Genome Sequence of *Idiomarina* sp. Strain A28L, Isolated from Pangong Lake, India[▽]

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***Idiomarina* sp. strain A28L was isolated from the alkaline brackish water of a high-altitude lake, Pangong Lake. Here, we present the draft genome of *Idiomarina* sp. strain A28L, which contains 2,591,567 bp with a G+C content of 45.5 mol% and contains 2,299 protein-coding genes and 56 structural RNAs.**

The genus *Idiomarina* belongs to the family *Idiomarinaceae* of the class *Gammaproteobacteria*. The genus contained 19 species at the time of writing (12). All of these bacteria were isolated from saline habitats with a wide range of salinities, such as coastal and oceanic waters, coastal sediments, submarine hydrothermal fluids, solar salt-making works, and inland hypersaline wetlands (5). Strain A28L was isolated by culture on alkaline bacillus agar (pH 9.5) containing 1.5% NaCl from the alkaline brackish water of Pangong Lake, which is situated at an altitude of 4350 m in Ladakh, India. This strain is a Gram-negative, aerobic, flagellar bacterium. Phylogenetic analysis of the *rrs* (16S rRNA) gene sequence revealed that strain A28L belongs to the genus *Idiomarina*. It showed the highest *rrs* gene sequence identity, 95.2%, with the type strain of *Idiomarina maris* (12).

The genome of *Idiomarina* sp. strain A28L was sequenced by a whole-genome shotgun strategy using 454 GS FLX (Roche) at the Institute of Genomics and Integrative Biology, Delhi, India. A total of 282,412 sequence reads were generated by FLX Titanium sequencing with a genome coverage of 38-fold. The sequence was assembled into 31 contigs by Newbler software, version 2.3 (Roche). The 28 large contigs (>500 bp to 394,143 bp) were used for gene prediction and annotation by the IMG ER system (7), which uses Prodigal (4) for gene prediction. The IMG ER automated pipeline uses a homology search at the nonredundant proteins database (NR) of GenBank, pfam (2), and the TIGRFam (9), InterProScan (11), KEGG (6), and COG (10) databases for annotation (8). Annotated coding sequences from the IMG ER server were used for a round of manual curation by BLAST, and the noncoding RNA and RNA with miscellaneous features were analyzed by Rfam, before submission of the annotated draft genome to GenBank. The draft genome sequence was also uploaded to the RAST (1) server.

The *Idiomarina* sp. strain A28L unclosed draft genome was 2,591,567 bp in length, with a G+C content of 45.5 mol%. The genome, which has a coding density of 90%, contained 2,299

protein coding genes, 49 tRNA genes, and 4 rRNA genes. Comparison with genome sequences available at RAST showed that *I. loihiensis* L2TR (score, 517), *I. baltica* OS145 (score, 430) followed by *Pseudoalteromonas tunicata* (score, 321) were the closest neighbors of strain A28L. The strain A28L genome contained genes for glycolysis/gluconeogenesis, the tricarboxylic acid cycle, a high-affinity phosphate transporter and regulatory genes for sensing inorganic phosphate, and genes for flagellum assembly and function, while the genes for sugar transporters (phosphotransferase system, ABC-type sugar transporter, and sugar-phosphate permease), the Entner-Doudoroff pathway, inorganic sulfur assimilation, and siderophore biosynthesis were absent, which was similar to the reported *I. loihiensis* L2TR genome (3). In contrast to *I. loihiensis* L2TR, genes for thiamine biosynthesis, ammonia assimilation, and denitrification were absent in strain A28L. Detailed comparative analyses of *Idiomarina* sp. strain A28L with *I. loihiensis* L2TR and *I. baltica* OS145 should reveal their metabolic differences and the genetic basis of adaptation to their unique habitats.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AFPO00000000. The version described in this paper is the first version, AFPO01000000. The 28 large contigs have been deposited under accession numbers AFPO01000001 to AFPO01000028.

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