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Complete genome sequence of *Marivivens* sp. JLT3646, a potential aromatic compound degrader

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ABSTRACT

Marivivens sp. JLT3646 (CGMCC 1.15778), belonging to the phylum *Alphaproteobacteria*, was isolated from seawater, Kueishan Islet, offshore northeast of Taiwan. Here, we present the complete genome sequence of *Marivivens* sp. JLT3646, which contains a circular 2,978,145 bp chromosome with 56.2% G + C content, and one circular plasmid which is 169,066 bp in length. The genome data suggested that *Marivivens* sp. JLT3646 has the potential to degrade aromatic monomers, which might provide insight into biotechnological applications and facilitate the investigation of environmental bioremediation.

1. Introduction

Aromatic compounds are widely found in the environment as components of plant materials and as anthropogenic pollutants, and their degradation by bacteria has tremendous practical significance (Harwood and Parales, 1996; Gulvik and Buchan, 2013). Benzoate and *p*-hydroxybenzoate are common lignin-derived phenolic compounds (Feng et al., 2016). Benzoate produced from the degradative pathways of various aromatic chemicals is generally recognized as a pollutant (Kim et al., 2002) and found in food and dye processing effluents (Oie et al., 2007). Many attempts have been made to isolate bacteria degrading aromatic compounds and investigate the degradation mechanisms (Ren et al., 2016). The β-ketoadipate pathway is a chromosomally encoded convergent pathway for aromatic compound degradation (Harwood and Parales, 1996; MacLean et al., 2006) and its protocatechuate branch, in coastal marine environments, may be used to degrade aromatic monomers that arise during the decay of lignin and other vascular plant components (*e.g.*, vanillate, coumarate, cinnamate, ferulate, benzoate, and *p*-hydroxybenzoate) (Buchan et al., 2000). Here, we present the complete genome of *Marivivens* sp. JLT3646, which harbors genetic potential to utilize benzoate or *p*-hydroxybenzoate.

2. Data description

Strain JLT3646 was isolated from the surface water, Kueishan Islet, offshore northeast of Taiwan. It was an aerobic, motile, non-sporulating, short rods-shaped and colorless, Gram-negative bacterium (Table 1). The 16S rRNA gene in strain JLT3646 showed 99.8% sequence similarity with that in *Marivivens donghaensis* AM-4^T (Park et al., 2016).

Marivivens sp. JLT3646 was cultured with 2216E agar (Hopebio, China) and incubated at 28 °C. Genomic DNA was extracted with the TIANamp Bacteria DNA Kit (Tiangen Biotech, China) in accordance with the manufacturer's recommendations. DNA quantity and quality were determined by Agilent 2100 Bioanalyzer (Agilent Technologies, USA). The whole genome of JLT3646 was sequenced using PacBio RS II sequencing technology (Pacific Biosciences, USA). A total of 99,956 reads with the mean read length of 12,910 bp were generated. The reads were *de novo* assembled into the complete genome of strain JLT3646 using the HGAP pipeline of the SMRT Analysis v2.3.0 (Chin et al., 2013), resulting in 2 contigs with 430-fold average coverage. Gene annotation was performed using the NCBI Prokaryotic Genome Annotation Pipeline (Pruitt et al., 2012). As shown in Fig. 1, the complete genome was comprised of one circular chromosome of 2,978,145 bp with a G + C content of 56.2%, and one plasmid of 169,066 bp with 52.8% G + C content. A total of 3150 genes were predicted and 3045 of them were protein-coding sequences (Table 2). Each gene was functionally assigned to a category using the Non-Redundant Protein Database (Tatusov et al., 2000). A total of 9 rRNAs, 50 tRNAs, 3 other RNAs and 43 pseudo genes were found in the genome (Table 2).

Marivivens sp. JLT3646 possessed the complete repertoire of genes encoding for enzymes involved in protocatechuate branch of the β-ketoadipate pathway. These genes encode enzymes including protocatechuate 3,4-dioxygenase (the key enzyme cleaving the aromatic ring of protocatechuate) (*pcaGH*, BSK21_00725, BSK21_00720), 3-carboxy-cis-cis-muconate cycloisomerase (*pcaB*, BSK21_00735), γ-

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Table 1
General features of *Marivivens* sp. JLT3646 and MIxS mandatory information (Yilmaz et al., 2011).

Items	Description
General features	
Classification	Domain *Bacteria* Order *Rhodobacetrales* Family *Rhodobacteraceae*
Particle shape	Short rods
Gram stain	Negative
Pigmentation	Colorless
Temperature	4–40 °C
Salinity	0.5–9%
pH range	5–9
Motility	Motile
MIxS data	
Submitted_to_insdc	CP018572; CP018573 (GenBank)
Investigation_type	Bacteria
Project_name	*Marivivens* sp. JLT3646 genome sequencing and assembly
Geo_loc_name	Kueishantao Islet, Taiwan, China
Lat_lon	24°50′ N, 121°57′ E
Depth	5 m
Collection_date	2015-05-27
Env_biome	Surface water (ENVO:00002042)
Env_feature	Coastal water body (ENVO: 02000049)
Env_ material	Sea water (ENVO: 00002149)
Env_package	Missing
Source_mat_id	CGMCC 1.15778
Biotic_relationship	Free living
Trophic_level	Chemoorganotroph
Rel_to_oxygen	Aerobic
Number of contigs	2
Seq_meth	Pacific Biosciences RS II
Assembly method	SMRT Analysis v 2.3.0
Finishing_strategy	430x, complete
Annot_source	NCBI

carboxymuconolactone decarboxylase (*pcaC*, BSK21_15695), 3-oxoadipate enol-lactonase (*pcaD*, BSK21_00710, BSK21_12240), β-ketoadipate succinyl-CoA transferase (*pcaIJ*, BSK21_11870, BSK21_11875) and acetyl-CoA acetyltransferase (*pcaF*, BSK21_01795, BSK21_04065, BSK21_05865, BSK21_09265, BSK21_13160). In addition, designated *pobA* gene (BSK21_00705), coding for the enzyme catalyzing the conversion of 4-hydroxybenzoate to protocatechuate, and *pcaQ* gene (BSK21_00700), a LysR transcriptional regulator, were localized on the bacterial chromosome. The presence of associated genes of the β-ketoadipate pathway in *Marivivens* sp. JLT3646 showed its potential to utilize aromatic compounds including benzoate and *p*-hydroxybenzoate.

To our knowledge, this study represents the first genome information of *Marivivens* genus, which provides genetic information for microbial aromatic compounds metabolism and hints at the potential application of this strain in bioremediation processes.

Table 2
Genome statistics of *Marivivens* sp. JTL3646.

Characteristics	Chromosome	Plasmid
Assembly size (bp)	2,978,145	169,066
G + C content (%)	56.2	52.8
Genes	2989	161
Protein-coding genes	2889	156
rRNA genes	3, 3, 3 (5S, 16S, 23S)	0
tRNA genes	50	0
ncRNA genes	3	0
Pseudo genes	38	5

3. Nucleotide sequence and strain accession numbers

The complete genome sequence of *Marivivens* sp. JLT3646 has been deposited at Genbank under the accession numbers of CP018572 and CP018573 for chromosome and plasmid, respectively. The strain is available from the Chinese General Microbiological Culture Collection Center with the preservation number CGMCC 1.15778.

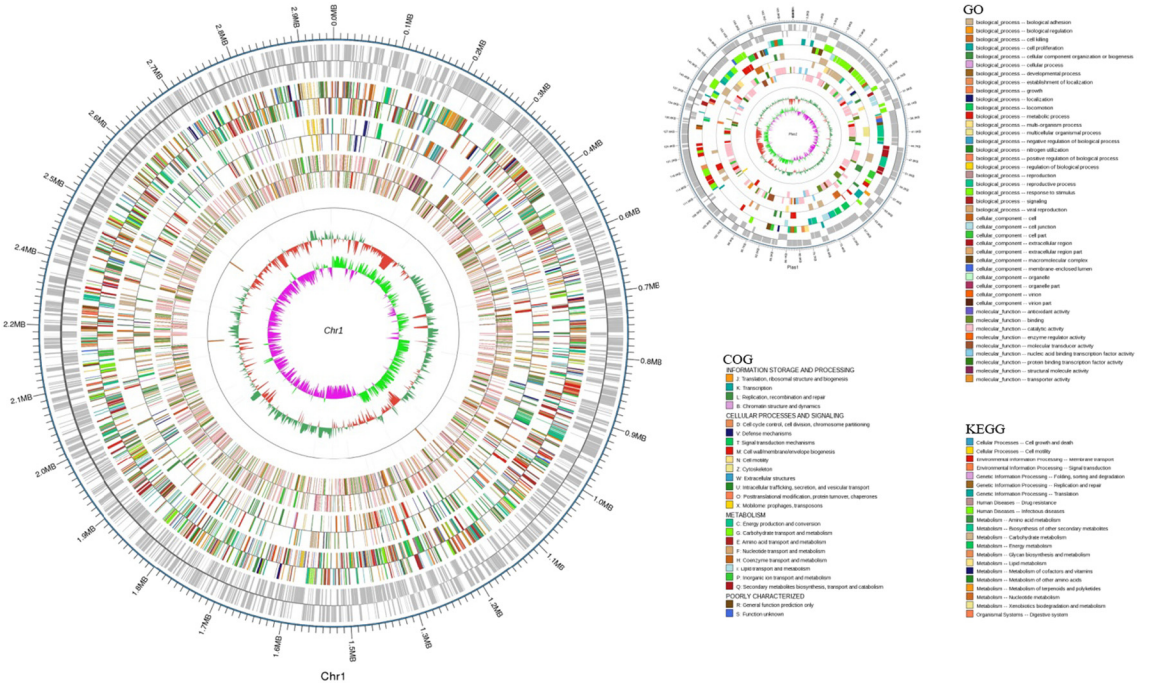

Fig. 1. Circular genome map of *Marivivens* sp. Strain JLT3646. The scales indicated the location in Mbp, starting with the initial coding region. From the innermost circles, circle (1) showed the GCskew (G-C/G + C). The value was plotted as the deviation from the average GC skew of the entire sequence. Circle (2) GC content, plotted using a sliding window. Circle (3) denoted tRNA/rRNA. Circle (4, 5, 6, 7, 8, 9) illustrated the CDSs, colored according to GO (4, 5), KEGG (6, 7), COG (8, 9) function categories, 4, 6 and 8 were backward strands, 5, 7 and 9 were forward strands. Circle (10, 11) indicated m4C and m6A sites in CDS/rRNA/tRNA, 10 was backward strand, 11 was forward strand. Circle (12) demonstrated m4C and m6A sites in the intergenomic regions.

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