

Genome Sequence of *Arenibacter algicola* Strain TG409, a Hydrocarbon-Degrading Bacterium Associated with Marine Eukaryotic Phytoplankton

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***Arenibacter algicola* strain TG409 was isolated from *Skeletonema costatum* and exhibits the ability to utilize polycyclic aromatic hydrocarbons as sole sources of carbon and energy. Here, we present the genome sequence of this strain, which is 5,550,230 bp with 4,722 genes and an average G+C content of 39.7%.**

Received 8 June 2016 Accepted 10 June 2016 Published 4 August 2016

Citation Gutierrez T, Whitman WB, Huntemann M, Copeland A, Chen A, Kyrpides N, Markowitz V, Pillay M, Ivanova N, Mikhailova N, Ovchinnikova G, Andersen E, Pati A, Stamatidis D, Reddy TBK, Ngan CY, Chovatia M, Daum C, Shapiro N, Cantor MN, Woyke T. 2016. Genome sequence of *Arenibacter algicola* strain TG409, a hydrocarbon-degrading bacterium associated with marine eukaryotic phytoplankton. *Genome Announc* 4(4):e00765-16. doi:10.1128/genomeA.00765-16.

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Arenibacter algicola strain TG409 was isolated from a laboratory culture of the marine diatom *Skeletonema costatum* (CCAP 1077/1C) by enrichment with polycyclic aromatic hydrocarbons (PAHs) as the sole carbon source (1). The strain represents the first *Arenibacter* species associated with a laboratory culture of *S. costatum* and shows the ability to degrade PAHs as a sole source of carbon and energy (1). Notably, work with this and other *Arenibacter* type strains has shown that PAH degradation may be a shared phenotype among members of this genus (1). Strain TG409 is a strictly aerobic and nonmotile rod-shaped bacterium that is associated with the cosmopolitan marine diatom *S. costatum*. It produces amphiphilic biopolymers (e.g., biosurfactants) on the cell surface that may facilitate attachment to oil droplets and increase the bioavailability of hydrocarbons (1).

Here, we report the genome sequence of *Arenibacter algicola* strain TG409. Genomic DNA was isolated, and the sequence generated at the Department of Energy (DOE) Joint Genome Institute (JGI) using the Pacific Biosciences (PacBio) technology. A PacBio SMRTbell library was constructed and sequenced on the PacBio RS platform, which generated 292,099 filtered subreads totaling 1074.1 Mbp. All general aspects of library construction and sequencing performed at the JGI can be found at <http://www.jgi.doe.gov>. The raw reads were assembled using HGAP (version: 2.1.1) (2). The final draft assembly produced three scaffolds containing three contigs totaling 5.6 Mbp in size and input read coverage of 185.2×.

Project information is available in the Genomes Online Database (3). Genes were identified using Prodigal (4), followed by a round of manual curation using GenePRIMP (5) as part of the JGI's microbial annotation pipeline (6). The predicted coding sequences (CDSs) were translated and used to search the National Center for Biotechnology Information (NCBI) nonredundant da-

tabase and the UniProt, TIGRFam, Pfam, KEGG, COG, and InterPro databases. The tRNA-ScanSE tool (7) was used to find tRNA genes, whereas rRNA genes were found by searches against models of the rRNA genes built from SILVA (8). Other noncoding RNAs, such as the RNA components of the protein secretion complex and the RNase P, were identified by searching the genome for the corresponding Rfam profiles using INFERNAL (<http://infernal.janelia.org>). Additional gene prediction analysis and manual functional annotation was performed within the Integrated Microbial Genomes—Expert Review (IMG ER) platform (<https://img.jgi.doe.gov/>) developed by the Joint Genome Institute, Walnut Creek, CA, USA (9).

The complete genome sequence length was 5,550,230 bp with a G+C content of 39.7%. The genome contains 4,722 genes (4,649 protein-coding genes) with functional predictions for 3,538 of them. A total of 73 RNA genes were detected. Other genes, characteristic for the genus, are given in the IMG database (9).

Nucleotide sequence accession number. The draft genome sequence of *A. algicola* strain TG409 obtained in this study was deposited in GenBank as part of BioProject no. PRJNA224116, with individual genome sequences submitted as whole-genome shotgun projects under the accession no. [JPOO0000000](https://doi.org/10.1101/000000).

ACKNOWLEDGMENTS

T.G. was supported by a Marie Curie International Outgoing Fellowship (PIOF-GA-2008-220129) within the 7th European Community Framework Program.

The work was conducted by the U.S. Department of Energy Joint Genome Institute, a DOE Office of Science User Facility, which is supported by the Office of Science of the U.S. Department of Energy under contract no. DE-AC02-05CH11231.

FUNDING INFORMATION

This work, including the efforts of Tony Gutierrez, was funded by European Commission (EC) (PIOF-GA-2008-220129). U.S. Department of Energy (DOE) provided funding to Tony Gutierrez, William B. Whitman, Marcel Huntemann, Alex Copeland, Amy Chen, Nikos C. Kyrpides, Victor Markowitz, Manoj Pillay, Natalia Ivanova, Natalia Mikhailova, Galina Ovchinnikova, Evan Andersen, Amrita Pati, Dimitrios Stamatis, T. Reddy, Chew Ngan, Mansi Chovatia, Chris Daum, Nicole Shapiro, Michael Cantor, and Tanya Woyke under grant number DE-AC02-05CH11231.

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