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GENOME SEQUENCES

Draft Genome Sequence of the Planctobacterium marinum Type Strain K7

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ABSTRACT *Planctobacterium marinum* strain K7 is a Gram-negative gammaproteobacterium of the *Alteromonadaceae* family and is the sole type strain in the genus *Planctobacterium*. Presented here is the draft whole-genome sequence of *P. marinum* strain K7.

The *Alteromonadaceae* are an ecologically diverse group, with members isolated from seafloor sediments (1), coastal (2), open, and hadal (3, 4) marine waters, marine invertebrates, fish, and algae (5). Members of this family are also notable for harboring degradative genes and secondary metabolite synthetic gene clusters with desirable activities in their genomes (5–7). *Planctobacterium marinum* strain K7, which was isolated from seawater collected in the South China Sea, is a Gram-negative, aerobic gammaproteobacterium of the *Alteromonadaceae* family (8). At the time of this writing, *P. marinum* strain K7 is the sole member of its genus. The increasing availability of next-generation sequencing technologies has made whole-genome sequences essential for the representation of taxa of interest and have generated new standard measurements of genomic taxonomy (9, 10). Because only phenotypic and 16S rRNA sequence data from *P. marinum* strain K7 were available for the analyses distinguishing two novel genera, *Ningiella* and *Marisediminitalea* (1, 3), the availability of a draft whole-genome sequence of another type strain will further elucidate taxonomic differences between related strains in the *Alteromonadaceae* family.

P. marinum strain K7 was obtained from the Belgian Co-ordinated Collection of Micro-Organisms (BCCM) LMG collection (LMG 28835). A *P. marinum* culture was grown overnight at 27°C on a plate of glycerol artificial seawater medium solidified with 1.5% agar (11). A plate culture of *P. marinum* derived from a single colony was grown at Southern Oregon University and sent to the Microbial Genome Sequencing Center (MiGS) (Pittsburgh, PA, USA) for genomic DNA extraction using the DNeasy blood and tissue kit (Qiagen, Hilden, Germany) according to the manufacturer's instructions. Raw reads were obtained from the MiGS, using 151-bp paired-end libraries prepared with the Illumina Nextera kit as described previously and run on the Illumina NextSeq 550 platform (12). Initial results of high-throughput sequencing produced 3,103,747 paired-end sequences. The raw read data quality was assessed using FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc), and read quality trimming and Illumina adapter sequence removal were performed using BBDuk within the BBMap package (http://sourceforge.net/projects/bbmap) as described previously (13), with the following parameters: ktrim=r, ordered, minlen=50, mink=11, comp=f, k=21, ow=t, ftm=5, zl=4, qtrim=rl, and trimq=20. The trimmed reads were assembled into a draft genome with SPAdes v. 3.14.0 using the --careful option and specifying kmers of 21, 33, 55, 77, 99, and 121.

This assembly produced 22 scaffolds, with a mean coverage of 34.2× and an N_{50} value of 877,771 bp. The draft genome sequence comprises a total of 5,239,599 bp, with a G+C

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content of 46.24%. Preliminary genome annotation using the Prokaryotic Genome Annotation Pipeline (PGAP) identified 4,619 total genes; 61 RNAs, 49 of which are tRNAs and 8 of which are rRNA sequences, were also identified (14).

Data availability. This whole-genome shotgun project was deposited in DDBJ/ENA/GenBank under the accession number JAJEWQ000000000. The version described in this paper is version JAJEWQ010000000. Raw sequence reads were deposited in the SRA under accession number SRR16643386 and are associated with BioSample number SAMN22563709.

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