

GENOME ANNOUNCEMENT

Complete Genome Sequence of “*Candidatus Puniceispirillum marinum*” IMCC1322, a Representative of the SAR116 Clade in the *Alphaproteobacteria*[∇]

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The complete genome sequence of “*Candidatus Puniceispirillum marinum*” IMCC1322, the first cultured representative of the SAR116 clade in the *Alphaproteobacteria*, is reported here. The genome contains genes for proteorhodopsin, aerobic-type carbon monoxide dehydrogenase, dimethylsulfoniopropionate demethylase, and C₁ compound metabolism. The genome information proposes the SAR116 group to be metabolic generalists in ocean nutrient cycling.

Ever since the first description of the SAR116 clade (2, 4), members of this unique alphaproteobacterial group have been found in various marine environments based on culture-independent approaches (4, 10). The SAR116 clade has been regarded as a ubiquitous but uncultured lineage of marine bacterioplanktons (5). Isolated from a surface seawater sample from the Western Pacific Ocean Margin (East Sea of Korea), “*Candidatus Puniceispirillum marinum*” IMCC1322 was subjected to whole-genome sequencing. Here we report the complete genome sequence of IMCC1322, the first cultured representative of the SAR116 clade. Genomic DNA of IMCC1322 was prepared, shotgun sequenced, and analyzed by Macrogen, Inc. (Seoul, South Korea). Open reading frame (ORF) prediction and annotation were done with the EMFAS software program (Ensoltek, Inc., Daejeon, South Korea) using homology searches in the NCBI/UniProt databases and non-homology-based function annotations (genome context analysis).

The circular chromosome of IMCC1322 was 2,753,527 bp in length (48.85 G+C mol%) with a single rRNA operon and no extrachromosomal genetic element. A putative prophage sequence was found at base pair positions 405,417 to 424,699 (19,283 bp in length) by the phage_finder software program (3). Two thousand, five hundred forty-six predicted ORFs of the IMCC1322 genome showed the best blast hits to genomes of *Magnetospirillum magneticum* AMB-1 (210; 8.2%) and *Rho-*

dospirillum rubrum ATCC 11170 (190; 7.2%), members of the *Rhodospirillaceae* that have been proposed to be distant phylogenetic affiliates of the SAR116 clade (5). IMCC1322 had an impaired Embden-Meyerhoff-Parnas pathway due to the lack of 6-phosphofructokinase, but it possessed Entner-Doudoroff pathway genes encoding 6-phosphogluconate dehydratase and 2-dehydro-3-deoxyphosphogluconate aldolase. The IMCC1322 genome contained nitrate reductase, sulfate reductase, and an inorganic phosphate uptake system, including the phosphate regulon sensor *phoR* and a high-affinity ABC phosphate transporter system, polyphosphate kinase, and exopolyphosphatase/GppA phosphatase.

The most interesting features of the IMCC1322 genome are genes of biogeochemical importance in the ocean surface, encoding proteorhodopsin (PR), carbon monoxide dehydrogenase (CODH), C₁ compound metabolism, and dimethylsulfoniopropionate (DMSP) demethylase (encoded by *dmdA*). The IMCC1322 PR gene was followed by retinal biosynthesis gene clusters of the rhodopsin chromophore (*crtE-crtI-crtB-crtY*). PR, known as the light-driven proton pump (1, 11), may help IMCC1322 compete in the ocean surface because IMCC1322 has many ATP-independent electrochemical transporters, as well as ABC-type transporter genes. The genome is predicted to contain genes for the form II (*Bradyrhizobium*, *Mesorhizobium*, and *Sinorhizobium* [BMS]) large subunit of CODH (*coxL*) with the AYXGAGR active-site motif (8), along with the medium (*coxM*) and small (*coxS*) subunits in the arrangement *coxSLM*. Strain IMCC1322 possesses genes for metabolism of C₁ compounds: methanol, formaldehyde, formate, formamide, and methanesulfonate. The genome of strain IMCC1322 contained a gene for glycine/serine hydroxymethyltransferase to enter into an assimilatory serine cycle via the serine pathway (9). Strain IMCC1322 had a DMSP demethylase gene similar to *dmdA* of “*Candidatus Pe-*

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lagibacter ubique" HTCC1062 (6, 7) and *Silicibacter pomeroyi* DSS-3 (7), and IMCC1322 also had dimethyl sulfide (DMSO) reductase.

"*Candidatus* Puniceispirillum marinum" IMCC1322 is expected to be a metabolic generalist carrying functional genes for utilizing resourceful sunlight, DMSP, CO, and C₁ compounds in the surface ocean. Such metabolic potential of strain IMCC1322, the first cultured representative of the SAR116 clade, might reflect ecological niches for even more dominant marine bacterioplankton clades SAR11, *Roseobacter*, and SAR86.

Nucleotide sequence accession number. The complete genome sequence of strain IMCC1322 is available in GenBank under accession number CP001751.

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