Complete Genome Sequence of a Psychrophilic Bacterium, *Pseudoalteromonas* sp. Strain APM04, Isolated from the Seafloor of the South Mariana Trough, Pacific Ocean

Mahoko Taguchi,[a] ⓘYong Guo,[b] ⓘTomoyasu Nishizawa,[a,b] Shigeru Chohnan,[a,b] Yasurou Kurusu[a]

[a]Graduate School of Agriculture, Ibaraki University, Ami, Ibaraki, Japan
[b]Ibaraki University College of Agriculture, Ami, Ibaraki, Japan

ABSTRACT The complete genome sequence of *Pseudoalteromonas* sp. strain APM04, which is a psychrophilic bacterium that inhabits the seabed of the South Mariana Trough, Pacific Ocean, was determined to characterize the genetic features associated with evolution in extremophilic and oligotrophic deep seawater.

Psychrophiles found in the deep sea, which remains at 5°C or less throughout the year, are thought to grow very slowly to conserve limited nutritional resources (1–3). Here, we carried out complete genome sequencing of a psychrophilic bacterium strain, APM04, which was predicted to be a member of the genus *Pseudoalteromonas* based on the 16S rRNA sequence; it was obtained from a depth of 2,880 m (4.1 m below the seafloor at the Snail site) on the seafloor of the South Mariana Trough (12°57′N, 143°37′E) during the voyage conducted as a part of the Archaean Park Project (4, 5).

APM04, isolated as a single colony, was grown on 1/2 TZ medium (g/l): Polypepton (Nihon Pharmaceutical), 2.5; Bacto yeast extract (Thermo Fisher Scientific), 0.5; HEPES (Merck KGaA), with Kester's artificial seawater-1.5% Bacto agar (Merck KGaA) (6), and the APM04 DNA was extracted from multiple colonies grown on the solid plate using a PowerSoil kit (Qiagen). A paired-end library was established using a TruSeq DNA PCR-free kit (Illumina), and a long-read library was prepared using a 1D genomic DNA library kit (Oxford Nanopore Technologies). Then the paired-end library and the long-read library were sequenced on Illumina MiSeq (2 × 150 bp) and GridION instruments, respectively, to generate 2,493,442 reads with a total length of 376,509,732 bases and 424,961 reads with a total length of 3,134,375,494 bases, respectively. Read processing and genome assembly were performed as described previously (7). Briefly, the paired-end reads were processed using Cutadapt v1.11 with the options of –overlap 10, –minimum-length 51, and –quality-cutoff 20 (8), and the Nanopore reads were trimmed using Nanofilt v2.0.0 with the options of –l 1000 and –q 9 (9). The processed paired-end and long reads were assembled and circularized using Unicycler v0.4.6 with default settings (10). The genome sequences were annotated using GeneMarkS-2+ (11), as implemented in the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v6.1 (12).

The APM04 genome was composed of two chromosomes, i.e., 3,457,294-bp circular chromosome 1 with an average GC content of 39.8%, containing 25 rRNAs (9 of 5S rRNA, 8 of 16S rRNA, and 8 of 23S rRNA) and 102 tRNAs, and 694,804-bp circular chromosome 2 with a GC content of 39.6%, containing 3 rRNAs (1 of rRNA gene operon). Of all protein coding sequences (CDSs) (3,655 CDSs), 3,060 CDSs (83.7%) were found on chromosome 1 and 595 CDSs (16.3%) were present on chromosome 2. The APM04 genome shared average nucleotide identities of 97.90%, 97.77%, 97.74%, 97.50%, and 97.46% with the closest sequenced genomes of *Pseudoalteromonas* sp. strain BSi20480 (GenBank accession number GCF_000241365.1), *Pseudoalteromonas marina* DSM 17587[T] (GenBank accession number GCF_000238335.3), *Pseudoalteromonas marina* 13-15 (GenBank accession number GCF_900141965.1), *Alteromonadales* bacterium TW-7 (GenBank accession number

GCF_000169055.1), and *Pseudoalteromonas marina* ECSMB14103 (GenBank accession number GCF_002407085.1), respectively, which were estimated using JSpeciesWS v3.9.3 (13). The genetic features of the psychrophilic bacterium *Pseudoalteromonas* sp. strain APM04 may help us to infer the evolutionary characteristics in oligotrophic ecosystems and provide genetic information on useful enzymes that function under low-temperature conditions.

Data availability. The genome sequences of *Pseudoalteromonas* sp. strain APM04 were deposited in the DDBJ/ENA/GenBank database with the accession numbers CP094441 and CP094442 for the circular chromosomes. The SRA accession numbers are SRR18360445 and SRR18360446 for the MiSeq and Nanopore raw reads, respectively.

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