

BCM scientists sequence microbes as part of Jumpstart for Human Microbiome Project

Baylor College of Medicine
HOUSTON -- (May 21, 2010) -- A consortium of genome sequencing leaders including the [Baylor College of Medicine](#) [1] Human Genome Sequencing Center released data on the first 178 microbial reference genomes representative of those in the human body in a report that appears in today's issue of the journal [Science](#) [2].

Others participating were the Broad Institute in Cambridge, Mass., the Genome Center at Washington University in St. Louis, Mo., and the J. Craig Venter Institute.

The Human Microbiome Project Jumpstart Consortium, consisting of the four institutions, was charged with selecting strains of microbes to sequence which represent those found in the human gastrointestinal tract, mouth, urogenital tract, skin and the respiratory tract. The 178 genomes released in this first publication from the Human Microbiome Project were submitted to detailed annotation and analysis. The Human Microbiome Project seeks to sequence at least 900 microbial genomes.

"One of the most interesting things from the work is that we have greatly increased the number of genes in the database of the [National Center for Biotechnology Information](#) [3] that are relevant to human microbes," said [Dr. Sarah Highlander](#) [4], associate professor of molecular virology and microbiology at BCM and a senior author of the Science report. "The results show that we are choosing the right organisms to sequence and that they are representative of members of the human microbiome."

Having these genomes as "reference" helps scientists understand and put into context the data as they are accumulated.

Dr. Karen E. Nelson of the non-profit Venter Institute, said, "This is a major study that moves us in the right direction to understanding the complex microbiota associated with the human body, and outlines how we benefit from this relationship. We will continue to learn more about the impact of these species in health and disease conditions."

Other BCM researchers who took part in this work include Dr. Kim.C. Worley; Dr. Richard A. Gibbs; Dr. Joseph .F. Petrosino; Donna M. Muzny; Dr. Xiang Qin; Lan Zhang; Andrew Cree; Lisa D. Hemphill; Vandita Joshi; Christie Kovar; Christian J. Buhay; Dr. Yi Ding; Shannon Dugan-Rocha; Michael Holder; Katarzyna Wilczek-Boney, and Dianhui Zhu.

Funding for this work came from the [National Human Genome Research Institute](#) [5]; the [Crohn's and Colitis Foundation of Canada](#) [6]; the Fund for Scientific Research; the [Canadian Cystic Fibrosis Foundation](#) [7] and the [Canadian Institutes](#)

[of Health Research](#) [8].

For more information on basic science information at Baylor College of Medicine, please go to www.bcm.edu/fromthelab [9].

[SOURCE](#) [10]

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http://www.mdtmag.com/news/2010/05/bcm-scientists-sequence-microbes-part-jumpstart-human-microbiome-project?qt-most_popular=0

Links:

[1] <http://www.bcm.edu/>

[2] <http://www.sciencemag.org/>

[3] <http://www.ncbi.nlm.nih.gov/>

[4] <http://www.bcm.edu/molvir/faculty/sarahh.htm>

[5] <http://www.genome.gov/>

[6] <http://www.cfc.ca/English/index.html>

[7] <http://www.cysticfibrosis.ca/en/index.php>

[8] <http://www.cihr-irsc.gc.ca/e/193.html>

[9] <http://www.bcm.edu/fromthelab/>

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