

Genome Sequence of the Marine *Janibacter* Sp. Strain HTCC2649[∇]

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***Janibacter* sp. strain HTCC2649 is a novel marine member of the Actinobacteria, family Intrasporangiaceae, and is closely related to *Janibacter melonis* CM2104^T and *Knoellia sinensis* HKI 0119^T. The organism was isolated from a sample collected at Hydrostation S south of Bermuda by using high-throughput culturing techniques. Here we present the genome sequence of *Janibacter* sp. strain HTCC2649.**

Ongoing high-throughput culturing (HTC) studies to isolate and characterize novel bacterioplankton resulted in the cultivation of a novel marine *Actinobacteria*, *Janibacter* sp. strain HTCC2649. Distinct from the more abundant, and as-yet-uncultured, canonical and monophyletic “marine *Actinobacteria*” clade (OM1 clade) often recovered in culture-independent studies (2, 3, 8), HTCC2649 is more closely related to *Janibacter melonis* CM2104^T (13) and *Knoellia sinensis* HKI 0119^T (5), even though these three strains are found in very different habitats. Water collected at Hydrostation S, 12 miles southeast of Bermuda (see reference 10), from a depth of 10 m, was used to inoculate low-nutrient heterotrophic medium (LNHM) with amended mixed carbon compounds (9). After initial cultivation using previously described HTC techniques (1, 11), the dilution culture was plated on marine agar 2216. HTCC2649 was isolated as a single colony and transferred into liquid medium. The organism was selected for sequencing due to the unique phylogenetic position among the *Actinobacteria*.

Here we present the genome sequence of HTCC2649. DNA shotgun sequencing using a combination of Sanger and pyrosequencing (4) was conducted at the J. Craig Venter Institute as part of the Moore Foundation Microbial Genome Sequencing Project (<http://www.moore.org/microgenome>). A draft, unclosed genome consisting of 14 contigs (AAMN01000001 to AAMN01000014) was obtained and annotated with the GenDB annotation application program (7) at the Center for Genome Research and Biocomputing at Oregon State University, similarly to work previously described for another marine strain (12), and through the Joint Genome Institute IMG/M website (<http://img.jgi.doe.gov/cgi-bin/pub/main.cgi>) (6).

The unclosed draft genome has 4,228,723 bases comprising 4,156 predicted open reading frames (ORFs), with a G+C content of 68.44%. There are two predicted copies of the 5S, 16S, and 23S rRNA genes each and 50 predicted tRNAs. The genome contains putative genes for complete glycolysis, tricarboxylic acid cycle, pentose-phosphate, and Entner-Doudoroff

pathways and predicted genes for the utilization of starch, fructose, sucrose, and galactose. There are 144 predicted ABC transporters, and most of the *sec* genes are predicted to be present. Predicted genes exist for the synthesis of all essential amino acids, except histidine, and many essential vitamins/cofactors, except biotin and thiamine. In addition, there are four predicted phage-related genes, three of which are annotated integrases.

Nucleotide sequence accession number. The draft genome sequence of HTCC2649 is available in GenBank under accession number AAMN00000000. The GenDB-generated data were also processed to be accessible in the Marine Microbial Genomics database at Oregon State University (<http://bioinfo.cgrb.oregonstate.edu/microbes/>).

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