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Draft Genome Sequence of *Psychrobacter piscatorii* Strain LQ58, a Psychrotolerant Bacterium Isolated from a Deep-Sea Hydrothermal Vent

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Here, we report the 3.1-Mb draft genome sequence of *Psychrobacter piscatorii* strain LQ58, isolated from a deep-sea hydrothermal vent on the East Pacific Rise. The sequence will provide further insight into the environmental adaptation of psychrotolerant bacteria and the development of novel cold-active enzymes for industrial application.

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Members of the genus *Psychrobacter* are psychrotolerant or psychrophilic bacteria, which are widely distributed in marine and terrestrial environments (1–3). They have been considered good sources of cold-active enzymes for industrial and environmental uses (4–6). *Psychrobacter piscatorii* strain LQ58 (=MCCC 1A10701) is an aerobic, psychrotolerant, chemoorganotrophic bacterium, isolated from a deep-sea hydrothermal vent sediment sample collected on the East Pacific Rise at a depth of 2,906 m (3.10 S, 102.55 W). Growth was observed at temperatures between 0°C and 35°C with an optimum at 22°C in the presence of 2% NaCl. Strain LQ58 showed highest 16S rDNA sequence similarity with *P. piscatorii* T-3-2 (99.3%) (7), followed by *Psychrobacter aquaticus* CMS56 (98.6%) (8). *P. piscatorii* was reported to exhibit an extraordinarily high catalase activity (9). To date, there is no reference *P. piscatorii* genome sequence available publicly. Here, we report the draft genome sequence of strain LQ58, the first released *P. piscatorii* genome sequence, which will provide further insight into the environmental adaptation of psychrotolerant bacteria and the development of novel cold-active enzymes for industrial application.

Extraction of genomic DNA from strain LQ58 was carried out using a bacterial DNA kit (Omega) according to the manufacturer's instructions. The genome of strain LQ58 was sequenced by whole-genome shotgun sequencing using the Illumina MiSeq system at Shanghai Majorbio Bio-pharm Technology Co., Ltd. (Shanghai, China). A total of 804,651,728 reads were generated, representing an approximately 260-fold coverage of the genome. These reads were assembled using SOAPdenovo version 2.0 (10) and resulted in 139 contigs with an N_{50} of 47,940 bp. The size of the longest contig was 149,861 bp. The draft genome of strain LQ58 was analyzed and annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok). Genes of interest were manually evaluated.

The draft genome sequence of strain LQ58 was 3,089,314 bp in length, with a G+C content of 44.1%. The genome contains 2,676 predicted open reading frames and 2,562 predicted protein-coding sequences). There were 33 tRNA genes, 3 rRNA genes, and 1 noncoding RNA (ncRNA) gene predicted from this assembly.

In silico DNA-DNA hybridization (DDH) and average nucleotide identity values of LQ58 against *P. aquaticus* CMS56 were 22.6 ± 2.36% and 79.3% (11), respectively, which was significantly lower than the recommended cutoff value for species delineation (12, 13).

Sequence analysis revealed that the LQ58 genome encodes 37 lipolytic enzymes, 58 peptidases, 2 formate dehydrogenases, 12 alcohol dehydrogenases, and 7 glycosyltransferases for potential biotechnology applications. LQ58 genome also encodes 3 cold-shock proteins (CspA, CspC and CspD), 1 capsular polysaccharide synthesis gene cluster, and 1 GroES-GroEL operon associated with cold stress (14). In addition, compared with other sequenced *Psychrobacter* genomes, LQ58 contains more catalase genes, including 1 HPII-like monofunctional catalase gene and 1 HPI-like bifunctional catalase gene (15), which may be favorable for its adaptation to an oxidative environment.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number LNDJ00000000. The version described in this paper is the first version, LNDJ01000000.

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