

Genome Sequence of Strain IMCC9480, a Xanthorhodopsin-Bearing Betaproteobacterium Isolated from the Arctic Ocean[∇]

Hyun-Myung Oh,¹ Kiyoung Lee,¹ Yoonra Jang,¹ Innam Kang,¹ Hee-Jin Kim,²
Tae-Wook Kang,² Seon-Young Kim,² and Jang-Cheon Cho^{1*}

Division of Biology and Ocean Sciences, Inha University, Incheon, Republic of Korea,¹ and Medical Genomics Research Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon, Republic of Korea²

Received 14 April 2011/Accepted 25 April 2011

Strain IMCC9480 is a novel member of the family Oxalobacteraceae of the Betaproteobacteria, isolated from the Arctic Ocean by dilution-to-extinction culturing. Here we present the draft genome sequence of strain IMCC9480. The genome is predicted to contain genes for xanthorhodopsin, retinoid biosynthesis, carbon monoxide dehydrogenase, and C₁ metabolism.

An Arctic marine bacterium, designated strain IMCC9480, was isolated from a surface seawater sample collected off the coast near the Dasan Korean Arctic Station in Ny-Ålesund, Svalbard, Norway (79°00'07"N, 11°18'33"E). The Arctic seawater sample was used as the inoculum for low-nutrient heterotrophic medium (LNHM) (3) and incubated at 10°C for 12 weeks. After initial cultivation using high-throughput culturing techniques (3), the extinction culture was spread on marine 1/10 R2A agar medium (2) and purified as a single colony. Phylogenetic analysis of 16S rRNA gene sequences placed strain IMCC9480 in the family *Oxalobacteraceae* of the class *Betaproteobacteria*. Strain IMCC9480 was closely related to the validly published species *Hermiimonas fonticola* (AY676462; 96.7%), *Aquaspirillum arcticum* (AB074523; 96.4%), and *Undibacterium pigrum* (AM397630; 95.4%). Many closely related isolates have been retrieved mainly from polar environments, including Antarctic bacterium CCQ from Collins Glacier, Antarctica (EU636040; 100%), Arctic sea ice bacterium ARK10118 (AF468343; 99.2%), and Alaska Glacier bacterium Gu-R-31 (AB545765; 98.6%). The strain was chosen for genome sequencing to supply more genomic information on Arctic marine bacteria and because of the unique phylogenetic position of the strain in the family *Oxalobacteraceae*.

A library for Illumina single-read sequencing was prepared from 5 µg DNA of IMCC9480 using a genomic DNA sample prep kit (FC-102-1001; Illumina Inc., San Diego, CA) at KRIBB (Daejeon, Republic of Korea). Single-read sequencing in 76 cycles was performed using proprietary reagents according to the manufacturer's protocol, and the resulting sequence reads were assembled by Velvet (8). Open reading frames (ORFs) and non-coding RNAs were predicted by using rapid annotation using subsystem technology (RAST) (1). The unclosed draft genome has 4,501,499 bases comprising 4,033 predicted ORFs, one rRNA operon, and 29 tRNAs, with a G+C content of 59.4 mol%.

The IMCC9480 genome is predicted to contain 151 putative

genes for ABC transporters, including inorganic ion uptake systems for phosphate, nitrate, ammonium, sulfate, chromate, iron, cobalt, zinc, cadmium, and molybdenum as well as urea, carbohydrates, and amino acids. The interesting features of the genome are genes of ecological importance in the ocean surface, encoding xanthorhodopsin (XR), retinoid biosynthesis, aerobic-type carbon monoxide dehydrogenase (CODH), ribulose biphosphate carboxylase (RubisCO), and C₁ compound metabolism. Considering that the XR gene is also found in *Methylophilales* bacterium HTCC2181 (4) and strain KB13 (GenBank accession no. ABXG000000000) in the OM43 clade (7), one of the most abundant coastal bacterioplankton lineages (6), XR may help IMCC9480 to survive better in the coastal seawater. The genome is predicted to encode genes for form I large (*coxL*), medium (*coxM*), and small (*coxS*) subunits of CODH (5), as well as accessory genes (*coxG*, *coxD*, *coxE*, *coxF*). The IMCC9480 genome also encodes genes for RubisCO, glycine/serine hydroxymethyltransferase, and proteins for assimilating methanol and formate.

Nucleotide sequence accession number. The genome sequence of strain IMCC9480 is available in GenBank under accession number AEPR00000000.

This study was supported by the Polar Academic Program (PAP) of the Korea Polar Research Institute (KOPRI).

REFERENCES

1. Aziz, R., et al. 2008. The RAST server: rapid annotations using subsystems technology. *BMC Genomics* **9**:75.
2. Cho, J.-C., and S. J. Giovannoni. 2004. Cultivation and growth characteristics of a diverse group of oligotrophic marine *Gammaproteobacteria*. *Appl. Environ. Microbiol.* **70**:432–440.
3. Connon, S. A., and S. J. Giovannoni. 2002. High-throughput methods for culturing microorganisms in very-low-nutrient media yield diverse new marine isolates. *Appl. Environ. Microbiol.* **68**:3878–3885.
4. Giovannoni, S. J., et al. 2008. The small genome of an abundant coastal ocean methylophilic bacterium. *Environ. Microbiol.* **10**:1771–1782.
5. King, G. M., and C. F. Weber. 2007. Distribution, diversity and ecology of aerobic CO-oxidizing bacteria. *Nat. Rev. Microbiol.* **5**:107–118.
6. Rappé, M. S., and S. J. Giovannoni. 2003. The uncultured microbial majority. *Annu. Rev. Microbiol.* **57**:369–394.
7. Rappé, M. S., P. F. Kemp, and S. J. Giovannoni. 1997. Phylogenetic diversity of marine coastal picoplankton 16S rRNA genes cloned from the continental shelf off Cape Hatteras, North Carolina. *Limnol. Oceanogr.* **42**:811–826.
8. Zerbino, D. R., and E. Birney. 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. *Genome Res.* **18**:821–829.

* Corresponding author. Mailing address: Division of Biology and Ocean Sciences, Inha University, Incheon 402751, Republic of Korea. Phone: 82-32-860-7711. Fax: 82-32-232-0541. E-mail: chojc@inha.ac.kr.

[∇] Published ahead of print on 13 May 2011.