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GENOME SEQUENCES

Complete Genome Sequence of *Marinobacterium aestuarii* ST58-10^T, a Benzene-Degrading Bacterium Isolated from Estuarine Sediment

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ABSTRACT *Marinobacterium aestuarii* ST58-10^T was identified as a benzene-degrading aerobic bacterium isolated from estuarine sediment in the Republic of Korea. The genome of strain ST58-10^T was found to be composed of a single circular chromosome (5,191,608 bp) with a G+C content of 58.78% and harboring 4,473 protein-coding genes. The assembled sequence data will help elucidate potential metabolic pathways and mechanisms responsible for the hydrocarbon-degrading ability of *M. aestuarii* ST58-10^T.

The genus *Marinobacterium* was proposed by Gonzalez et al. (1), with the description of *Marinobacterium aestuarii* as the type species. To date, 17 type strains from different species in this genus have been identified (http://www.bacterio.net/marinobacterium.html), and these strains have been isolated from various marine habitats. *M. aestuarii* ST58-10^T shows benzene-degrading activity of up to 70%, which was first observed within reported *Marinobacterium* species (2). To date, 10 genomes of *Marinobacterium* species have been published in the NCBI genome database; however, the genome of only *M. aestuarii* ST58-10^T has been sequenced completely. Considering the unique benzene-degrading properties of this strain and its dominant composition in hydrocarbon-rich environments, such as oil reservoirs (3, 4), we conducted genome sequencing to elucidate the physiological roles and metabolic potential of *M. aestuarii* ST58-10^T.

The genomic DNA was purified from cells after overnight culture in marine broth 2216 at 25°C using an AccuPrep bacterial genomic DNA extraction kit (Bioneer, South Korea) according to the manufacturer's instructions. The genome was sequenced from a 20-kbp library by using the single-molecule real-time (SMRT) sequencing method with a PacBio RS II system (Pacific Biosciences, USA). The 81,479 reads were assembled using Hierarchical Genome Assembly Process version 3 with default parameters. Genome annotation was performed using the NCBI Prokaryotic Genome Annotation Pipeline (5).

As a result of the final assembly, a single contig with an N_{50} value of 5,191,608 bp was generated, with coverage of 154× and 58.78% G+C content. In total, 4,473 protein-coding sequences were predicted, with 110 RNA genes, including 21 rRNAs (7 copies of 5S, 16S, and 23S), 85 tRNAs, 4 noncoding RNAs, and 51 pseudogenes. In the genome, we detected genes encoding mechanisms for xenobiotic biodegradation and metabolism-related enzymes, such as phenol hydroxylase and benzoate and/or toluene 1,2-dioxygenase. Many other aromatic hydrocarbon-metabolizing genes, such as protocatechuate 3,4-dioxygenase, anthranilate 1,2-dioxygenase large and small subunit, and haloacid dehalogenase, were also located on the chromosome. In addition, genes annotated as [2Fe-2S]-binding proteins, a component of the ring-hydroxylating dioxygenase alpha subunit responsible for the biodegradation of aromatic hydrocarbons, were identified (6).

In conclusion, the assembled genome sequence of *M. aestuarii* ST58-10^T presented

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here will contribute to the elucidation of regulatory pathways and metabolic networks involved in hydrocarbon degradation.

Data availability. *Marinobacterium aestuarii* ST58-10^T was deposited at the Korean Collection for Type Cultures (KCTC 52193^T) and Biological Resource Center, National Institute of Technology and Evaluation (NBRC 112103T). The BioSample and BioProject accession numbers are SAMN04939310 and PRJNA320435, respectively. The complete genome sequence of *Marinobacterium aestuarii* ST58-10^T has been deposited at DDBJ/EMBL/GenBank under the accession number CP015839.

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REFERENCES

1. González JM, Mayer F, Moran MA, Hodson RE, Whitman WB. 1997. *Microbulbifer hydrolyticus* gen. nov., sp. nov., and *Marinobacterium georgiense* gen. nov., sp. nov., two marine bacteria from a lignin-rich pulp mill waste enrichment community. Int J Syst Bacteriol 47:369–376. https://doi.org/10.1099/00207713-47-2-369.
2. Bae SS, Jung J, Chung D, Baek K. 2018. *Marinobacterium aestuarii* sp. nov., a benzene-degrading marine bacterium isolated from estuary sediment. Int J Syst Evol Microbiol 68:651–656. https://doi.org/10.1099/ijsem.0.002561.
3. Kobayashi H, Endo K, Sakata S, Mayumi D, Kawaguchi H, Ikarashi M, Miyagawa Y, Maeda H, Sato K. 2012. Phylogenetic diversity of microbial communities associated with the crude-oil, large-insoluble-particle and formation-water components of the reservoir fluid from a non-flooded high-temperature petroleum reservoir. J Biosci Bioeng 113:204–210. https://doi.org/10.1016/j.jbiosc.2011.09.015.
4. Sierra-Garcia IN, Dellagnezze BM, Santos VP, Chaves B MR, Capilla R, Santos Neto EV, Gray N, Oliveira VM. 2017. Microbial diversity in degraded and non-degraded petroleum samples and comparison across oil reservoirs at local and global scales. Extremophiles 21:211–229. https://doi.org/10.1007/s00792-016-0897-8.
5. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. Nucleic Acids Res 44:6614–6624. https://doi.org/10.1093/nar/gkw569.
6. Parales RE, Resnick SM. 2006. Aromatic ring hydroxylating dioxygenases, p 287–340. *In* Ramos JL, Levesque RC (ed), Pseudomonas. Springer, New York, NY.