Draft Genomes of Gammaproteobacterial Methanotrophs Isolated from Terrestrial Ecosystems

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

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 Methylmicobium 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). Methylovulum 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 (= IMV-B-3098)</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, H₄FP, pSC, dPPP, RuMP, EDD, EMP, TCA</td>
<td>ATYJ00000000</td>
</tr>
<tr>
<td>M. fibrata AML-C10T (= ATCC 700909)</td>
<td>Illumina</td>
<td>Allpaths, Velvet 1/1/05, Phrap 4.24</td>
<td>1,112</td>
<td>5</td>
<td>8 (34)</td>
<td>pMMO, Mxa, Xox, FDH, H₂MTP, H₄FP, pSC, dPPP, RuMP, EDD, EMP, TCA</td>
<td>ARCU00000000</td>
</tr>
<tr>
<td>M. miyakonense HT12T (= ATCC BAA-2070)</td>
<td>Illumina</td>
<td>Allpaths, Velvet 1/1/05, Phrap 4.24</td>
<td>1,199</td>
<td>4.7</td>
<td>9 (32)</td>
<td>pMMO, Mxa, Xox, FDH, H₂MTP, H₄FP, pSC, dPPP, RuMP, EDD, EMP, TCA</td>
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</tr>
<tr>
<td>M. agile ATCC 35068</td>
<td>PacBio</td>
<td>Prodigal, GenePRIMP</td>
<td>210.3</td>
<td>4.5</td>
<td>4 (4)</td>
<td>pMMO, Mxa, Xox, FDH, H₂MTP, H₄FP, pSC, dPPP, RuMP, EDD, EMP, TCA</td>
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</tr>
<tr>
<td>M. whittenburyi UCM-B-3033</td>
<td>PacBio</td>
<td>Prodigal, GenePRIMP</td>
<td>209.5</td>
<td>5.4</td>
<td>7 (7)</td>
<td>pMMO, Mxa, Xox, FDH, H₂MTP, H₄FP, pSC, dPPP, RuMP, EDD, EMP, TCA</td>
<td>JQNS00000000</td>
</tr>
</tbody>
</table>

pMMO, membrane-bound methane monoxygenase; Mxa, PQQ-linked methanol dehydrogenases; Xox, PQQ-linked methanol and formaldehyde dehydrogenases; FDH, formate dehydrogenases; H₂MTP, methanotperin-linked C1 transfer; H₄FP, folate-linked C1 transfer; pSC, partial serine cycle (i.e., no evidence for glyoxylate regeneration pathway is found); dPPP, dissimilatory 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.
losarcina fribra AML-C10	extsuperscript{7} (= ATCC 700909) was isolated from a landfill site (11).

The draft genome sequences were generated at the DOE Joint Genome Institute (JGI), using the Illumina (12) and/or PacBio technology (13) (Table 1). Raw reads were assembled using Allpaths, version 39750 (14), Velvet, version 1.1.05 (15) HGAP, version 2.1.1 (16), and/or Phrap, version 4.24 (High Performance Software, LLC). Possible misassemblies were corrected by manual editing in Consed (17–19). All general aspects of library construction and sequencing performed at the JGI can be found at http://www.jgi.doe.gov. Genome annotation was performed using Prodigal (20) and GenePRIMP (21). Additional gene prediction analyses were performed within the IMG (22) and MaGe (23) platforms.

Genome statistics and predicted core metabolic pathways are shown in Table 1. Genes encoding a soluble methane monoxygenase were detected only in the M. miyakonense HT112	extsuperscript{7} genome (24). A functional operon encoding methane monoxygenase was present in all genomes, and a homologous operon encoding related proteins (pxmAABC) (25) was found in all except M. miyakonense HT112	extsuperscript{7}. Each genome contains at least one homologue of the large subunit of methanol dehydrogenase (26). Two types of the structural organization of the gene cluster encoding 3-hexulose-6-phosphatesynthase (HPS) and 6-phospho-3-hexulosiomerase (PHI) were found. The genomes of M. miyakonense HT112	extsuperscript{7} and M. fribra AML-C10	extsuperscript{7} contain the hps-phi operon and another hpsi gene encoding an HPS PHI fused protein (27). M. lutes 98 and M. whittenburyi UCM-B-3033 possess only the hpsi operon. The genome of M. agile ATCC 35068 has only the hpsip gene. Genes encoding respiratory nitrate reductase (28) were identified only in the genome of M. fribra AML-C10	extsuperscript{7}. The genome sequences indicated that all strains can import and assimilate ammonium (amitB/ghnA/gdhB/ald) or urea (urtaBCDE/uratEBCDEFG) as the sole source of nitrogen. M. miyakonense HT112	extsuperscript{7}, M. lutes 98, and M. whittenburyi UCM-B-3033 possess the key genetic elements for nitrogen fixation (nifKDHWENX).

Many methanotrophic species (including Methylobacter spp.) produce cysts (7). We were not able to identify homologues of known cyst formation genes in any of the sequenced genomes, suggesting that this stage in the life cycle of some methanotrophs might be unique. Production of bacteriocins has been reported for many methanotrophic species (including M. luteus) as the sole source of nitrogen. Genes encoding respiratory nitrate reductase (29) were identified only in the genome of M. fribra AML-C10	extsuperscript{7}. Two gene clusters encoding a bacteriocin-producing peptide C39 and a putative precursor (31) were identified in this strain. The contribution of these genes to the production of the biologically active bacteriocin will require experimental validation by mutagenesis studies.

**Nucleotide sequence accession numbers.** The genome sequences have been deposited in GenBank under the accession numbers listed in Table 1.

**ACKNOWLEDGMENTS**

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**REFERENCES**


