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Draft Genome Sequence of *Halomonas smyrnensis* AAD6^T

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***Halomonas smyrnensis* AAD6^T is a Gram-negative, aerobic, exopolysaccharide-producing, and moderately halophilic bacterium that produces levan, a fructose homopolymer with many potential uses in various industries. We report the draft genome sequence of *H. smyrnensis* AAD6^T, which will accelerate research on the rational design and optimization of microbial levan production.**

Halomonas smyrnensis AAD6^T was isolated from soil samples taken from the Çamaltı Saltern area (Turkey) and was found to excrete high levels of levan exopolysaccharide (5). Further research on the potential uses of levan produced by *Halomonas* sp. as a bioflocculating agent (7), its nanostructured thin films (9), its suitability for peptide-based drug nanocarrier systems (8), and a scheme for economical production from waste (4) have been reported. Moreover, the first genome scale metabolic model of *Chromohalobacter salexigens* DSM 3043 was reported, which in turn formed the basis for the reconstruction of a generic *in silico* metabolic model of levan-producing *Halomonas* sp. (1). Recently, *H. smyrnensis* strain AAD6^T was identified as a Gram-negative, nonmotile, dark-yellow-pigmented, aerobic, moderately halophilic bacterium (6).

In this study, whole-genome sequencing of *H. smyrnensis* AAD6^T was performed by using a combination of 454 GS FLX+ (454 Life Sciences, Branford, CT) and Ion Proton (Ion Torrent Systems, Inc., Guilford, CT) sequencers. The shotgun sequence data generated consisted of 1,082,564 reads (mean length of 498.36 bp) and 359,877 reads (mean length of 122.42 bp), respectively, providing 140-fold coverage. The duplicates in the sequence data were eliminated with CLC Genomics Workbench (v5.0.1). *De novo* assembly of the whole sequencing reads was carried out with Newbler Assembler (v2.3). One hundred ninety-two contigs, with a minimum length of 500 bp, were obtained. Alignment of these contigs and elimination of the overlaps using Sequencher 5.0 (3) resulted in 81 high-quality contigs. These contigs were mapped to the raw data with CLC Genomics Workbench (v5.0.1) to estimate the terminals, and using overlapping terminal regions, the contigs were assembled into 34 supercontigs via Geneious Pro (v5.5.6) software. The draft genome of *H. smyrnensis* AAD6^T was structured with 34 supercontigs (total assembly size of 3,561,919 bp). Gene prediction and annotation were carried out using the RAST server (2).

The draft genome that resulted had a mean GC content of 67.9%, 3,237 coding sequences, 1,756 subsystems, and 64 RNA genes. Putative functions could be assigned to 2,436 protein-coding genes, whereas 801 hypothetical proteins had no match to any known proteins. Genome analysis revealed a number of genes related to exopolysaccharide biosynthesis, including the genes for levansucrase and ExoD.

Phylogenetic analysis of the draft genome revealed a rather close relationship to other species of the genus *Halomonas*, where *Halomonas salina* (99.5%) and *Halomonas halophila* (99.5%) were found to be the closest species on the basis of 16S rRNA sequence (GenBank accession no. DQ131909.2) comparison. However, whole-genome comparison with genome sequences available at the RAST server pointed out the closest similarity to *Chromohalobacter salexigens* DSM 3043 (score, 524), followed by *Halomonas elongata* DSM 2581 (score, 346).

The whole-genome sequence of *H. smyrnensis* AAD6^T marks an important step toward the rational genetic and metabolic optimization of levan production. Furthermore, the information provided by the whole-genome sequence here will facilitate future studies on the genetic and metabolic diversity of halophilic bacteria and contribute to the understanding of important processes such as osmoadaptation and exopolysaccharide biosynthesis.

Nucleotide sequence accession numbers. This genome project has been deposited at DDBJ/EMBL/GenBank under accession no. AJKS00000000. This is the second version, with accession numbers AJKS02000001 to AJKS02000034.

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