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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Pelagibacterium halotolerans* B2^T

Ying-Yi Huo,[a] Hong Cheng,[a] Xi-Fang Han,[b] Xia-Wei Jiang,[a] Cong Sun,[a] Xin-Qi Zhang,[a] Xu-Fen Zhu,[a] Yong-Feng Liu,[b] Peng-Fei Li,[b] Pei-Xiang Ni,[b] and Min Wu[a]

College of Life Sciences, Zhejiang University, Hangzhou, People's Republic of China,[a] and Beijing Genomics Institute (BGI)-Shenzhen, Shenzhen, People's Republic of China[b]

***Pelagibacterium halotolerans* B2^T is a marine halotolerant bacterium that was isolated from a seawater sample collected from the East China Sea. Here, we present the complete genome sequence of the type strain *P. halotolerans* B2^T, which consists of one chromosome (3,944,837 bp; 61.4% G+C content) and one plasmid (4,050 bp; 56.1% G+C content). This is the first complete genome of a member of the *Pelagibacterium* genus.**

Strains of the family *Hyphomicrobiaceae* are ubiquitous (found in freshwater, lake sediment, soil, plant root, sewage, swamps, activated sludge, etc.), but only a few have been isolated from marine environments. *Cucumibacter marinus* (6), *Filomicrobium fusiforme* (11), *Hyphomicrobium aestuarii* (4), *Pelagibacterium halotolerans* (14), and *Zhangella mobilis* (13) have been isolated from marine environments. Strain B2^T, isolated from a seawater sample from a depth of 70 m in the East China Sea, is the type strain of *Pelagibacterium halotolerans*, which in turn is the type species of the genus *Pelagibacterium* in the family *Hyphomicrobiaceae* (14). Strain B2^T showed tolerance to NaCl up to 13% (wt/vol). Here, we present the complete genome sequence of *P. halotolerans* B2^T, which is the first complete genome of the genus *Pelagibacterium* and only the second complete genome for a member of the family *Hyphomicrobiaceae*.

Whole-genome shotgun (WGS) DNA sequencing of *Pelagibacterium halotolerans* B2^T was performed using Solexa paired-end sequencing technology (1). Two libraries with insert sizes of 500 bp and 6,000 bp were constructed, and sequences a total of ~600 Mbp long were produced. The sequences were assembled into 322 contigs and 22 scaffolds using the SOAPdenovo v.1.04 (9). Gaps were closed by PCR, and the amplicons were sequenced by primer walking. Coding sequences (CDSs) were predicted using Glimmer v.3.0 (2) and analyzed using the KEGG (7), Pfam (3), COGs (12), Swiss-Prot and NCBI NR protein databases for genome annotation. tRNAs and rRNAs were identified using tRNAscan-SE (10), RNAmmer (8), and Rfam database (5).

The genome of *P. halotolerans* B2^T consists of a single circular chromosome (3,944,837 bp; 61.4% G+C content) and a plasmid (4,050 bp; 56.1% G+C content). The entire genome contains 3,881 CDSs, 3,878 genes on the chromosome, and 3 genes on the plasmid. The genome includes 47 tRNA genes and two copies of 16S-23S-5S rRNA gene operons located next to each other. The genome sequence confirms that strain B2^T is an obligate chemoheterotroph. The genome contains many genes coding for proteins involved in major metabolic pathways, such as glycolysis, the tricarboxylic acid (TCA) cycle, the pentose phosphate pathway, amino acid metabolism, amino acid biosynthesis, the urea cycle, porphyrin metabolism, etc. The genome of strain B2^T contains several ectoine biosynthesis, choline and betaine uptake, and betaine biosynthesis genes, which may play an important role in the accumulation of compatible solutes in osmotic stress adaptation. Additionally, the genome sequence reveals that strain B2^T has a remarkable capacity for resistance to heavy metals, including arsenic, cadmium, cobalt, copper, nickel, and mercury.

This is the first complete genome sequence of a member of the genus *Pelagibacterium*, and further analysis of this genome and comparative analysis with other genomes will provide further insights into the adaptive evolution of genomes and the mechanism of adaptation to the sea environment.

Nucleotide sequence accession numbers. The complete genome sequence of *Pelagibacterium halotolerans* B2^T is available in NCBI GenBank under accession numbers CP003075 (chromosome) and CP003076 (plasmid).

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Address correspondence to Min Wu, wumin@zju.edu.cn.

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