Draft Genome Sequences of Gammaproteobacterial Methanotrophs Isolated from Marine Ecosystems


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This is contribution 12 from OMeGA.

The genome sequences of *Methylobacter marinus* A45, *Methylobacter* sp. strain BBA5.1, and *Methylomarinum vadi* IT-4 were obtained. These aerobic methanotrophs are typical members of coastal and hydrothermal vent marine ecosystems.

**TABLE 1** General genome statistics and accession numbers

<table>
<thead>
<tr>
<th>Species</th>
<th>Sequencing platform(s)</th>
<th>Genome assembly and annotation</th>
<th>Genome coverage (×)</th>
<th>Genome size (Mb)</th>
<th>No. of scaffolds (no. of contigs)</th>
<th>Core (accessory) metabolic pathways*</th>
<th>NCBI accession no.</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>M. marinus</em> A45</td>
<td>Illumina</td>
<td>Velvet 1.1.05, AllPaths, Phrap 4.24, Prodigal 2.5</td>
<td>1,237</td>
<td>4.99</td>
<td>9 (49)</td>
<td>pMMO, pXmo, Mxa, XoxF1, XoxF2, H,F, H,MPT, FDH, RuMP, EMP, EDD, dPPP, PPP, pSC, TCA</td>
<td>ARVS000000000</td>
</tr>
<tr>
<td><em>Methylomarina</em> sp. BBA5.1</td>
<td>Illumina, PacBio RS</td>
<td>AllPaths, Prodigal 2.5</td>
<td>290</td>
<td>5.07</td>
<td>87 (91)</td>
<td>pMMO, pXmo, Mxa, XoxF1, XoxF2, H,F, H,MPT, FDH, RuMP, EMP, EDD, dPPP, PPP, pSC, TCA</td>
<td>JQKS000000000</td>
</tr>
<tr>
<td><em>M. vadi</em> IT-4</td>
<td>Illumina, PacBio RS</td>
<td>Prodigal 2.5</td>
<td>272</td>
<td>4.33</td>
<td>1 (1)</td>
<td>pMMO, Mxa, XoxF, H,F, H,MPT, FDH, RuMP, EMP, EDD, dPPP, PPP, pSC, TCA</td>
<td>JPON000000000</td>
</tr>
</tbody>
</table>

* dPPP, dissipatory pentose-phosphate pathway; EDD, Entner-Doudoroff pathway; EMP, Embden-Meyerhof-Parnas pathway; FDH, formate dehydrogenases; H,F, folate-linked C4 transfer; H,MPT, methanopterin-linked C4 transfer; Mxa, PQQ-linked methanol dehydrogenases; pMMO, membrane-bound methane monooxygenase; pSC, partial serine cycle; pXmo, methane/ammonia monooxygenase-related proteins of unknown function; PPP, pentose-phosphate pathway; RuMP, assimilatory ribulose monophosphate pathway; Xox, PQQ-linked methanol and formaldehyde dehydrogenases (i.e., no evidence for the glyoxylate regeneration pathway was found); TCA, tricarboxylic acid cycle.

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Methylomarinum vadi IT-4 (= JCM 13665T = DSM 18976T) was isolated from a
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REFERENCES