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GENOME ANNOUNCEMENT

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

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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.

Strain HIMB55 was isolated from surface seawater of Kaneohe Bay on the northeastern shore of Oahu, Hawaii, via dilution-to-extinction culturing methods in low-nutrient heterotrophic medium (3). rRNA gene sequencing revealed that HIMB55 belongs to the OM60/NOR5 clade, a monophyletic lineage of marine bacterioplankton first identified via 16S rRNA gene cloning and sequencing from the Sargasso Sea (13), coastal waters off Cape Hatteras, North Carolina (14), and the North Sea (4). Cells of this lineage have been detected in high abundance (>10% of total cell counts) in the surface layer of the coastal ocean (5). A number of cultured strains from the OM60/NOR5 clade have been interrogated via whole genome sequencing, including *Congregibacter litoralis* KT71 (6), two strains isolated from Oregon coastal seawater (16), and one from the Yellow Sea (9). Comparative genomics and physiological experimentation show that members of the OM60/NOR5 clade possess diverse metabolic potential, including bacteriochlorophyll-based anoxygenic phototrophy and chemoheterotrophy (1, 2, 6, 15). Recently, a proteorhodopsin gene was also identified within the genome of OM60/NOR5 strain IMCC3088 (9).

The genome of HIMB55 was shotgun sequenced by the J. Craig Venter Institute as part of the Moore Foundation Microbial Genome Sequencing Project (http://camera.calit2.net/microgenome), resulting in 623,303 reads of 454 FLX Titanium sequence data. A draft genome was assembled to 95× coverage from 619,671 reads (260,601,228 bases) of sequence data. Gaps between contigs of the initial draft genome assembly were closed by sequencing PCR amplicons from genomic DNA, resulting in a single contig containing one unclosed gap. Functional annotation was performed with the Integrated Microbial Genomes Expert Review (IMG-ER) pipeline (12). Genes were identified using Prodigal (8) and were translated and used to search the NCBI nonredundant protein database and the UniProt, TIGRFam, Pfam, PRIAM, KEGG, COG, and InterPro databases. Nontranslated genes were predicted using tRNAScanSE (11), RNAmmer (10), and Rfam (7). Additional gene prediction analysis and manual functional annotation were performed within IMG-ER.

The draft genome of HIMB55 comprised 2,736,988 bases and had 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_6, para-aminobenzoic acid, folate, lipoic acid, nicotinic acid and nicotinamide, pantothenic acid, coenzyme A, and ubiquinone. Pathways for the synthesis of biotin, hemin, retinal, riboflavin, thiamines, and vitamin B_{12} 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.

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