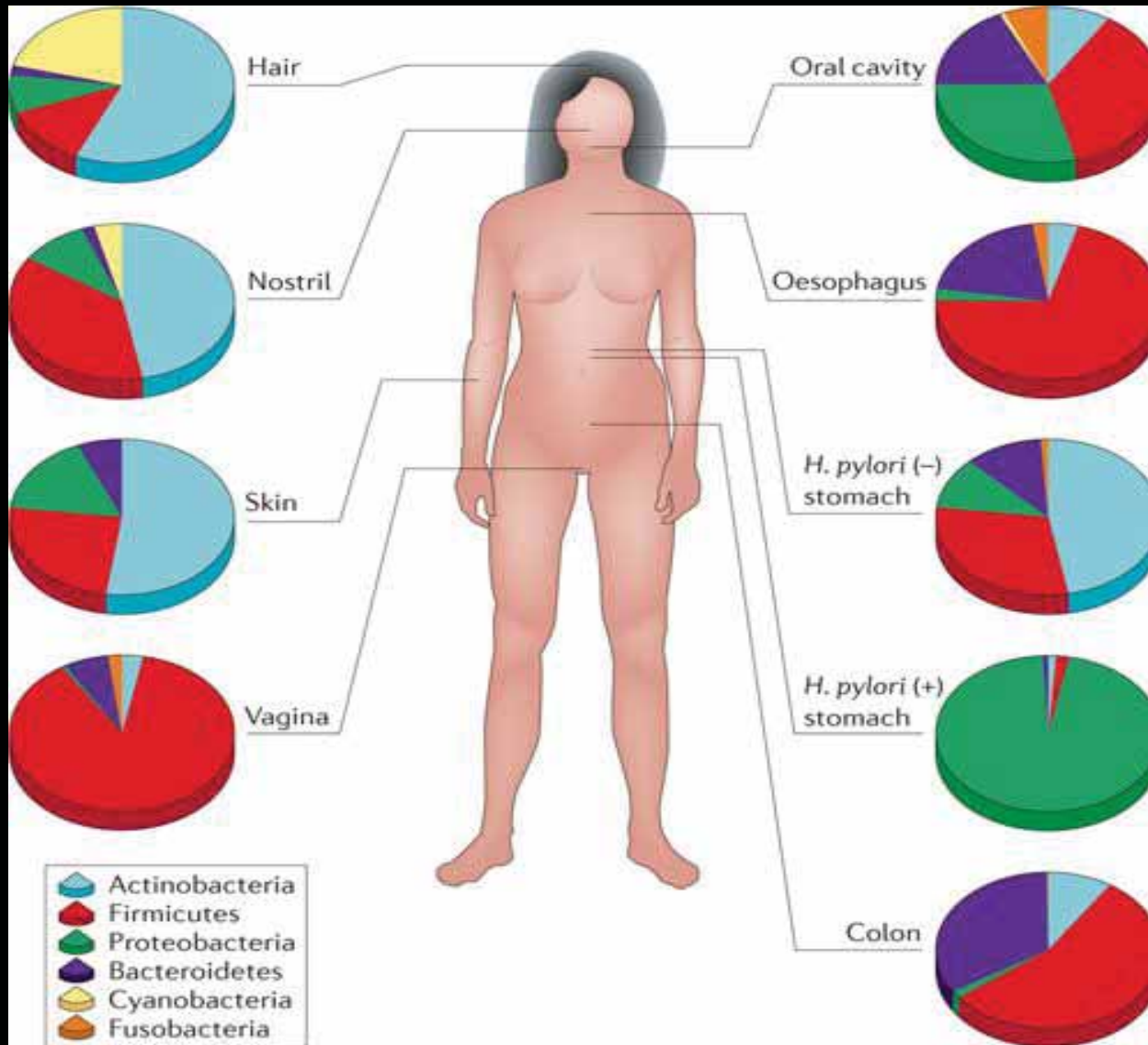
**Skin**

**Large intestine**

**Urinary and  
genital systems  
(lower urethra in  
both sexes and  
vagina in females)**

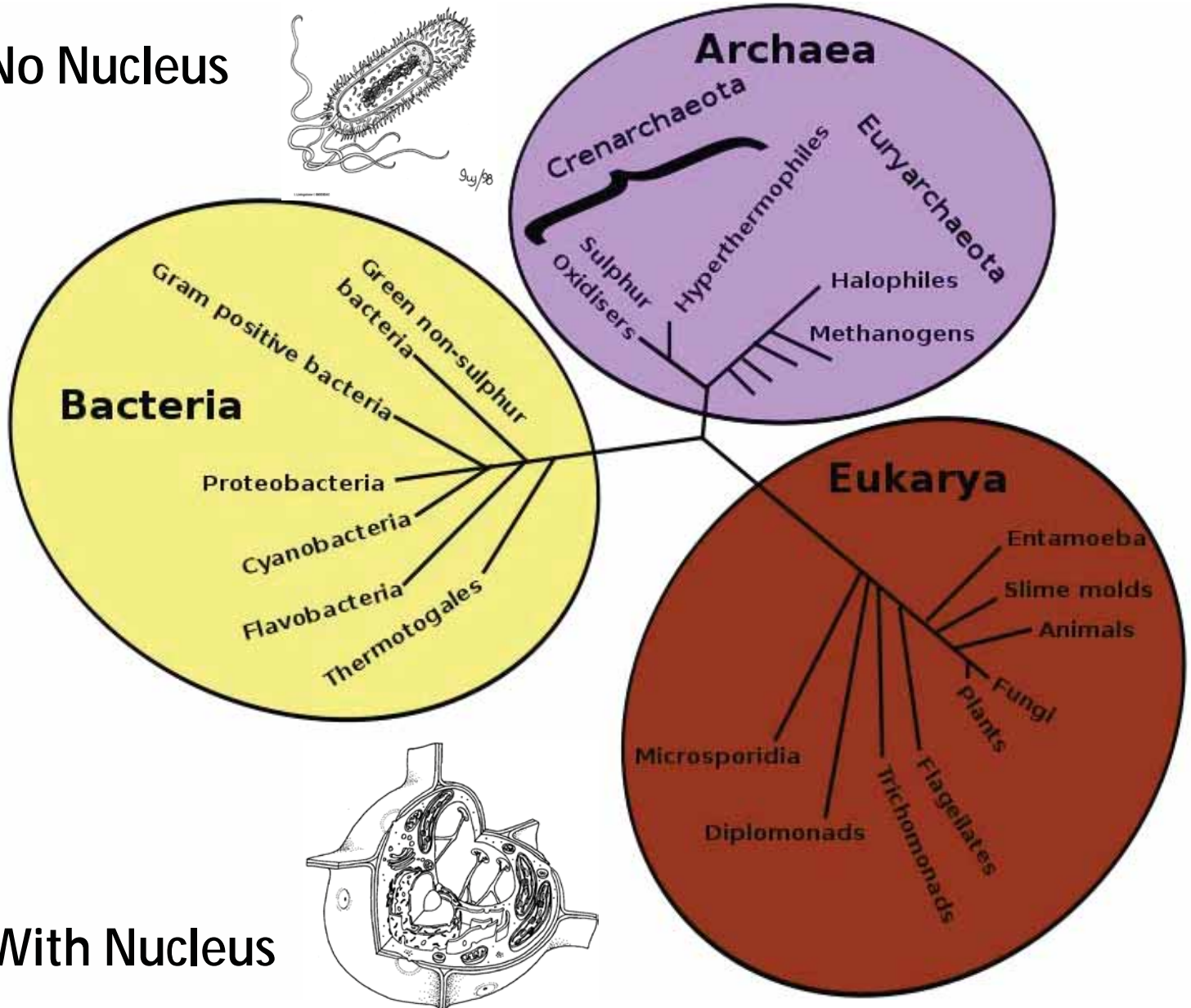
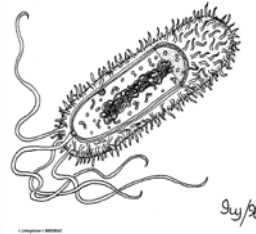


# Diversity across body regions

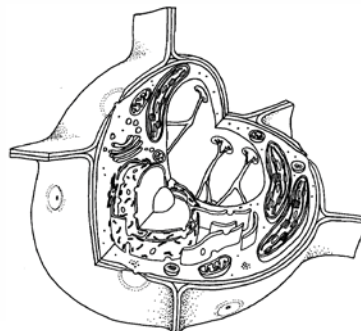


# Includes species from each major domain

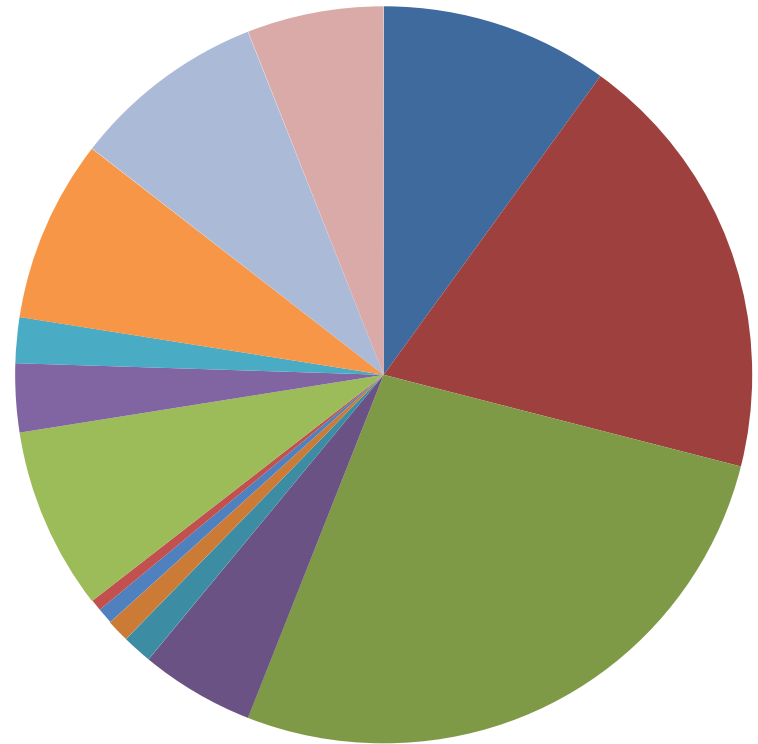
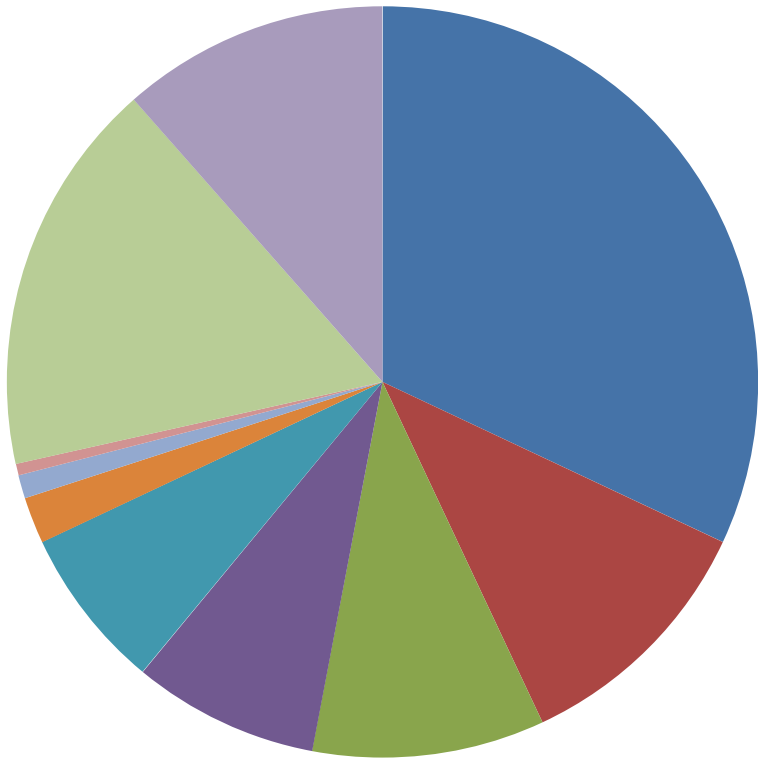
No Nucleus

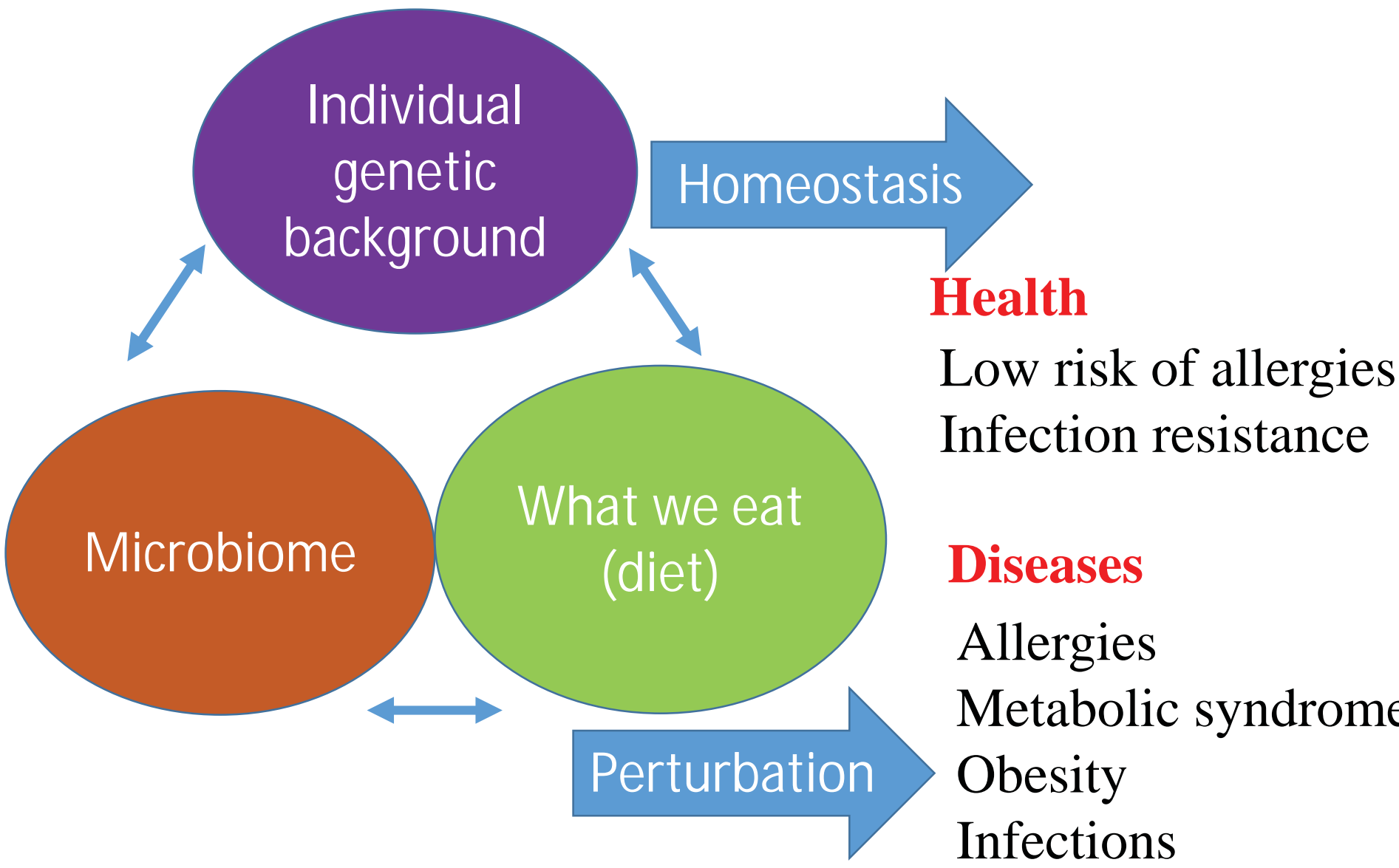


With Nucleus



# Diversity across individuals same body region








The understanding of the relationship of “our second genome” with that of our own genome is just beginning to emerge.

- DNA sequences to categorize organisms into taxonomic groups

Broadest  Narrowest  
domain, kingdom, phyla, class, order, family, genus, species

Two organisms from different domains would have less DNA sequence similarity than two organisms that belong to the same domain.

The more related the taxonomic unit for two organisms, the more similar their DNA sequences will be.

## Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans

Tommi Vatanen,<sup>1,2,22</sup> Aleksandar D. Kostic,<sup>1,3,4,22</sup> Eva d’Hennezel,<sup>5,22</sup> Heli Siljander,<sup>6,7,8</sup> Eric A. Franzosa,<sup>1,4</sup> Moran Yassour,<sup>1</sup> Raivo Kolde,<sup>3</sup> Hera Vlamakis,<sup>1</sup> Timothy D. Arthur,<sup>1</sup> Anu-Maaria Hämäläinen,<sup>9</sup> Aleksandr Peet,<sup>10</sup> Vallo Tillmann,<sup>10</sup> Raivo Uibo,<sup>11</sup> Sergei Mokurov,<sup>12</sup> Natalya Dorshakova,<sup>13</sup> Jorma Ilonen,<sup>14,15</sup> Suvi M. Virtanen,<sup>16,17,18</sup> Susanne J. Szabo,<sup>5</sup> Jeffrey A. Porter,<sup>5</sup> Harri Lähdesmäki,<sup>2</sup> Curtis Huttenhower,<sup>1,4</sup> Dirk Gevers,<sup>1,23</sup> Thomas W. Cullen,<sup>5,23</sup> Mikael Knip,<sup>6,7,8,19,23</sup> on behalf of the DIABIMMUNE Study Group, and Ramnik J. Xavier<sup>1,3,20,21,23,\*</sup>

nature  
genetics

## The effect of host genetics on the gut microbiome

Marc Jan Bonder<sup>1,19</sup>, Alexander Kurilshikov<sup>1–3,19</sup>, Etti F Tigchelaar<sup>1,4</sup>, Zlatan Mujagic<sup>4,5</sup>, Floris Imhann<sup>6</sup>, Arnau Vich Vila<sup>6</sup>, Patrick Deelen<sup>1,7</sup>, Tommi Vatanen<sup>8,9</sup>, Melanie Schirmer<sup>8,10</sup>, Sanne P Smeekens<sup>11,12</sup>, Daria V Zhernakova<sup>13</sup>, Soema A Janringradings<sup>13</sup>, Martin Leong<sup>11,12</sup>, Merie Osting<sup>11,12</sup>

## Temporal and spatial variation of the human microbiota during pregnancy

Daniel B. DiGiulio<sup>a,b,c,1</sup>, Benjamin J. Callahan<sup>a,d,1</sup>, Paul J. McMurdie<sup>a,d</sup>, Elizabeth K. Costello<sup>a,e</sup>, Deirdre J. Lyell<sup>a,f</sup>, Anna Robaczewska<sup>a,b,c</sup>, Christine L. Sun<sup>a,e</sup>, Daniela S. A. Goltsman<sup>a,e</sup>, Ronald J. Wong<sup>a,g</sup>, Gary Shaw<sup>a,g</sup>, David K. Stevenson<sup>a,g</sup>, Susan P. Holmes<sup>a,d</sup>, and David A. Relman<sup>a,b,c,e,2</sup>

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***Gut Microbiome and Health***

Sharmila Mande, Pune

***Novel Insights into The Human Microbiome***

Vineet K. Sharma, Bhopal

***The Microbiome in Skin Health and Disease***

Souvik Mukherjee (Kolkata)

***Towards a National Microbiome Project***

Shekhar Mande, Pune