

News from the NIH Human Microbiome Project

The National Institutes of Health Human Microbiome Project (HMP) is a 5-year initiative begun in 2008 to support foundational studies on the human microbiome and to develop community resources for the field. The HMP has been a capacity building enterprise for the study of complex microbial communities involved in human health and disease and has increased the appreciation for how personalized the human microbiome is. Host genetics, the environment, diet and the immune system all interact with the human microbiota to regulate the composition and function of the microbiome. As a community resource, the HMP has contributed over 1000 reference microbial genome sequences with a project goal of 3000 and the healthy human cohort study alone has contributed 4 Tbp of metagenomic microbial sequence, millions of 16S reads and a comprehensive body-wide survey of the human microbiome in hundreds of individuals.

Three recent developments emerging from HMP activities are highlighted below:

On May 24, 2011, Drs. Dirk Gevers (Broad Institute) and Curtis Huttenhower (Harvard School of Public Health), representing the HMP Research Consortium, will be reporting on key findings from the largest study of adult microbiomes to date at a late breaking session at the ASM annual meeting in New Orleans (item #1). They will report on major insights into the structure and function of microbiomes from 200 healthy adults sampled multiple times across 5 major body areas ([http://www.gm.asm.org/index.php/scientific-program/daily-schedule/tuesday-may-24#Late-Breaker Abstracts](http://www.gm.asm.org/index.php/scientific-program/daily-schedule/tuesday-may-24#Late-Breaker_Abstracts))

The HMP is making publically available at www.hmpdacc.org a very large set of data from this study: over 70 million targeted 16S sequences from over 5000 human microbiome samples as well as metagenome assemblies from over 600 human microbiome samples (item #2).

The metagenomics visualization tool, SitePainter, is being made publically available to the scientific community. This tool, developed by the lab of Rob Knight at the University of Colorado – Boulder for the HMP, allows the user to directly visualize the microbial composition and biochemical functions of microbiomes at key body sites (<http://www.hmpdacc.org/sp/>) (item #3).

For more information, contact: Lita Proctor, HMP Coordinator, NHGRI/NIH, lita.proctor@nih.gov

Item #1

Drs. Dirk Gevers and Curtis Huttenhower, representing the HMP Research Consortium, were selected by the ASM Late Breaking Session review committee, to report on recent key findings of the microbiomes of 200 healthy adults sampled multiple times across five major body areas (oral, nasal, skin, GI tract and urogenital). These analyses include studies of the microbial composition and metabolic functions of these microbiomes and are based on very large targeted 16S and metagenome assembly datasets of these microbiomes.

American Society for Microbiology General Meeting, New Orleans, LA
Late-Breaker Session, May 24, 2011, 3:00 PM – 5:30 PM

Session conveners: Roberto G. Kolter; Harvard Med. Sch., Boston, MA and Stanley R. Malloy; San Diego State Univ., San Diego, CA

Presentations for the HMP Research Consortium:

Microbial Community Composition of the Normal Human Microbiome

Dirk Gevers; The Broad Institute, Cambridge, MA

Microbial Community Function in the Normal Human Microbiome

Curtis Huttenhower; Harvard School of Public Health, Boston, MA

Item #2

Press Release: Human Microbiome Project data available to research community
Baltimore, Maryland

The Human Microbiome Project (HMP), a roadmap initiative funded through the National Institutes of Health, is now releasing reads and assembled sequences from whole metagenome shotgun sequencing of 690 microbiomes and ~ 72 million reads from targeted 16S sequencing of 5034 microbiomes from healthy human subjects for use by the scientific community via the [HMP Data Analysis and Coordination Center \(DACC\)](#), which is located at the Institute for Genome Sciences (IGS) at the University of Maryland School of Medicine.

Since its launch in 2008, the Human Microbiome Project has generated a huge volume of sequence, annotation and metadata. The HMP DACC is charged with the task of organizing this information and facilitating its use in analysis by researchers outside the HMP.

Now, on behalf of the HMP, the DACC is releasing both processed reads and assemblies from whole metagenome shotgun sequencing for an initial group of 690 metagenomes from a subset of >17,000 samples collected from 300 healthy human volunteers. Fifteen body habitats are represented in this collection. Assembly was carried out by the HMP Assembly Working Group. The DACC is in the process of generating a gene index of all proteins predicted from these assemblies which will be made available to the public upon completion. In addition ~72 million reads corresponding to deconvoluted, trimmed 16S sequences from 5034 samples are also available. 16S variable region V3-5 was sequenced for all 5034 samples, with variable regions V1-3 and V6-9 also sequenced for subsets of the samples. 18 body sites are represented in this 16S collection.

Sampling of the subjects was done at the Baylor College of Medicine and Washington University and sequencing was carried out by Washington University, Baylor College of Medicine, the J. Craig Venter Institute, and the Broad Institute.

Owen White, PhD, Director of Bioinformatics at the Institute for Genome Sciences, Professor of Epidemiology and Preventive Medicine at the University of Maryland School of Medicine, and Principal Investigator of the DACC explained, "These data provide the research community with a key resource for their human metagenomic studies, facilitating research into complex human diseases."

The whole metagenome read and assembly data is available at www.hmpdacc.org/HMASM/.
The 16S reads are available at www.hmpdacc.org/HM16STR/.

About IGS

The Institute for Genome Sciences (IGS) at the University of Maryland School of Medicine is an international research center dedicated to advancing the use of genomics to improve healthcare. Led by Dr. Claire Fraser-Liggett, a preeminent genome scientist and microbiologist, IGS is located in a 10-acre BioPark on the University of Baltimore's campus in downtown Baltimore. IGS scientists integrate genomics, bioinformatics and metagenomics into biomedical research. For more information, see www.igs.umaryland.edu.

Item #3

SitePainter is software developed by Antonio Gonzalez in the lab of Rob Knight at the University of Colorado –Boulder that allows information about microbial communities, including taxonomic and functional information, easily and visually accessible by showing abundance information or other features of microbial diversity on images supplied by the users. The HMP version of SitePainter allows particular bacteria and biochemical functions associated with different parts of the body to be identified rapidly (www.hmpdac.org/sp/)