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Genome Announcement

Draft genome sequence of *Vitellibacter aquimaris* D-24^T isolated from seawater

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ABSTRACT

Vitellibacter aquimaris D-24^T (=KCTC 42708^T = DSM 101732^T), a halophilic marine bacterium, was isolated from seawater collected from Desaru beach, Malaysia. Here, we present the draft genome sequence of D-24^T with a genome size of approximately 3.1 Mbp and G + C content of 39.93%. The genome of D-24^T contains genes involved in reducing a potent greenhouse gas (N_2O) in the environment and the degradation of proteinaceous compounds. Genome availability will provide insights into potential biotechnological and environmental applications of this bacterium.

Over the last few decades, marine microorganisms have received considerable attention for their applications in biotechnology. Prime focus has been given on identification of halophilic enzymes with potential applications.[1,2] Halophilic enzymes boast unique properties such as the sustainability at extreme ranges of salt concentration, temperature, pH, and organic solvents.[3,4] Characterization of marine bacteria through their genome sequence has provided great opportunities for mining and identifying of enzymes with biotechnological importance.

Vitellibacter aquimaris D-24^T, previously isolated from seawater, was confirmed as a new species in genus *Vitellibacter*.[5] This bacterium is a Gram negative, rod-shape and yellow-orange pigmented bacterium. In this study, we report the draft genome of *V. aquimaris* D-24^T.

V. aquimaris D-24^T was grown in Marine Broth 2216 (BD Difco) and the genomic DNA was extracted using the DNeasy Blood and Tissue kit (Qiagen, Hilden, Germany) per manufacturer instructions. The genome of the *V. aquimaris* D-24^T sequence was generated using pair-end sequencing in an

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Table 1 – Genome features of *Vitellibacter aquimaris* D-24^T.

Attributes	Values
Genome size	3,147,268 bp
G + C content	39.93%
Number of contigs	66
Protein coding genes	2790
rRNA genes	7
tRNA genes	35
Pseudo genes	134
Frame shifted genes	8
Genes with signal peptides	376
Genes with transmembrane helices	727

Illumina MiSeq sequencing platform (Illumina, California, USA). *De novo* assembly was performed using IDBA-UD version 1.0.9,[6] obtaining 66 contigs with a N_{50} contig length of 439,587. Genome annotations were carried out using NCBI Prokaryotic Genome Annotation Pipeline 2.8[7] and Integrated Microbial Genomes Expert Review (IMG-ER).[8] Protein coding sequences were predicted by using GeneMarkS+ version 2.8 with the best-placed reference protein method[9] and Prodigal,[10] respectively.

The draft genome of *V. aquimaris* D-24^T is comprised of 3,147,268 nucleotides with a mean G + C content of 39.93%. A total of 2967 genes were predicted, of which 2790 (94.03%) protein-coding genes were assigned with putative function or hypothetical proteins. The genome consists of three 5S rRNA, one 16S rRNA, one 23 rRNA, and 35 tRNA genes (Table 1). The genome *V. aquimaris* D-24^T contains genes encoded for nitrite reductase (*nirK*) (WP_045079976.1), nitric oxide reductase subunit B (*norB*) (WP_062619270.1), nitric oxide reductase subunit C (*norC*) (WP_062619272.1), and nitrous oxide reductase (*nosZ*) (WP_062619280.1), all of which are involved in the denitrification pathway (NO_2^- to N_2). Nitrous oxide (N_2O) is a potent greenhouse gas which also damages the Earth's ozone layer. Due to intensive agricultural and industrial practices, the release of this gas into the atmosphere has greatly increased.[11,12] Nitrous-oxide reductase plays an important role in catalyzing the reduction of nitrous oxide to nitrogen (N_2).[13] The nitrous oxide reductase (*nosZ*) from *V. aquimaris* D-24^T is a promising candidate for removing nitrous oxide, a potent greenhouse gas, from the environment.

Genome analysis also revealed a total of twelve genes encoded for proteases, including two metalloproteases (KXO00999.1; KXN98592.1); two serine proteases (KXO01375.1; KXN97930.1); five proteases (KXO00989.1; KXO00819.1; KXN99950.1; KXN99951.1; KXO00100.1); two zinc metalloproteases (KXO00568.1; KXN98177.1); and an acid protease (KXO00796.1). Genes encoding proteases were also present in the genome of another species of *Vitellibacter*.[14] The draft genome sequence of *V. aquimaris* D-24^T will facilitate understanding and development of potential applications of *Vitellibacter* species.

The Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number JRWG00000000. The first version (accession number JRWG01000000) is described in this paper.

Conflicts of interest

The authors declare no conflicts of interest.

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