Complete Genome Sequence and Methylome of the Type Strain of *Shewanella algae*

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ABSTRACT We report the complete genome sequence and base modification analysis of the *Shewanella algae* type strain CECT 5071 (=OK-1 = ATCC 51192 = DSM 9167 = IAM 14159). The genome is composed of a single chromosome of 4,924,764 bp, with a GC content of 53.10%.

The gammaproteobacterium *Shewanella algae* was first described as a tetrodotoxin-producing epiphyte of the red alga *Jania* sp. (1), and the type strain was designated OK-1 following the original nomenclature by Kotaki et al. (2). *S. algae* is the most relevant human pathogen within the genus *Shewanella*, causing bacteremia, otitis, skin and soft tissue infections, and a variety of other diseases, with the emergence of multidrug-resistant isolates being a concern (3, 4). *S. algae* is also known for its ability to produce secondary metabolites like iron-scavenging siderophores (5). Its versatile physiology is considered a hallmark of the genus *Shewanella*. In the past 3 years, genomes of several clinical and environmental isolates of *S. algae* have been sequenced (6–9), but no complete genome sequence of a reference strain has been available. We have investigated *S. algae* from different angles (10–14). Here, we report the complete genome sequence of the *S. algae* type strain OK-1 (1), which was obtained from the Spanish Type Culture Collection (strain CECT 5071).

The strain was grown in LB medium at 37°C to exponential phase, and the DNA was isolated with the Genomic-tip 500/G kit (Qiagen). Multiplexed sequencing libraries with a target insert size of 8 kb were prepared using the SMRTbell Express template preparation kit v2.0 and barcoded overhang adapter kit 8A (Paciﬁc Biosciences [PacBio], Menlo Park, CA, USA). After removal of adapter dimers, the libraries were sequenced on a Sequel single-molecule real-time (SMRT) cell following the manufacturer's recommendations (PacBio). Barcode splitting was done using SMRT Link v8.0 (PacBio) and resulted in 622,115 reads totaling 3,045,548,325 bases, with an N50 value of 7,709 bases. A total of 693,216,159 bases from unique reads were used in the microbial assembly pipeline included in SMRT Link v8.0 (PacBio) with default parameters.

The genome of the *S. algae* type strain CECT 5071 is composed of a single chromosome of 4,924,764 bp, with a GC content of 53.10% (Fig. 1). No extrachromosomal elements were detected. Genome annotation by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v5.0 (15) predicted 4,400 genes, of which 4,225 are protein-coding genes. A total of 136 RNAs were predicted, including 107 tRNAs, 25 rRNAs (5S, 9 copies; 16S, 8 copies; 23S, 8 copies), and 4 noncoding RNAs. SMRT sequencing offers the possibility of assessing genome-wide DNA methylation patterns. Detected methylation motifs are summarized in Table 1, and the methylome is available in the REBASE database (16).

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Of note, the rpoS gene is truncated in the type strain of S. algae (10), consistent with evidence from the draft genomes of equivalent strains, namely, ATCC 51192 (GenBank accession no. GCA_012396675.1), NBRC 103173 (GenBank accession no. GCA_001598875.1), and JCM 21037 (GenBank accession no. GCA_000615045.1), suggesting that this truncation was already present in the original OK-1 isolate. In Escherichia coli, the RpoS protein is the stress sigma factor of the RNA polymerase required for stationary-phase transcription (17). However, natural E. coli rpoS mutants exist (18, 19). The ecological and physiological significance of the rpoS truncation in the S. algae type strain remains to be determined.

Data availability. The complete genome sequence of S. algae CECT 5071T was deposited in DDBJ/ENA/GenBank under the accession no. CP068230. Sequencing raw data are available at the SRA under the accession no. SRR14739658. The methylome of S. algae CECT 5071T is available at the REBASE database under the organism accession no. 46337.

**TABLE 1** Summary of methylation motifs detected in the complete genome sequence of S. algae CECT 5071T and associated methyltransferases

| Motif     | Center position | Modification type | No. detected | No. in genome | Type | Methyltransferase locus tag |
|-----------|-----------------|-------------------|--------------|---------------|------|----------------------------|
| GATC      | 2               | m6A               | 41,451       | 41,456        | II   | ——a                        |
| TGANNNNNNNTTCC | 3       | m6A               | 827          | 827           | ly   | E1N14_007370               |
| TGGCCA    | 4               | m4C               | 4,218        | 8,820         | llα  | E1N14_009720               |

a ——, GATC could not be matched unambiguously by REBASE because there is more than one candidate.
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