

After the human genome project: The human microbiome project

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Earth Day may be more than a month away, but another, more personal, ecosystem has been shown to also be worth protecting—within our bodies are communities of microbes that affect the behavior of human cells hosting them. These communities, called the "microbiome," is so crucial to our health that some consider it to be a complex "second genome." Understanding the interaction of these microbes among one another and their human hosts has the potential to yield insights into numerous diseases and complex human disorders from obesity to susceptibility to infection.

In a new report appearing in the March 2013 issue of <u>*The FASEB</u></u> <u><i>Journal*</u>, scientists take an important step toward designing a uniform protocol for microbiome research that ensures proper controls and considerations for variations among people. By doing this, future researchers should be able to better assess how what we ingest, whether drugs or food, affects our bodies.</u>

"While historically pre and probiotics have dominated the microbiome landscape, emerging data from numerous labs as to the impact of dietary interventions and antibiotic exposure will play formative roles in tailoring therapy," said Kjersti M. Aagaard, M.D., Ph.D., from the Department of <u>Obstetrics and Gynecology</u> at Baylor College of Medicine in Houston, Texas. "We may find that the answers to our most common and prevalent health and disease states lies not in manipulating the <u>human genome</u>, but rather, in utilizing subtle shifts in diet and components of the diet, efficacy trials in prophylactic or preventative



antibiotic therapies, and care attention to the over prescription of steroids and antibiotics."

Aagaard and colleagues completed comprehensive body site sampling in healthy 18-40 year old adults, creating an unparalleled reference set of microbiome specimens. Researchers then screened 554 individuals to enroll 300 (149 males, 151 females, mean age 26, mean BMI 24, 20.0 percent racial minority and 10.7 percent Hispanic). Scientists obtained specimens from several body sites to evaluate the longitudinal changes in an individual's microbiome by sampling 279 participants twice (mean 212 days after first sampling, range 30-359), and 100 individuals three times (mean 72 days after second sampling, range 30-224). This sampling strategy yielded 11,174 primary specimens, from which 12,479 DNA samples were submitted to four centers for metagenomic sequencing. This clinical design and well-defined reference cohort has laid a baseline foundation for microbiome research.

"Whether it is yogurt, penicillin, or diet soda, each alters the microbial communities that live within us," said Gerald Weissmann, M.D., Editorin-Chief of *The* FASEB Journal. "This pioneering study promises to provide their names and numbers, so that we can understand how diet, disease or drugs affect our internal ecosystem."

More information: Kjersti Aagaard, Joseph Petrosino, Wendy Keitel, Mark Watson, James Katancik, Nathalia Garcia, Shital Patel, Mary Cutting, Tessa Madden, Holli Hamilton, Emily Harris, Dirk Gevers, Gina Simone, Pamela McInnes, and James Versalovic. The Human Microbiome Project strategy for comprehensive sampling of the human microbiome and why it matters. FASEB J March 2013 27:1012-1022, <u>doi:10.1096/fj.12-220806</u>



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