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.

Microbial methane oxidation is one of the key drivers of oxygen consumption in marine sediments and the overlying water column (1). Methanotrophic bacteria are the primary producers of many cold and hot seep ecosystems (2, 3). Here, we report three genome sequences of gammaproteobacterial methanotrophs isolated from three marine ecosystems. *Methylobacter marinus* A45 (a methanol-adapted strain, formerly *Methylomonas methanica* A4, ACM 4717) was isolated from sewage outfall sediment near Los Angeles, CA (4). *Methylobacter* sp. strain BBA5.1 was isolated from the surface layer of estuary sediment collected at low tide near Newport, Bay Estuary (CA) (5). *Methylomarinum vadi* IT-4 (= JCM 13665T = DSM 18976T) was isolated from a

### 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 pathwaysa</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, H2F, H2MPT, FDH, RuMP, EMP, EDD, dPPP, PPP, pSC, TCA</td>
<td>ARVS00000000</td>
</tr>
<tr>
<td><em>Methylomarinum</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, H2F, H2MPT, FDH, RuMP, EMP, EDD, dPPP, PPP, pSC, TCA</td>
<td>JQKS00000000</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, H2F, H2MPT, FDH, RuMP, EMP, EDD, dPPP, PPP, pSC, TCA</td>
<td>JPON00000000</td>
</tr>
</tbody>
</table>

a dPPP, dissipatory pentose-phosphate pathway; EDD, Entner-Doudoroff pathway; EMP, Embden-Meyerhof-Parnas pathway; FDH, formate dehydrogenases; H2F, folate-linked C1 transfer; H2MPT, methanopterin-linked C1 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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REFERENCES


