



Complete genome sequence of a deeply branched marine *Bacteroidia* bacterium *Draconibacterium orientale* type strain FH5^T



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ABSTRACT

Draconibacterium orientale strain FH5^T isolated from a marine sediment sample from coast of Weihai, China, was a new species within the proposed new genus *Draconibacterium* in class *Bacteroidia*. Here, we present the genome sequence of *D. orientale* FH5^T, which contains 5,132,075 bp with a G + C content of 41.31%. The genome sequence will contribute to a better understanding of the physiology of this species.

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1. Introduction

Draconibacterium orientale FH5^T (= DSM 25947^T = CICC 10585^T) was originally isolated from a marine sediment sample from coast of Weihai, China (122°03'44.01"E, 37°32'01.93"N) and was first described by Du in 2014 (Du et al., 2014). This bacterium is a facultative anaerobe, light pink to tawny Gram-negative, non-motile bacterium. The novel isolate showed the highest 16S rRNA gene sequence similarity with the established genera *Marinifilum* (Ruvira et al., 2013) and *Prolixibacter* (Holmes et al., 2007). Based on the distinct genotype compared with members of the most closely related taxon, the novel strain FH5^T is proposed as representing a novel genus and species for which the name *D. orientale* gen. nov., sp. nov. is proposed (Du et al., 2014). The GenBank accession number for the 16S rRNA gene sequences of *D. orientale* FH5^T is JQ683778 (Du et al., 2014). Fig. 1 shows the phylogenetic relationship of *D. orientale* FH5^T with closely related species based on 16S gene rRNA. *D. orientale* strain FH5^T has been deposited in the China Center of Industrial Culture Collection (accession number: CICC 10585^T) and the

Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (accession number: DSM 25947^T). Here, we report the complete genome sequence of *D. orientale* FH5^T.

2. Data description

D. orientale FH5^T was cultured with 2216 Marine Broth (MB, Difco) and incubated at 28 °C (Du et al., 2014). DNA was extracted and purified using a bacteria genomic DNA Mini kit (TaKaRa Bio) following the manufacturer's standard protocol. The genome was sequenced with Illumina and 454 sequencing platforms. Pyrosequencing reads were assembled using the Newbler assembler (Roche). A total of 222,320 high-quality Roche 454 reads were trimmed and assembled using the Newbler assembler, and scaffolded with 11 million paired end reads of Illumina (insert size 3000 bp) using SSPACE (Boetzer et al., 2011). The gaps were closed with PCR amplification, primer walking and edited with phrap and CONSED tools (Ewing and Green, 1998; Ewing et al., 1998). The open reading frames were predicted by Glimmer version 3.02 (Delcher et al., 2007). The tRNAs and rRNAs were predicted using tRNAscan-SE (Lowe and Eddy, 1997) and RNAmmer (Lagesen et al., 2007), respectively. The functions of encoding genes were annotated by using the NCBI nr (Karsch-Mizrachi and Ouellette, 2001), COG (Tatusov et al., 2003), KEGG (Moriya et al., 2007) and InterProScan (Quevillon et al., 2005).

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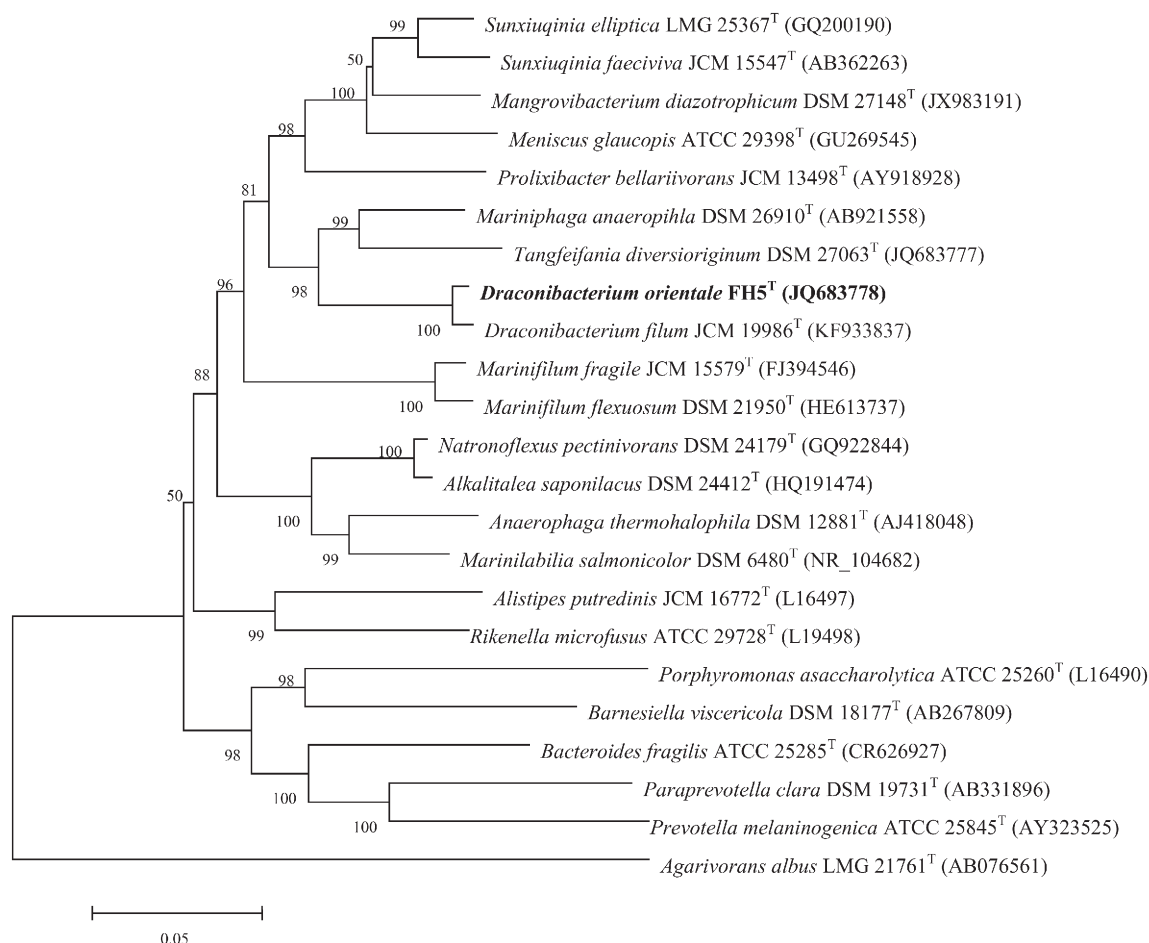


Fig. 1. Neighbor-joining phylogenetic tree reconstructed with 16S rRNA gene sequences, showing the phylogenetic position of strain FH5^T within the class *Bacteroidia*.

The complete genome of *D. orientale* FH5^T is made up of a circular chromosome of 5,132,075 bp with 41.31% GC content and no plasmid (Table 1). The graphical map of the chromosome of *D. orientale* FH5^T was illustrated in Fig. 2. The genome of *D. orientale* FH5^T encodes 4518 proteins, and the total length of genes was 5,074,790 bp, which makes up 98.88% of genome (Table 1). The genome also encodes 45 tRNAs and 6 rRNAs, which make up 1.12% of the genome (Table 1). Physiological and biochemical key features of *D. orientale* FH5^T was illustrated in Table 2 following the MlxS mandatory information of the MlxS checklist and environmental packages.

3. Nucleotide sequence accession number

The complete genome sequence of *D. orientale* FH5^T is available in GenBank under the accession number CP007451.

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Table 1
General features of *D. orientale* FH5^T complete genome.

Attribute	Value
Genome size (bp)	5,132,075
Contig	1
DNA coding region (bp)	4,485,657
GC content %	41.31%
Total genes	4569
RNA	51
rRNA	6
tRNA	45
Protein coding genes	4518
Genes with prediction function	2214

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