Genome sequence of strain HIMB55, a novel marine gammaproteobacterium of the OM60/NOR5 clade

Megan Huggett

Michael Rappe
Genome Sequence of Strain HIMB55, a Novel Marine Gammaproteobacterium of the OM60/NOR5 Clade

Megan J. Huggett and Michael S. Rappé

Genome Sequence of Strain HIMB55, a Novel Marine Gammaproteobacterium of the OM60/NOR5 Clade

Megan J. Huggett and Michael S. Rappé
Hawaii Institute of Marine Biology and Center for Microbial Oceanography: Research and Education, School of Ocean and Earth Science and Technology, University of Hawaii at Manoa, Kaneohe, Hawaii, USA

Strain HIMB55 is a phylogenetically unique member of the OM60/NOR5 clade of the Gammaproteobacteria isolated from coastal seawater of Kaneohe Bay on the northeastern shore of Oahu, Hawaii, by extinction culturing in seawater-based oligotrophic medium. Here we present the genome sequence of strain HIMB55, including genes for bacteriochlorophyll-based phototrophy.

The draft genome of HIMB55 comprised 2,736,988 bases and a G+C content of 52.90%. A total of 2,515 predicted open reading frames and 2,470 predicted protein-coding genes were identified, of which 2,085 have a predicted function. There are predicted single copies of the 5S, 16S, and 23S rRNA genes and 38 predicted tRNAs. A complete glycolysis pathway and tricarboxylic acid (TCA) cycle are predicted from the genome sequence, but the pentose-phosphate and Entner-Doudoroff pathways are incomplete. The genome contains complete pathways for the synthesis of all essential amino acids and a number of vitamins, including vitamin B<sub>6</sub>, para-amino benzoic acid, folate, lipic acid, nicotinic acid and nicotinamide, pantothenic acid, coenzyme A, and ubiquinone. Pathways for the synthesis of biotin, hemin, retinal, riboflavin, thiamine, and vitamin B<sub>12</sub> are incomplete.

The genome of strain HIMB55 contains genes for bacteriochlorophyll-based phototrophy but does not contain a proteorhodopsin gene comparable to that described for strain IMCC3088 (9). HIMB55 also contains genes that encode two phosphoenolpyruvate carboxylases and a carbonic anhydrase, indicating the potential for autotrophic carbon fixation.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at GenBank under accession number AGIF00000000. The version described in this paper is the second version, AGIF02000001.1.

ACKNOWLEDGMENTS

We thank Steve Ferriera, Justin Johnson, and other JCVI scientists for performing the sequencing and assembly of this genome, which was performed by the J. Craig Venter Institute through support provided by the Gordon and Betty Moore Foundation Marine Microbial Sequencing Project (http://www.moore.org/marinemicro). We also thank Maria Kim of the JCVI for her assistance.

Strain preparation, genomic DNA extraction, and annotation were supported by the Center for Microbial Oceanography: Research and Education (NSF Science and Technology Center Award EF-0424599).

REFERENCES


Received 3 February 2012 Accepted 13 February 2012
Address correspondence to Michael S. Rappé, rappe@hawaii.edu.
Copyright © 2012, American Society for Microbiology. All Rights Reserved.
doi:10.1128/JB.00171-12