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**Citation for published version:**

Kiseleva, L, Garushyants, SK, Briliute, J, Simpson, DJW, Cohen, MF & Goryanin, I 2015, 'Genome Sequence of the Electrogenic Petroleum-Degrading *Thalassospira* sp. Strain HJ' *Genome announcements*, vol. 3, no. 3, e00483-15. DOI: 10.1128/genomeA.00483-15

**Digital Object Identifier (DOI):**

[10.1128/genomeA.00483-15](https://doi.org/10.1128/genomeA.00483-15)

**Link:**

[Link to publication record in Edinburgh Research Explorer](#)

**Document Version:**

Publisher's PDF, also known as Version of record

**Published In:**

Genome announcements

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# Genome Sequence of the Electrogenic Petroleum-Degrading *Thalassospira* sp. Strain HJ

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We present the draft genome of the petroleum-degrading *Thalassospira* sp. strain HJ, isolated from tidal marine sediment. Knowledge of this genomic information will inform studies on electrogenesis and means to degrade environmental organic contaminants, including compounds found in petroleum.

Received 8 April 2015 Accepted 14 April 2015 Published 14 May 2015

**Citation** Kiseleva L, Garushyants SK, Briliute J, Simpson DJW, Cohen MF, Goryanin I. 2015. Genome sequence of the electrogenic petroleum-degrading *Thalassospira* sp. strain HJ. *Genome Announc* 3(3):e00483-15. doi:10.1128/genomeA.00483-15.

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Inadvertently, through oil spills large and small, humans have amplified petroleum-degrading microorganisms on an unprecedented global scale (1). Strains isolated from shoreline sediments that regularly receive petroleum contaminants could potentially be exploited to break down petroleum in controlled environments, such as in microbial fuel cells (2).

Members of genus *Thalassospira* are Gram-negative, halophilic, and often facultative anaerobic alphaproteobacteria with the ability to utilize hydrocarbons as their sole source of carbon and energy (3). There are currently eight validly named species of *Thalassospira* (<http://www.bacterio.net>), and the genomes of seven strains are available in the GenBank database (<https://www.ncbi.nlm.nih.gov/genbank/>). Strain HJ was isolated from stagnant tidal marine sediment at Kaichu-doro Beach, Okinawa, Japan (26°19'56.1"N 127°54'0"E), in October 2013, 5 km from a large petroleum storage facility that has been in operation since the early 1970s. Strain HJ can grow on petroleum as a sole carbon source, it generates power in a microbial fuel cell and, based on *in silico* studies, and it possesses several catabolic pathways of interest (our unpublished data).

The genome of strain HJ was sequenced using the Illumina MiSeq sequencing platform (Illumina, Inc., San Diego, CA). The generated reads were trimmed and assembled *de novo* using SPAdes version 3.1.1 (4). The resulting sequence was then submitted to the NCBI Prokaryotic Genomes Automatic Annotation Pipeline for autoannotation (5). The size of the genome of strain HJ was found to be 4,269,399 bp, comprising 22 contigs, with a G+C content of 54.9%. Strain HJ contains 3,909 predicted genes, 3,838 putative coding sequences (CDS), 7 rRNAs, and 57 tRNAs.

*In silico* DNA-DNA hybridization (DDH) comparisons (6) between the genome of strain HJ and other accessible *Thalassospira* genome sequences in GenBank indicate the closest match to *Thalassospira profundimaris* WP0211 (7), with an estimated DDH value of 73.2% ± 3.8%, while comparisons with other *Thalassospira* strains gave values from 12.8% to 57.0% (high-scoring

segment pair length/total length, generalized linear model based). The aligned 16S rRNA gene sequences of these two organisms show 99.7% identity (1,449 bp/1,453 bp).

**Nucleotide sequence accession number.** The genome data have been deposited at NCBI under BioProject no. PRJNA275638 and accession no. [JYII00000000](https://ncbi.nlm.nih.gov/assembly/JYII00000000) for *Thalassospira* sp. HJ.

## ACKNOWLEDGMENT

This work was supported by the Okinawa Institute of Science and Technology.

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