Letters

Studying the Human Microbiome

We would like to respond to Theodore White’s letter (“Is the Human Microbiome too Bacteriocentric?, Microbe, December 2009, p. 536) on the National Institutes of Health’s (NIH) Human Microbiome Project (HMP). Dr. White’s letter may give readers the impression that HMP is focused solely on the bacterial aspect of the human microbiome. While HMP’s early work emphasizes bacterial community characterization, the HMP is also actively studying eukaryotic microbes, viruses, including bacteriophages, and archaea from five areas of the body: the digestive tract, the mouth, the skin, the nose, and the vagina. In addition, several of the Demonstration Projects funded as part of the HMP have a focus on viruses or consider both prokaryotic as well as eukaryotic organisms as potential disease correlates.

Beyond the 16S rDNA sequence analysis work that is used for identifying bacteria, HMP sequencing centers are deploying whole-genome shotgun sequencing strategies, as well as more targeted sequencing approaches, such as virus isolation and 18S amplification, for identification of the viruses and eukaryotic microorganisms. Furthermore, HMP also includes many viruses and eukaryotic microbes as part of a collection of nearly 1,000 reference prokaryotic, eukaryotic, archaeal, and viral genomes that are being sequenced and made freely and publicly available to researchers.

For more information about the NIH HMP, please see the paper in Genome Research (19:2317–2323, 2009) that describes the project and keep up to date on HMP at http://www.hmpdacc.org and http://nihroadmap.nih.gov/hmp/.

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Correction

In the letter “Original Articles Versus Press Reports” in the January 2010 Microbe, p. 1, the letter misquotes the Forum in the October 2009 Microbe, p. 440, as ‘The authors “seized on extremophiles, giving the impression that such microbes have been discovered recently.”’ The October Forum stated, ‘Thus, NASA’s publicity machine has seized on “extremophiles,” giving the impression that such microbes have been discovered recently. . .’ Microbe regrets the error.