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Draft Genomes of Gammaproteobacterial Methanotrophs Isolated from Terrestrial Ecosystems

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Genome sequences of Methylobacter luteus, Methylobacter whittenburyi, Methylosarcina fibrata, Methylomicrobium agile, and Methylolovulum miyakonense were generated. The strains represent aerobic methanotrophs typically isolated from various terrestrial ecosystems.

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Methane is a potent greenhouse gas (1–3). Methanotrophic bacteria of terrestrial ecosystems contribute to methane sinks not only by mitigating methane emissions but also by consuming atmospheric methane (1–6). Here we report five genomes of gammaproteobacterial methanotrophs isolated from various terrestrial ecosystems. Methylobacter whittenburyi (formerly "Methylobacter capsulatus" = UCM-B-3033), and Methylomicrobium agile (ATCC 35068) are methanotrophic bacteria commonly found in sediment samples from wetlands (7, 8). Methylobacter luteus strains (formerly Methylobacter bovis, represented here by the strain 98 [IMV-B-3098]) have typically been obtained from meadows, dry hay, and cow mouth samples (7–9). Methylolovulum miyakonense HT12T (= ATCC BAA-2070) was isolated from a forest soil (10).

TABLE 1 General genome statistics and accession numbers

<table>
<thead>
<tr>
<th>Species and strain</th>
<th>Sequencing platform</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 metabolic pathways</th>
<th>NCBI accession number</th>
</tr>
</thead>
<tbody>
<tr>
<td>M. luteus 98</td>
<td>Illumina, PacBio</td>
<td>Allpaths, Velvet 1/1/05, Phrap 4.24</td>
<td>1.288</td>
<td>5.1</td>
<td>4 (17)</td>
<td>pMMO, Mxa, Xox, FDH, H₂MTP, H₄F₄, pSC, dPPP, RuMP, EDD, EMP, TCA</td>
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<td>M. fibrata AML-C10T</td>
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<td>8 (34)</td>
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<td>M. miyakonense HT12T</td>
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<td>Allpaths, Velvet 1/1/05, Phrap 4.24</td>
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<td>M. agile ATCC 35068</td>
<td>PacBio</td>
<td>Prodigal, GenePRIMP</td>
<td>210.3</td>
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<td>4 (4)</td>
<td>pMMO, Mxa, Xox, FDH, H₂MTP, H₄F₄, pSC, dPPP, RuMP, EDD, EMP, TCA</td>
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<td>M. whittenburyi</td>
<td>PacBio</td>
<td>Prodigal, GenePRIMP</td>
<td>209.5</td>
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<td>7 (7)</td>
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<td>JQNS00000000</td>
</tr>
</tbody>
</table>

pMMO, membrane-bound methane monoxygenase; Mxa, PQQ-linked methanol dehydrogenases; Xox, PQQ-linked methanol and formaldehyde dehydrogenases; FDHI, formate dehydrogenases; H₂MTP, methanoterin-linked C1 transfer; H₄F₄, folate-linked C1 transfer; pSC, partial serine cycle (i.e., no evidence for glyoxylate regeneration pathway is found); dPPP, dissipatory pentose phosphate cycle; RuMP, assimilatory ribulose monophosphate pathway; EDD, Entner-Doudoroff pathway, EMP, Embden-Meyerhof-Parnas pathway, TCA, tricarboxylic acid cycle; sMMO, soluble methane monoxygenase.
Table 1

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REFERENCES


