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.

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

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<th>TABLE 1 General genome statistics and accession numbers</th>
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<tr>
<td>M. marinus A45</td>
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<td>Methylobacter sp. BBA5.1</td>
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<td>M. vadi IT-4</td>
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- dPPP, dissimilatory pentose-phosphate pathway; EDD, Entner-Doudoroff pathway; EMP, Embden-Meyerhof-Parnas pathway; FDH, formate dehydrogenases; H4F, folate-linked C4 transfer; H4MPT, 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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microbial mat of a shallow submarine hydrothermal system near Taketomi Island, Okinawa, Japan (6).

DNA samples from the three strains were prepared using the standard phenol-chloroform method (7). DNA sequence data were obtained at the Joint Genome Institute using a combination of PacBio (8) and Illumina (9) technologies, and draft genome sequences were assembled. The computational tools used for genome sequencing and assembly are listed in Table 1.

All three sequenced marine methanotrophs are obligate methane and methanol utilizers. All three genomes harbor genes typical for type I methanotrophs, including genes encoding particulate methane monoxygenase (pmoCAT), the PQQ-dependent methanol dehydrogenases (mxaFI and multiple copies of xoxF), genes for tetrahydrodronopterin (H4MPT) and tetrahydrofolic acid (H4F)-dependent C1-transfer pathways, genes of the ribulose monophosphate pathway, including its phosphoketolase variant (10), and genes encoding a complete tricarboxylic acid (CIA) cycle and a partial serine cycle (10) (Table 1). The gdna ABC gene clusters (11) linked to a distant homologue of the nitrate-nitrite transporter (nark) were found in the Methylobacter sp. strain BBS.5 and M. marinus A45 genomes. A phosphoenolpyruvate carboxylase gene (ppc) was found in M. vadi IT-4 only. Genes encoding soluble methane monoxygenase, known glyoxylate regeneration pathways, and Rubisco (cbbL and cbbS) were not detected. Genes involved in ammonium and nitrate assimilation are present in all three genomes. The genomes of strains A45 and BBA5.1 contain all genes necessary to provide for urea hydrolysis and nitrogen fixation. M. vadi IT-4 has the potential for dissimilatory nitrite reduction to nitric oxide, as suggested by the presence of nir genes. The NADH:ubiquinone reductase (H+-)-translocating genes (nuoABCDEFGHJKLMN) were identified in M. marinus A45 only. All strains possess genes encoding Na+ transporting NADH:ubiquinone oxidoreductase (napA/B/C/DEF), ubiquinol-cytochrome bc1 complex, cytochrome b, cytochrome c oxidase, cytochrome P450 and P460, and cytochrome d ubiquinol oxidase. Cytochrome bo, quinol oxidase was found in M. vadi IT-4 only. Both Methylobacter species possess genes encoding the Na+-translocating ferredoxin:NAD+ oxidoreductase complex (mrfABCDGE). All genomes contain genes encoding pyruvate-ferredoxin/flavodoxin oxidoreductases, and all three strains possess ectoine biosynthesis genes.

The genome of M. marinus A45 includes a chromosomally integrated complete copy of a bacteriophage genome (predicted size, 65 kb) integrated in the chromosome, indicating the possibility of lysogenic infection in methanotrophic bacteria. These genomes provide a valuable resource to obtain new insights into environmental controls of fitness and diversity in methanotrophs, mechanisms of genetic exchange within methanotrophic communities, and the potential for the development of new genetic tools for methanotrophs.

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

**ACKNOWLEDGMENTS**

We thank all members of the Organization for Methanotroph Genome Analysis for collaboration (OMeGA) and Genoscope (France) for access to its MicroScope platform for comparative genome analysis (http://www.genoscope.cns.fr/agc/microscope/home/).

This report is based upon work supported by the National Science Foundation under award MCB-0842686 and by faculty start-up funds from San Diego State University to M. G. Kalyuzhnaya. Work conducted by the U.S. Department of Energy Joint Genome Institute was supported by the Office of Science of the U.S. Department of Energy under contract no. DE-AC02-05CH11231.

**FUNDING INFORMATION**

The National Science Foundation (NSF) provided funding to Marina G. Kalyuzhnaya under grant number MCB-0842686. The U.S. Department of Energy (DOE) provided funding to Tanya Woyke under grant number DE-AC02-05CH11231. San Diego State University (SDSU) provided funding to Marina G. Kalyuzhnaya.

**REFERENCES**