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Genome Sequence of *Photobacterium halotolerans* MELD1, with Mercury Reductase (*merA*), Isolated from *Phragmites australis*

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Here, we present the whole-genome sequence of *Photobacterium halotolerans* strain, MELD1, isolated from the roots of a terrestrial plant *Phragmites australis* grown in soil heavily contaminated with mercury and dioxin. The genome provides further insight into the adaptation of bacteria to the toxic environment from where it was isolated.

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Photobacterium spp. are Gram-negative bacteria belonging to the family *Vibrionaceae*. Though they are found to be primarily associated with marine environments (1), *Photobacterium halotolerans* MELD1 was isolated from the rhizosphere of a terrestrial weed, *Phragmites australis*, found growing in mercury- and dioxin-contaminated land located near the seacoast (2). In our previous study, we demonstrated that *P. halotolerans* MELD1 helped with the phytoprotection of *Vigna unguiculata* from mercury stress (2). To gain insight into the genetic traits among the closely related *P. halotolerans* strains, whole-genome sequencing of terrestrial environment dwelling *P. halotolerans* MELD1 was performed.

The MELD1 whole-genome sequence was obtained using Illumina technology. Ten micrograms of total DNA was sonicated by a Misonix 3000 sonicator to sizes ranging from 400 to 500 bp. DNA sizing was checked by a bioanalyzer DNA 1000 chip (Agilent Technologies, Santa Clara). One-microgram sonicated DNA was end repaired, A tailed, and adaptor ligated following Illumina's Trueseq DNA preparation protocol. The sequences generated went through a filtering process to obtain the qualified reads. ConDeTri (3) was implemented to trim or remove the reads according to the quality score. Cleaned and filtered nuclear reads were assembled *de novo* using ABySS (4). Genome annotations were created in MAKER 2.00 (5) using a GeneMark (6) model trained for MELD1 via self-training. The resulting predictions were searched against the NCBI nonredundant (nr) database by using BLASTp.

The whole-genome draft of *P. halotolerans* MELD1 consists of 57 contigs for a total of 4,758,037 bp with an overall G+C content of 51%, 258 pseudogenes, 17 rRNA genes, and 88 tRNA genes. In our previous work, we identified the presence of a *merA* gene and its mercury reductase activity, as well as resistance to toxic compounds like cadmium, lead, and dioxin (2). As a trait of adaptation to the mercury-contaminated habitat, the genome of MELD1 contains a *mer* operon containing a mercury reductase gene (*merA*). Furthermore, MELD1 had a cluster of genes responsible for stress resistance, multidrug efflux pumps, and aerobactin siderophore. They also bear *lux* genes and genes responsible for gamma aminobutyric acid (GABA) (7) and pyrroloquinoline quinone (PQQ) (8). These unique characteristics make the strain *P. halotolerans* MELD1 an effective plant growth-promoting bacterium in heavy metal-contaminated environments.

Nucleotide sequence accession numbers. The whole-genome sequence of *P. halotolerans* MELD1 was deposited at DDBJ/EMBL/GenBank under the accession no. JWYV00000000. The version described in this paper is the first version, JWYV01000000.

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