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# Genome Sequence of “*Candidatus Aquiluna*” sp. Strain IMCC13023, a Marine Member of the *Actinobacteria* Isolated from an Arctic Fjord

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**We report the genome sequence of actinobacterial strain IMCC13023, isolated from arctic fjord seawater. Phylogenetic analysis of 16S rRNA gene showed that the strain is related to “*Candidatus Aquiluna rubra*.” The genome information suggests that strain IMCC13023 is a photoheterotroph carrying actinorhodopsin, with the smallest genome ever reported for a free-living member of the *Actinobacteria*.**

Members of the class *Actinobacteria*, such as the marine *Actinobacteria* clade (OM1 clade) (10), have been recognized as significant, if not major, contributors to marine microbial communities through culture-independent studies, including pyrosequencing of 16S rRNA genes, metagenome sequencing, and metaproteomics (5, 7, 8, 13, 14). “*Candidatus Aquiluna rubra*” in the family *Microbacteriaceae* of the *Actinobacteria* was initially proposed as an indigenous freshwater species based on the cultivation study from freshwater lakes (4). Many 16S rRNA gene sequences highly similar to “*Candidatus Aquiluna rubra*,” however, have been also obtained from saline environments, which makes the ecology and evolution of this lineage interesting (6, 9).

Strain IMCC13023 was isolated from a surface seawater sample collected off Kongsfjorden (Svalbard, Norway) during the glacier-melting season using high-throughput extinction-to-dilution culturing (HTC) (2). Pyrosequencing of 16S rRNA genes showed that gene clusters related to strain IMCC13023 comprised a significant portion of the bacterial community of Kongsfjorden seawater at the time of sampling. Phylogenetic analysis based on 16S rRNA gene sequences revealed that strain IMCC13023 is closely related to “*Candidatus Aquiluna rubra*” strain MWH-CanK2 (4) with 98.4% sequence similarity. Interestingly, many 16S rRNA gene sequences with more than 99% similarity to that of strain IMCC13023 have been found in both freshwater and marine environments, including the Arctic Ocean (JN177602), the Bering Sea (GQ452883), saline Lake Bonney, Antarctica (DQ015852), brine of Lake Vida, Antarctica (DQ521545 and GQ167333), freshwater Lake Saelenvannet, Norway (AJ575519), Smeerenburg Fjord, Svalbard (GQ259247), and Saanich Inlet, Canada (GQ347775). Because of the distribution of similar sequences from freshwater and saline environments, largely located in high-latitude regions, we performed genome sequencing of strain IMCC13023.

Genomic DNA was extracted from colonies formed on marine agar 2216 and used to prepare libraries for 100-bp paired-end sequencing with an Illumina genome analyzer. Sequencing reads were assembled by using the CLC Genomics Workbench (CLC Bio, Denmark), resulting in 6 contigs with an average coverage of 1,621-fold. The summed length of the contigs was 1,359,862 bp, the smallest genome size ever reported for free-living *Actinobacteria*, as of April 2012. The G+C ratio of the genome was 51.7 mol%, a slightly higher value than the range predicted for abundant freshwater actinobacterial groups (3).

Annotation of the genome sequence was performed by using the RAST server (1), which predicted 43 tRNA genes, one copy of each 16S, 23S, and 5S rRNA gene, and 1,365 open reading frames (ORFs). Functional annotation of ORFs was further improved by searching against the COG database and KEGG pathway maps. The genome of strain IMCC13023 contains a gene encoding actinorhodopsin, a microbial rhodopsin-family protein previously reported from actinobacterial isolates and metagenome sequences (11, 12). The amino acid sequence of IMCC13023 actinorhodopsin is most similar to those of freshwater members of “*Candidatus Aquiluna rubra*” and has residues known to be essential for light-driven proton pumping, suggesting the potential for photoheterotrophy of strain IMCC13023.

**Nucleotide sequence accession numbers.** This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AJKR00000000](#). The version described in this paper is the first version, AJKR01000000.

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