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Complete Genome Sequence of Antarctic Bacterium *Psychrobacter* sp. Strain G

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Here, we report the complete genome sequence of *Psychrobacter* sp. strain G, isolated from King George Island, Antarctica, which can produce lipolytic enzymes at low temperatures. The genomics information of this strain will facilitate the study of the physiology, cold adaptation properties, and evolution of this genus.

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The genus *Psychrobacter* was described to accommodate Gram-negative, psychrotolerant, halotolerant, aerobic, nonmotile bacteria (1). *Psychrobacter* species have been isolated from a wide range of habitats, including Antarctic ornithogenic soils (2), sea ice (3), Siberian permafrost (4), marine crustaceans (5), clinical specimens (6), and seafood (7). *Psychrobacter* sp. strain G was collected from King George Island, Antarctica (62°12′39″S, 58°54′41″W), and it can produce extracellular lipolytic enzymes with activity at low temperatures (8).

The *Psychrobacter* sp. G genome was sequenced with 454 GS-FLX and Illumina platforms. A total of 157,071 high-quality 454 reads with an average of 371 bp were produced, providing about 17× coverage, while the Illumina reads provide about 454× coverage with mate-pair reads of 100 bp (insert size, ~3,000 bp). Primary assembly was performed with Newbler version 2.3 and then scaffolded with Illumina mate-pair reads using SSPACE (9). The gaps were closed with GapFiller (10) and PCR walking. Open reading frames were identified and annotated with the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (11). The functions of genes were also annotated by Clusters of Orthologous Groups (COG) (12), KEGG (13), and InterProScan (14).

The complete genome of *Psychrobacter* sp. G consists of a circular chromosome of 3,079,438 bp (42.44% G+C content) plus 3 plasmids: PsyG_26 (26,087 bp), PsyG_4 (4,518 bp), and PsyG_3 (3,956 bp). The chromosome contains 2,614 protein-encoding genes (CDSs), 12 rRNA operons, and 48 tRNAs. A total of 1,967 of the CDSs were assigned to COGs, and 1,345 CDSs can be annotated into 165 pathways by using KAAS (15). The genome sequence enables the further study of the cold adaptation properties, lipolytic enzymes, and evolution of this genus.

Nucleotide sequence accession numbers. The genome sequence data have been deposited in GenBank under the accession no. CP006265 (chromosome), CP006266 (PsyG_26), CP006267 (PsyG_4), and CP006268 (PsyG_3).

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