

Genome Sequence of Strain IMCC1989, a Novel Member of the Marine *Gammaproteobacteria*[∇]

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Strain IMCC1989 is a novel member of the oligotrophic marine *Gammaproteobacteria* (OMG) group and is closely related with a symbiont group of the genera *Teredinibacter* and “*Candidatus Endobugula*.” Here we present the genome sequence of strain IMCC1989, which was isolated from the Yellow Sea by using dilution-to-extinction culturing.

A marine bacterium designated strain IMCC1989 was isolated from a surface seawater sample collected off the coast near Deokjeok Island, in the Yellow Sea, by using high-throughput culturing techniques based on dilution-to-extinction culturing (6). The extinction culture of strain IMCC1989 was originally cultivated in a low-nutrient heterotrophic medium that was prepared with 0.2- μ m-filtered and autoclaved natural seawater. The initial extinction culture was successfully subcultured on marine 1/10 R2A medium as tiny colonies, which were subsequently maintained on marine agar 2216 (BD Difco).

Phylogenetic analysis of 16S rRNA gene sequences positioned strain IMCC1989 in a phylogenetic clade affiliated with the oligotrophic marine *Gammaproteobacteria* (OMG) group (5). The OMG group includes five distinct bacterial clades (BD1-7, KI89A, OM60, OM182, SAR92), together with several oligotrophic marine bacterial clades, such as a bacterial symbiont group represented by *Teredinibacter* and “*Candidatus Endobugula*.” The described species that is most closely related to strain IMCC1989 was *Eionea nigra* 17X/A02/237^T (96.6% 16S rRNA gene sequence similarity), isolated from the Mediterranean Sea (10). Strain IMCC1989 was also closely related to “*Candidatus Endobugula sertula*” (95.0%) (7, 9) and *Pseudoterredinibacter isopora* SW-11^T (94.2%) (4). Members of “*Candidatus Endobugula*” and related species that belong to a bacterial symbiont group affiliated with the OMG clade have gained attention because these microbial symbionts have the bryostatin polyketide synthase gene cluster (7, 9). Other close relatives included uncultured gamma-proteobacterial clone H102, isolated from seahorses (*Hippocampus guttulatus*) (FM878644; 96.3%) (2), and surface sediment clone B78-56, retrieved from the Arctic Ocean (EU287020; 95.0%) (8).

Genomic DNA of strain IMCC1989 was prepared using the DNeasy blood and tissue genomic DNA kit (Qiagen Korea Ltd., Seoul, South Korea). Tagged genomic library generation

and whole-genome shotgun sequencing based on Solexa paired-end sequencing technology (3) were performed by Macrogen, Inc. (Seoul, South Korea). About 8.5 million short reads, totaling 647,001,680 bp, were initially obtained for the genome library tagged for strain IMCC1989. After quality filtering and trimming, 3,028,681 reads were assembled into 455 contigs (AEVK01000001 to AEVK01000455) using Velvet (11), with a depth of 112-fold genome coverage for the unclosed draft genome of strain IMCC1989. The IMCC1989 genome has 3,939,451 bp, with a mean G+C content of 42.06%. Annotation of the open reading frames (ORFs) and noncoding RNAs were performed using the RAST (rapid annotations using subsystem technology) server (1). Predicted ORFs were 2,844 in number, and noncoding RNA genes for 31 tRNAs and one copy of 16S-23S-5S rRNA were also predicted. Although strain IMCC1989 was closely related to “*Candidatus Endobugula sertula*,” the IMCC1989 genome does not encode genes for the modular polyketide synthase system. As expected from the morphology of the cells, the genome contained a full set of flagella biosynthesis genes. The genome is also predicted to encode genes for the glyoxylate bypass, capsular polysaccharide synthesis and export, Mu-like prophage proteins, and inorganic ion metabolisms, including high-affinity phosphate transporter (*pho* regulon).

Nucleotide sequence accession number. The draft genome sequence of strain IMCC1989 is available in GenBank under accession number AEVK00000000.

This work was supported by the National Research Foundation of Korea (NRF) grant funded by the Korean government (MEST) (no. 2010-0014604) and by the 21C Frontier Program of Microbial Genomics and Applications.

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[∇] Published ahead of print on 20 May 2011.

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