

GENOME ANNOUNCEMENTS

Complete Genome Sequence of Strain IMCC9063, Belonging to SAR11 Subgroup 3, Isolated from the Arctic Ocean[▽]

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Strain IMCC9063 is a novel isolate of the SAR11 clade and is distantly related to other cultured representatives in this clade. The strain was isolated off the coast of Svalbard, Norway, by applying high-throughput culturing methods based on dilution to extinction. Here we present the finished genome sequence of strain IMCC9063.

The SAR11 clade (4), the most abundant group of the *Bacteria* in the ocean (5), consists of at least four subgroups (3, 6) and plays an important role in marine carbon and nutrient cycling. Despite a high abundance of SAR11 cells, only a few strains have been successfully isolated from the Pacific and Atlantic Oceans solely by dilution-to-extinction culturing (8–10). Currently all the isolates in the SAR11 clade belong to the subgroup 1 and do not form colonies on any solid medium. In this report, we present the complete genome sequence of strain IMCC9063, a representative of the SAR11 subgroup 3.

Strain IMCC9063 was isolated from a surface seawater sample collected off the coastal region near the Dasan Korean Arctic Station in Ny-Ålesund, Svalbard, Norway (79°00′07″N, 11°18′33″E). The seawater sample was used as the inoculum for low-nutrient heterotrophic medium (LNHM) (2) and incubated at 10°C for 12 weeks. After the initial extinction culture was obtained using high-throughput culturing techniques (2), the strain was purified through several passages in LNHM. Strain IMCC9063 was only distantly related to the cultured representative strain in the SAR11 group 1A, “*Candidatus* Pelagibacter ubique” HTCC1062 (8), with a 16S rRNA gene sequence similarity of 88.3%. Phylogenetic analysis of 16S rRNA gene sequences placed strain IMCC9063 in the SAR11 subgroup 3, showing the closest relationship with several Norwegian coastal clones, such as 16_09_03B11 (GenBank accession no. FR685368; 100% similarity) from Raunefjord, Bergen, and s133 (GenBank accession no. EU919858; 99% similarity) from Kongsfjorden, Svalbard (11).

To prepare genomic DNA for genome sequencing, IMCC9063 was grown in acid-cleaned polycarbonate carboys containing 20 l LNHM. Eighty liters of cultured cells were harvested by filtration through a 0.2- μ m Supor membrane (Pall Corporation). Genomic DNA was directly ex-

tracted from filters by the phenol-chloroform method and finally purified using the Qiagen DNeasy Blood and Tissue genomic DNA kit (Qiagen Korea Ltd., Seoul, South Korea). Using 5.5 μ g of genomic DNA preparation, paired-end sequencing was performed on a GS FLX Titanium sequencing instrument (454 Life Sciences) by Chunlab, Inc. (Seoul, South Korea). The draft genome sequence consisted of 6 contigs in a scaffold of 1,283,256 bp in length (from 345,800 reads) with 49-fold coverage. Combinatorial PCR was used for filling gaps between contigs as previously described (7); chromatograms generated by BigDye terminator chemistry were analyzed in the draft genome assembly using the Consed/Phred/Phrap software program. Finally a circular genome with 1,284,727 bp (31.7 G+C mol%) was obtained, and open reading frames (ORFs) and noncoding RNAs were predicted by using RAST (rapid annotation using subsystem technology) (1). The genome contained a single rRNA operon and 32 tRNA genes. The predicted 1,432 ORFs of the IMCC9063 genome included genes that encode enzymes for retinoid biosynthesis and proteorhodopsin in addition to gluconeogenesis, TCA cycle, and ABC transporters for inorganic ions and amino acids.

Nucleotide sequence accession number. The complete genome sequence of strain IMCC9063 has been deposited in GenBank under accession number CP002511.

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