Genome Announcement

Draft genome sequence of Vitellibacter aquimarís D-24\(^T\) isolated from seawater

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ABSTRACT

Vitellibacter aquimarís 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 (\(\text{N}_2\text{O}\)) in the environment and the degradation of proteinaceous compounds. Genome availability will provide insights into potential biotechnological and environmental applications of this bacterium.

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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 aquimarís 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 \(V.\) aquimarís D-24\(^T\).

\(V.\) aquimarís 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 \(V.\) aquimarís D-24\(^T\) sequence was generated using pair-end sequencing in an...
Table 1 – Genome features of Vitellibacter aquimaris D-24T.

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

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.

**Acknowledgments**

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**References**

