

Genome Sequence of the Agar-Degrading Marine Bacterium *Alteromonadaceae* sp. Strain G7

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Here, we present the high-quality draft genome sequence of the agar-degrading marine gammaproteobacterium *Alteromonadaceae* sp. strain G7, which was isolated from coastal seawater to be utilized as a bioresource for production of agar-derived biofuels. The 3.91-Mb genome contains a number of genes encoding algal polysaccharide-degrading enzymes such as agarases and sulfatases.

Agar is a major constituent in the cell wall of red algae, which is a highly abundant biomass in the ocean (10). Due to its gelling property, this galactan carbohydrate has been broadly used in the food industry as a food additive (7) and in scientific laboratories as a major ingredient for solid culture media. Use of marine biomass such as seaweeds for producing biofuels may avoid problems resulting from competition between fuel and food (6). For this and other reasons, there is a growing interest from the bioindustry sector in utilizing marine microbes that are capable of processing agarose or agaropectin (3).

Members of the family *Alteromonadaceae*, which contains the genera *Alteromonas*, *Agarivorans*, *Alishewanella*, *Catenovulum*, *Glaciecola*, *Marinobacter*, *Marinobacterium*, *Microbulbifer*, and *Saccharophagus*, are mostly of marine origin. Among them, *Saccharophagus degradans* 2-40, of which genomic and proteomic information has been provided (4), can degrade many complex polysaccharides such as agar. Recently, a new member of the family, strain G7, was identified from coastal seawater in an effort to isolate agar-degrading microbes, and *Gayadomonas joobiniege* gen. nov., sp. nov., was proposed for the bacterium (W. J. Chi, Y. K. Chang, and S. K. Hong, submitted for publication) that is phylogenetically close to another agar degrader in the family, *Catenovulum agarivorans* (11).

Illumina/Solexa HiSeq 2000 was used for the genome sequencing of the G7 bacterium (National Instrumentation Center for Environmental Management [NICEM], Republic of Korea). A total of 71,156,138 reads with 1,710-fold coverage were generated from a 400-bp paired-end library. Sequence trimming and *de novo* assembly were performed with CLC Genomics Workbench, version 4.8, and scaffolding was carried out with SSPACE (2). Optical mapping (OpGen, Inc., Gaithersburg, MD) was performed to validate the scaffold structure. IMAGE (9) and Perl scripts developed in-house were used for *in silico* walking. Primer walking was conducted to close gaps and to proofread the regions of polymorphism among reads. Structural gene prediction was performed using Glimmer, version 3, and functional annotation was carried out with AutoFact (5a) using GenBank, KEGG, COG, UniProt, Pfam, and Subsystem databases. tRNA and rRNA were predicted with tRNAscan-SE and RNAmmer.

The draft genome of G7 is composed of seven contigs

(3,140,906 bp, 41.44% G+C) that can be built up into a single chromosome and one completely assembled plasmid (769,523 bp, 41.12% G+C) with *oriC*. From this ca. 3.91-Mb genome, 3,439 protein-coding sequences, 6 rRNA operons, and 56 tRNA genes were annotated. The G7 genome has many genes encoding hydrolytic enzymes that may play important roles in the complete breakdown of sulfated algal polysaccharides (8): 50 sulfatases, 17 glycoside hydrolases, 13 agarases, 8 β -galactosidases, 3 altronate hydrolases, and 1 cellulase. One interesting observation is the presence of many of them on the plasmid, for example, 32 sulfatase genes and 11 agarase genes. These genomic features represent the potential for the bacterium to be used as a bioresource for biofuel production.

Nucleotide sequence accession numbers. The assembled whole-genome shotgun sequences of G7 have been deposited in GenBank under accession number [AMRX000000000](https://www.ncbi.nlm.nih.gov/nuccore/AMRX000000000), of which the first version, AMRX010000000, is described in this paper. The sequence and annotation are also available from the Genome Encyclopedia of Microbes (GEM; <http://www.gem.kr>) (5).

ACKNOWLEDGMENTS

We thank Dong Su Yu and Choi Jae-Pil for assistance with depositing genome information at the GEM database, Dae-Hee Lee for helpful comments, and Choong Hoon Lee for critically reading the manuscript.

We are grateful for the financial assistance from the National Research Foundation (grant no. 2012-0005726) of the Ministry of Education, Science and Technology, Republic of Korea, and the Next-Generation BioGreen 21 Program (grant no. SA00004146 and PJ00820101), Rural Development Administration, Republic of Korea. Financial support also came in part from the Yonsei University Research Fund of 2012 (to J.F.K.).

Received 30 September 2012 Accepted 2 October 2012

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doi:10.1128/JB.01931-12

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