



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 multi-drug-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^T).

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 N_{50} 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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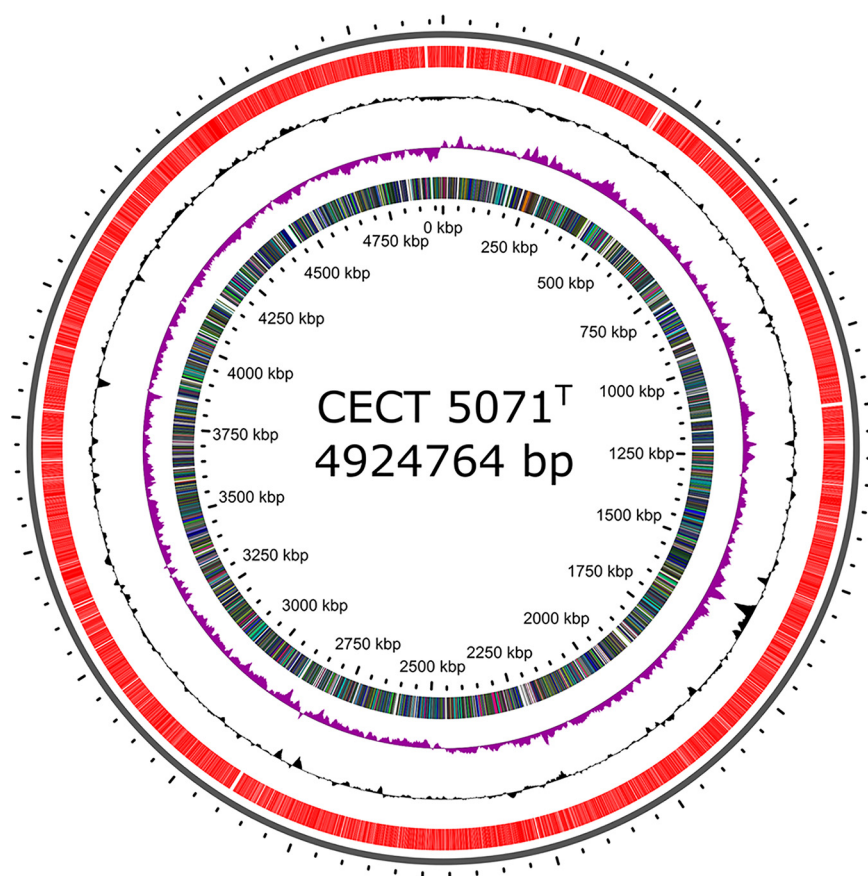


FIG 1 Circular map of the *Shewanella algae* CECT 5071^T chromosome. Circles from outside to inside represent the coding sequences (red), GC content (black), GC skew (purple), and color-coded Clusters of Orthologous Groups (COG) assignments of protein-coding genes. The map was generated with CGView (20).

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](https://www.ncbi.nlm.nih.gov/nuccore/GCA_012396675.1)), NBRC 103173 (GenBank accession no. [GCA_001598875.1](https://www.ncbi.nlm.nih.gov/nuccore/GCA_001598875.1)), and JCM 21037 (GenBank accession no. [GCA_000615045.1](https://www.ncbi.nlm.nih.gov/nuccore/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 5071^T was deposited in DDBJ/ENA/GenBank under the accession no. [CP068230](https://www.ncbi.nlm.nih.gov/nuccore/CP068230). Sequencing raw data are available at the SRA under the accession no. [SRR14739658](https://www.ncbi.nlm.nih.gov/sra/SRR14739658). The methylome of *S. algae* CECT 5071^T is available at the REBASE database under the organism accession no. [46337](https://www.ncbi.nlm.nih.gov/rebase/methyl/46337).

TABLE 1 Summary of methylation motifs detected in the complete genome sequence of *S. algae* CECT 5071^T 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
TGANNNNNNTTCC	3	m6A	827	827	I _γ	E1N14_007370
TGGCCA	4	m4C	4,218	8,820	II _α	E1N14_009720

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

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