Idiomarina xiamenensis strain 10-D-4T was isolated from an oil-degrading consortium enriched from surface seawater around the Xiamen island. Here, we present the draft genome of strain 10-D-4T, which contains 2,899,282 bp with a G+C content of 49.48% and contains 2,673 protein-coding genes and 43 tRNA genes.

The genome sequence of I. xiamenensis 10-D-4T was determined by Shanghai Majorbio Bio-pharm Technology Co., Ltd. (Shanghai, China), using Solexa paired-end sequencing technology. A total of 5,983,729 paired-end reads (500-bp library) were generated to reach a 334-fold depth of coverage with Illumina/Solexa Genome Analyzer IIx (Illumina, San Diego, CA), and the gaps among scaffolds were closed by custom primer walks or by PCR amplification followed by DNA sequencing. The genome of I. xiamenensis 10-D-4T consists of 77 contigs (>200 bp; N50 = 18) of 2,899,282 bp and had an average G+C content of 49.48%. Automatic gene annotation was carried out by the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html), followed by manual editing. The genome contains 2,673 candidate protein-encoding genes (with an average size of 988 bp), giving a coding intensity of 91.2%. A total of 1,984 proteins were assigned to cluster of orthologous groups (COG) families (5). Forty-three tRNA genes for all 20 amino acids and one 16S-23S-5S rRNA operon were identified.

Strain 10-D-4T cannot utilize n-alkanes or polycyclic aromatic hydrocarbons as sole carbon and energy sources, though it was isolated from an oil-degrading consortium and can grow in diesel oil and crude oil. However, no alkane-degrading-related monooxygenase was found in the genome of strain 10-D-4T. Prior to strain 10-D-4T, three strains of genus Idiomarina have been genome sequenced, Idiomarina loihiensis L2TRT (3), Idiomarina balitica OS145T, and Idiomarina sp. strain A28L (2). Their genome sizes were 2.84 Mb, 2.72 Mb, and 2.59 Mb, respectively, and their GC contents ranged from 45.5 mol% to 47.3 mol%. All these features were similar to those for I. xiamenensis 10-D-4T. Detailed comparative analyses of I. xiamenensis 10-D-4T with the other three genome sequences of the genus Idiomarina should reveal their metabolic differences and the genetic basis of environment-specific genetic requirements. The genome sequence of strain 10-D-4T and its curated annotation are important assets to better understand the physiology and metabolic potential of Idiomarina xiamenensis and will open up new opportunities in the functional genomics of this species.

**Nucleotide sequence accession number.** The draft genome sequence of Idiomarina xiamenensis 10-D-4T has been deposited in GenBank under accession number AMRG00000000 (chromosome).

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