



# Genome Sequence of *Arenibacter algicola* Strain SMS7, Found in Association with the Marine Diatom *Skeletonema marinoi*

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**ABSTRACT** *Arenibacter algicola* strain SMS7 was isolated from a culture of the marine diatom *Skeletonema marinoi* strain ST54, sampled from top-layer sediments in Kosterfjord, Sweden. Here, we present its 5,857,781-bp genome, consisting of a circular chromosome and one circular plasmid, in all containing 4,932 coding sequences.

In an ongoing study of the microbiome of the chain-forming diatom *Skeletonema marinoi* strain ST54, we isolated and sequenced the associated bacterial strain SMS7.

The ST54 culture was established from a revived resting cell taken from top-layer sediment in Kosterfjord, Sweden (58°51.0'N, 10°45.7'E; 102 m depth) in May 2009. This bacterial strain was sampled from a colony formed after multiple-dilution streaking on marine agar. Genomic DNA was extracted using Plant DNAzol reagent (Invitrogen Life Technologies, USA) from pure cultures grown from a single bacterial colony, according to the manufacturer's instructions. Genome sequencing was performed with the PacBio RS II platform (Pacific Biosciences, Menlo Park, CA, USA) on a single-molecule real-time (SMRT) cell. The sequencing produced 98,352 uncorrected reads totaling 1.3 Gbp, which were assembled using Falcon version 1.7.5 (<https://github.com/PacificBiosciences/FALCON> [1]; seed read length, 17,000 bp). To ensure that the contigs were circular, the corresponding contig ends were joined, and the SMRT Portal version 2.3.0 RS\_Resequencing.1 protocol (Pacific Biosciences [2]) was used to remap the reads to the contigs; this included a correction step using Quiver (2). The assembly contains two circular contigs, a chromosome of 5,793,053 bp (G+C content, 39.8%) and a plasmid of 64,728 bp (G+C content, 43.8%), with an average assembly read coverage of 173.06× (statistics are summarized in Table 1).

The assembly was annotated with Prokka version 1.12beta (3); this inferred 4,932 coding sequences (CDSs; of which 4,061 have a predicted function), 17 pseudogenes, 47 tRNAs, 9 rRNAs, 22 noncoding RNAs (ncRNAs), and one transfer-messenger RNA (tmRNA) (statistics are summarized in Table 1). Strain SMS7's chromosome contains three identical 16S rRNA sequences, which share 99.9% identity with the three found in the *Arenibacter algicola* type strain TG409 (NCBI RefSeq accession number [NZ\\_LJPO000000000](https://.ncbi.nlm.nih.gov/RefSeq/ accession/nz_ljpo000000000)). In addition, the housekeeping genes *gyrB* and *rpoB* show 99.1% and 99.0% sequence similarity, respectively, between strain SMS7 and *A. algicola* strain TG409<sup>T</sup>. Given this similarity, strain SMS7 was compared to all whole-genome-sequenced *Flavobacteriaceae* species available in RefSeq (<ftp://ftp.ncbi.nlm.nih.gov/genomes/refseq/bacteria/>) using the phylotaxonomic analysis software PhyloPhlAn version 0.99 (4). This showed strain SMS7 as sister to the clade of *A. algicola* TG409<sup>T</sup> and *Arenibacter* sp. strain C-21, with 100% bootstrap support. Taking the above-described analyses together, we place strain SMS7 in the taxon *Arenibacter algicola*. In addition, colonies of strain SMS7 showed the characteristic orange pigmentation of *A. algicola*, attributed to its pigment absorbing at 450/470/476 nm.

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**TABLE 1** Summary of assembly and annotation statistics for *Arenibacter algicola* strain SMS7

Statistic	Value for:		
	Total assembly	Chromosome	pSMS7
Assembly			
No. of reads	98,352		
No. of bases	1,266,330,556		
Final assembly size (bp)	5,857,781	5,793,053	64,728
G+C content (%)	39.8	39.8	43.8
Avg read coverage (×)	173.06		
Annotation (no.)			
CDSs	4,932	4,852	80
Pseudogenes	17	17	0
tRNAs	47	47	0
rRNAs	9	9	0
ncRNAs	22	22	0
tmRNAs	1	1	0

*Arenibacter algicola* strain SMS7 contains a plasmid, pSMS7 (with 80 predicted CDSs), a feature not reported for strain TG409<sup>T</sup> (5). This plasmid was compared to the type strain assembly and SMS7 chromosome using BLASTn (6), and the result implies that pSMS7 is a unique replicon, as no sizable equivalent appears in the strain TG409<sup>T</sup> assembly or the SMS7 chromosome.

The *A. algicola* type strain TG409 was originally isolated from the *Skeletonema* type species, *S. costatum* (7). Our identification of another *A. algicola* strain associated with *S. marinoi* provides further evidence of functional links between the two organisms. One suggested link is the diatoms' ability to accumulate polycyclic aromatic hydrocarbons (PAHs) on their silica frustules, which associated *A. algicola* bacteria can use as a carbon source (7).

**Data availability.** This whole-genome project has been deposited in GenBank under the accession numbers [CP022515](#) and [CP022516](#) as part of BioProject number [PRJNA380207](#).

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