Genome Sequence of the Extreme Obligate Alkaliphile Bacillus marmarensis Strain DSM 21297

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Bacillus marmarensis strain DSM 21297 is an extreme obligate alkaliphile able to grow in medium up to pH 12.5. A whole-shotgun strategy and de novo assembly led to the generation of a 4-Mbp genome of this strain. The genome features alkaliphilic adaptations and pathways for n-butanol and poly(3-hydroxybutyrate) synthesis.

The draft genome consists of 98 large (>500 bp) contigs totaling 4.0 Mb, with a G+C content of 40.2%. A total of 4,195 predicted coding sequences were identified, and 1,889 coding sequences were assigned a predicted function. Among these, 37 tRNA sequences and 7 rRNA clusters were found. Several extraacellular hydrolases of industrial importance were annotated: 7 proteases, 6 amylases, 2 cellulases, and 1 lipase. Also, metabolic pathways for the production of the drop-in-ready biofuel n-butanol (9) and biodegradable plastic poly(3-hydroxybutyrate) (10) were annotated.

Several known adaptations of alkaliphiles were also found in the genome. These include a high number of sodium-proton antiporters (11), sodium-dependent flagellum rotor proteins (12), and a specialized F$_{1}$-F$_{0}$-ATPase of neutrophilic bacteria contains a GxGxGxG motif in the C subunit that mutates toward AxAxAxA in alkaliphiles; increasing A residues correlate with greater alkaliphilicity (14). However, B. marmarensis displays a novel variant of GxSxAxA. This finding, and the rest of the genome, may reveal other unique adaptations necessary for growth in medium beyond pH 12.0.

Nucleotide sequence and accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL-GenBank under the accession no. ATAE00000000. The version described in this paper is version ATAE01000000.

ACKNOWLEDGMENTS

This work was supported by the Kaiteki Institute and performed in a "co-laboratory" renovated by the National Science Foundation under grant no. 0963183 (funded under the American Recovery and Reinvestment Act of 2009).

We thank Matteo Pellegrini (UCLA) for assistance in genome sequencing and assembly.

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Received 22 October 2013 Accepted 27 October 2013 Published 27 November 2013

Citation Wernick DG, Choi K-Y, Tat CA, Lafontaine Rivera JG, Liao JC. 2013. Genome sequence of the extreme obligate alkaliphile Bacillus marmarensis strain DSM 21297. Genome Announc. 1(6):e00967-13. doi:10.1128/genomeA.00967-13.

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