Draft Genome Sequence of the Moderately Halophilic Methanotroph
Methylohalobius crimeensis Strain 10Ki

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Methylohalobius crimeensis strain 10Ki is a moderately halophilic aerobic methanotroph isolated from a hypersaline lake in the Crimean Peninsula, Ukraine. This organism has the highest salt tolerance of any cultured methanotroph. Here, we present a draft genome sequence of this bacterium.

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Methylohalobius crimeensis strain 10Ki tolerates up to 15% NaCl (1), almost double the level of any other cultured methanotroph (2). The draft genome was sequenced, assembled, and annotated by the U.S. Department of Energy Joint Genome Institute (JGI) using Illumina and Pacific Biosciences (PacBio) technologies. Using the Illumina HiSeq 2000 (3), 20,000,000 reads totaling 1,780 Mb were generated from a long-insert mate pair library and 20,000,000 reads totaling 3,000 Mb from a standard shotgun library. Illumina sequence data were passed through DUK to remove known library preparation and sequencing errors (L. Mingkun, A. Copeland, and J. Han, unpublished data). An SMRTbell library was constructed and sequenced on the PacBio RS platform; 115,902 raw PacBio reads yielded 147,692 adapter-trimmed and quality-filtered subreads totaling 446.8 Mb. Filtered reads comprising 1365.7 × Illumina and 1277.7 × PacBio genome coverage were assembled using AllpathsLG (4). The final draft assembly contained five contigs in five scaffolds. The estimated size of the genome is 3.5 Mb, with an average G+C content of 58.3%. In total, 3,404 protein-coding genes and 95 pseudogenes were predicted.

Diverse genetic systems for osmotolerance were present, including (i) ectABCD genes for ectoine and hydroxyectoine synthesis, along with a second copy of ectoine synthase ectC, (ii) a gene encoding a high-affinity importer of choline/glycine betaine driven by a sodium-motive force (5), (iii) three gene copies for choline dehydrogenase and a gene 40% identical to betaine aldehyde dehydrogenase from Bacillus subtilis, (iv) a putative Na+/H+ antiporter localized within an ATP synthase-encoding gene cluster, and (v) a gene encoding an Na+/H+ antiporter localized within an ATP synthase-encoding gene cluster, and (vi) a pathway for sucrose synthesis and degradation/reutilization, including genes for sucrose-phosphate synthase, sucrose synthase, and fructokinase.

Genes encoding for assimilatory nitrate (nasA) and nitrite reductase (nirB), as well as dissimilatory nitric oxide reductase...
(norCB) and hydroxylamine dehydrogenase (haoA), were present. Nitrogen fixation genes were not.

**Nucleotide sequence accession numbers.** The *Methylohalobius crimeensis* strain 10Ki genome sequence was deposited in GenBank under the accession numbers ATXB01000001 to ATXB01000005.

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**REFERENCES**