

Genome Sequence of the Algicidal Bacterium *Kordia algicida* OT-1[∇]

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***Kordia algicida* OT-1 is an algicidal bacterium against the bloom-forming microalgae. The genome sequence of *K. algicida* revealed a number of interesting features, including the degradation of macromolecules, the biosynthesis of carotenoid pigment and secondary metabolites, and the capacity for gliding motility, which might facilitate the understanding of algicidal mechanisms.**

Kordia algicida OT-1 is the first species to be assigned a new genus, *Kordia*, in the family *Flavobacteriaceae* and was isolated from surface seawater where a *Skeletonema costatum* bloom occurred (8). Comparative sequence analysis of its 16S rRNA gene revealed that this strain is most closely related to the very recently described *Kordia periserrulae* IMCC1422. *K. periserrulae* IMCC1422 was isolated from the digestive tract of a marine polychaete, *Periserrula leucophryna*, which was collected from a tidal flat (4). *K. algicida* OT-1 showed algicidal activity against several marine microalgal species, such as *S. costatum*, *Thalassiosira* sp., *Heterosigma akashiwo*, and *Cochlodinium polykrikoides*, which are known to cause red tide blooms (8).

Here, we present the genome sequence of *K. algicida*, which is the first genome report for the genus *Kordia*. Whole-genome shotgun sequencing was performed by the J. Craig Venter Institute (JCVI) as a part of the Moore Foundation Microbial Genome Sequencing Project (<http://www.camera.calit2.net/microgenome>). A draft, unclosed genome consisting of 34 contigs (ABIB01000001 to ABIB01000034) was obtained and annotated using JCVI's prokaryotic annotation pipeline and the National Center for Biotechnology Information prokaryotic genome automatic annotation pipeline (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>).

The *K. algicida* genome has 5,019,836 bases with a G+C content of 34.3%, and a total of 4,514 protein coding genes, 3 rRNA loci, and 61 tRNA genes were detected. Comparative bacterial genome analysis revealed that *K. algicida* shared the greatest proportion of homologous proteins with *Cellulophaga lytica* DSM 7489 (GenBank accession no. CP002534), isolated from the surface of the marine benthic macroalga *Fucus serratus* L. and the surrounding seawater, and with "*Gramella forsetii*" KT0803 (GenBank accession no. CU207366), isolated from North Sea surface waters during a phytoplankton bloom (2, 6).

K. algicida forms yellow-pigmented colonies (8), and the genome revealed the presence of genes coding for enzymes

required for carotenoid biosynthesis, including geranylgeranyl synthase, phytoene synthase, phytoene desaturase, lycopene cyclase, and β -carotene hydroxylase. The identification of several copies of genes coding for α -amylases, α -glucosidase, and various endo- and exopeptidases confirmed the physiological ability of the strain to degrade macromolecules such as gelatin, skim milk, and starch (8). Intriguingly, although gliding motility has not been observed in this strain, its genome contains homologs of all of the *gld* and *spr* gliding motility genes that have been identified in the genomes of gliding *Flavobacterium johnsoniae* UW101, *Flavobacterium psychrophilum*, and *Cytophaga hutchinsonii* and potentially gliding "*G. forsetii*" KT0803 (2, 5, 7, 9). The *K. algicida* genome has a gene cluster encoding a nonribosomal peptide synthetase, and some genes are homologous to the corresponding genes of a gene cluster spanning Fjoh_2083 to Fjoh_2104 of *F. johnsoniae* UW101 (7). A giant gene cluster containing genes with homology to polyketide synthase genes of modular organization in *Bacillus subtilis* and *Bacillus amyloliquefaciens* FZB 42 was identified, implying that the strain has the biosynthetic potential to produce a polyketide compound (1, 3). These interesting features might facilitate the understanding of algicidal mechanisms.

Nucleotide sequence accession number. The genome sequence is available in GenBank under accession number ABIB00000000.

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