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Genome Sequence of the Halotolerant Bacterium *Imtechella halotolerans* K1^T

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We report the 3.087-Mb genome sequence of *Imtechella halotolerans* K1^T, isolated from an estuarine water sample collected from Kochi, Kerala, India. Strain K1 was recently reported as a novel genus of the family *Flavobacteriaceae*.

The genus *Imtechella* contains strictly aerobic, Gram-negative, rod-shaped nonmotile bacteria and is commonly present in estuarine habitats (5). The type species of the genus *Imtechella*, *Imtechella halotolerans* K1, was isolated from an estuarine water body of Kochi, Kerala, India. Strain K1^T is known to possess various enzymatic activities, such as lipase, γ -glutamyl transferase, glycine arylamidase, and Glu-Gly-Arg-arylamidase (5). Since strain K1^T is halotolerant, the enzymes produced by this strain are likely to be halotolerant and therefore of industrial interest.

The genome of *Imtechella halotolerans* K1^T was sequenced using the Illumina-HiSeq 1000 paired-end technology, which produced a total of 35,288,314 paired-end reads (insert size of 350 bp) of 101 bp. We have used NGS QC Toolkit v2.2.1 (4) to filter the data for high-quality (HQ) (cutoff read length for HQ, 70%; cutoff quality score, 20), vector/adaptor free reads for genome assembly. A total of 33,202,176 high-quality, vector-filtered reads (~800 times coverage) were used for assembly with Velvet 1.2.03 (at a hash length of 61) (6). The final assembly contains 44 contigs with total size of 3,086,951 bp, with an N_{50} contig length of 337,071 nucleotides (nt). All assembly data were submitted to GenBank.

The draft genome (44 contigs) comprising 3,086,951 nt was annotated with the help of the RAST (Rapid Annotation using Subsystem Technology) system (1), RNAmmer 1.2 (2) servers, and tRNAscan-SE-1.23 (3) software. A total of 2,738 predicted coding sequences (CDSs), 3 rRNAs, and 38 tRNAs were predicted.

Comparison of the genome sequences available on the RAST server shows that “*Flavobacteriales bacterium*” HTCC2170 (score, 517), *Capnocytophaga ochracea* DSM 7271 (score, 488), and *Capnocytophaga sputigena* ATCC 33612 (score, 485) were the closest neighbors of strain K1^T. Strain K1^T contains genes of deoxyhypusine synthase, methylglutaconyl-coenzyme A (CoA) hydratase (EC 4.2.1.18), leucine dehydrogenase (EC 1.4.1.9), agmatinase (EC 3.5.3.11), saccharopine dehydrogenase (EC 1.5.1.9), α -amylase (neopullulanase) SusA (EC 3.2.1.135), α -glucosidase SusB (EC 3.2.1.20), 8-amino-7-oxononanoate synthase (EC 2.3.1.47), adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.62), deoxyhypusine synthase, 2-dehydropantoate 2-reductase (EC 1.1.1.169), formate-tetrahydrofolate ligase (EC 6.3.4.3), NAD(P)H oxidoreductase YRKL (EC 1.6.99.-), and isospartyl aminopeptidase (EC 3.4.19.5), which were absent in the RAST annotation of “*Flavobacteriales bacterium*”

HTCC2170. However, strain K1^T does not have genes coding for formyltetrahydrofolate deformylase (EC 3.5.1.10), the pyruvate dehydrogenase E1 component (EC 1.2.4.1), pterin-4- α -carbinolamine dehydratase (EC 4.2.1.96), 2-heptaprenyl-1,4-naphthoquinone methyltransferase (EC 2.1.1.163), and 6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.78) present in the “*Flavobacteriales bacterium*” HTCC2170 strain.

Nucleotide sequence accession numbers. The sequence from this Whole Genome Shotgun project has been deposited in DDBJ/EMBL/GenBank under accession no. [AJJU00000000](https://doi.org/10.1093/bioinformatics/btt000). The version described in this paper is the first version, AJJU01000000.

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