

SELECTED ORAL PRESENTATION

Open Access

A data analysis and coordination center for the human microbiome project

Jennifer Wortman^{1*}, Michelle Giglio¹, Heather Creasy¹, Amy Chen², Konstantinos Liolios³, Ken Chu², Noam Davidovics¹, Mark Mazaitis¹, Todd DeSantis², Navjeet Singh², Joshua Orvis¹, Jonathan Crabtree¹, Victor Felix¹, Catherine Jordan¹, Anup Mahurkar¹, Rob Knight⁴, Gary Andersen², Nikos Kyrpides³, Victor Markowitz², Owen White¹

From Beyond the Genome: The true gene count, human evolution and disease genomics
Boston, MA, USA. 11-13 October 2010

The Human Microbiome Project (HMP) was launched by the National Institutes of Health (NIH) Roadmap for Medical Research and is designed to fuel research into the microbes that live in the various environments of the human body [1]. A major goal of the HMP is to look for correlations between changes in the microbiome and human health. The HMP will generate unprecedented amounts of sequence, annotation and metadata. The analysis of this data requires the ability to collect, integrate, and standardize information of different types and from different sources.

The HMP Data Analysis and Coordination Center (DACC) is the central repository for all HMP data, providing a specialized data management and analysis infrastructure to support the collection, integration and standardization of HMP data and facilitate research. HMP data sets will include over 1000 reference genomes isolated from the human body, as well as 16S ribosomal RNA, and whole metagenome shotgun sequencing of samples collected from multiple body sites and individuals. Successful data integration and standardization will rely on the use of controlled vocabularies, the application of quality control measures, and the development of standard operating procedures. The DACC web portal (<http://hmpdacc.org>) will provide multiple analysis resources to the research community including data query and visualization, comparative genomics, 16S rRNA analysis, and comparative metagenomic community analysis. Reference genome status and relevant metadata are available through the HMP Project catalog (http://www.hmpdacc.org/project_catalog.html) while annotated HMP reference genomes are

provided as part of IMG/HMP (http://www.hmpdacc-resources.org/img_hmp), an HMP specific version of the Integrated Microbial Genomes (IMG) data management and analysis system. IMG/HMP serves as a community resource for comparative analysis of HMP genomes in the comprehensive integrated context of all publicly available microbial genomes.

Author details

¹Institute for Genome Sciences, University of Maryland School of Medicine, Baltimore, MD, USA. ²Lawrence Berkeley National Laboratory, Berkeley, CA, USA. ³Joint Genome Institute, Walnut Creek, CA, USA. ⁴University of Colorado at Boulder, Boulder, CO, USA.

Published: 11 October 2010

Reference

1. NIH HMP Working Group: The NIH Human Microbiome Project. *Genome Res.* 2009, **12**:2317-2323.

doi:10.1186/gb-2010-11-S1-O13

Cite this article as: Wortman et al.: A data analysis and coordination center for the human microbiome project. *Genome Biology* 2010 **11**(Suppl 1):O13.

Submit your next manuscript to BioMed Central and take full advantage of:

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

Submit your manuscript at
www.biomedcentral.com/submit

