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

Hyun Sook Lee,1,2 Sung Gyun Kang,1,2 Kae Kyoung Kwon,1,2 Jung-Hyun Lee,1,2 and Sang-Jin Kim1,2*

Korea Ocean Research & Development Institute, Ansan, P.O. Box 29, Seoul 425-600, South Korea; and Department of Marine Biotechnology, University of Science and Technology, Daejeon 305-333, South Korea

Received 6 May 2011/Accepted 16 May 2011

*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 *Cytophaga johnsoniae UW101*, *Flavobacterium psychrophilum*, and *Cytaphaga 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 *Bacillus subtilis* 42 was identified, implying that the strain has the biosynthetic potential to produce a polyketide compound (1, 5). 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.

This research was supported by the Gordon and Betty Moore Foundation Marine Microbial Sequencing Project, KORDI in-house program (PE98513), and the Marine and Extreme Genome Research Center program of the Ministry of Land, Transport, and Maritime Affairs, Republic of Korea.

**REFERENCES**