



Complete Genome Sequence of a Toxic and Bioactive Exopolysaccharide-Bearing Bacterium, *Sulfitobacter* sp. Strain AM1-D1

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ABSTRACT *Sulfitobacter* sp. strain AM1-D1, a toxic bacterium of the family *Rhodobacteraceae*, was isolated from the cultivable phycosphere microbiota of marine toxigenic dinoflagellate *Alexandrium minutum* amtk4. The complete 4.69-Mb genome comprises one single circular chromosome and five circular plasmids. It has 4,559 coding genes, including those for biosynthesis or degradation of saxitoxin and bioactive exopolysaccharides.

The phycosphere is a microscopic niche harboring interkingdom exchanges of diverse nutrients, infochemicals, and transferable genetic elements through complex alga-bacterium interactions (ABI) (1). Phycosphere microbiota (PM) inhabiting this microenvironment as a whole bacterial community has been reported in numbers of phytoplanktons in aquatic environments (2, 3). Here, we report the complete genome sequence of *Sulfitobacter* sp. strain AM1-D1, which was isolated from the cultivable PM of marine toxigenic dinoflagellate *Alexandrium minutum* amtk4 that produces paralytic shellfish poisoning toxins (PSTs) (4). This genomic information will enable improved mapping of bacterial roles during these dynamic interactions.

The bacterial isolation and extraction of genomic DNA were performed according to our previously described protocols (5). The complete genome sequence of *Sulfitobacter* sp. strain AM1-D1 was acquired by PacBio RS II single-molecule real time (SMRT) technology performed at Majorbio (Shanghai, China). For PacBio sequencing, genomic DNA was sheared to a standard 10-kb size using g-TUBE (Covaris) and converted into a proprietary SMRTbell library format using the RS DNA template preparation kit (Pacific Biosciences, CA) according to the manufacturer's instructions. Default parameters were used in this study for all software unless otherwise specified. A quality check of raw sequences was performed using FastQC (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc>). The genome sequence was *de novo* assembled from PacBio reads (186,958 reads; average length, 5,769 bp; coverage, 230×) into six contigs using SOAPdenovo2 v2.04 with the Fast Alignment and CONsensus (FALCON) v0.2.1 tools and circularized with Circos v0.64 (<http://circos.ca>). The 4.69-Mb genome of *Sulfitobacter* sp. strain AM1-D1 comprises one single circular chromosome (3,840,209 bp) and five circular plasmids (185,176 bp, 95,272 bp, 15,811 bp, 205,668 bp, and 348,874 bp). The G+C contents of these components are 64.9%, 65.6%, 60.3%, 58.7%, 63.7%, and 61.6%, respectively. The genome sequence was annotated by NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v1.2.1 (6). It harbors 43 tRNAs and 3 rRNAs. Of the 4,559 predicted coding genes, the key *sxtA* genes for starting the biosynthesis of saxitoxin (4) and those for the biosynthesis or degradation of cross-kingdom signals, namely, indole-3-acetic acid (IAA) (2) and bioactive exopolysaccharides (EPS) as promising natural biofloculants (7), are present in the bacterial chromosome.

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Data availability. The annotated complete genome sequence of *Sulfitobacter* sp. strain AM1-D1 was deposited in DDBJ/ENA/GenBank under the accession numbers [CP018076](#), [CP018077](#), [CP018078](#), [CP018079](#), [CP018080](#), and [CP018081](#) for the single circular chromosome and five circular plasmids, respectively. The raw reads are available under SRA accession number [SRR11216889](#).

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REFERENCES

1. Seymour JR, Amin SA, Raina JB, Stocker R. 2017. Zooming in on the phycosphere: the ecological interface for phytoplankton-bacteria relationships. *Nat Microbiol* 2:17065. <https://doi.org/10.1038/nmicrobiol.2017.65>.
2. Amin SA, Parker MS, Armbrust EV. 2012. Interactions between diatoms and bacteria. *Microbiol Mol Biol Rev* 76:667–684. <https://doi.org/10.1128/MMBR.00007-12>.
3. Landry ZC, Vergin K, Mannenbach C, Block S, Yang Q, Blainey P, Carlson C, Giovannoni S. 2018. Optofluidic single-cell genome amplification of sub-micron bacteria in the ocean subsurface. *Front Microbiol* 9:1152. <https://doi.org/10.3389/fmicb.2018.01152>.
4. Zhang X, Ma L, Tian X, Huang H, Yang Q. 2015. Biodiversity study of intracellular bacteria closely associated with paralytic shellfish poisoning dinoflagellates *Alexandrium tamarense* and *A. minutum*. *Int J Env Resour* 4:23–27.
5. Yang Q, Jiang Z, Zhou X, Zhang R, Xie Z, Zhang S, Wu Y, Ge Y, Zhang X. 2019. *Haliea alexandrii* sp. nov., isolated from phycosphere microbiota of the toxin-producing dinoflagellate *Alexandrium catenella*. *Int J Syst Evol Microbiol* 70:1133–1138. <https://doi.org/10.1099/ijsem.0003890>.
6. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. *Nucleic Acids Res* 44:6614–6624. <https://doi.org/10.1093/nar/gkw569>.
7. Mu J, Wang D, Yang G, Cui X, Yang Q. 2019. Preparation and characterization of a substitute for *Ruditapes philippinarum* conglutination mud as a natural biofloculant. *Bioresour Technol* 281:480–484. <https://doi.org/10.1016/j.biortech.2019.02.080>.