Draft Genome Sequences of Gammaproteobacterial Methanotrophs Isolated from Marine Ecosystems

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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

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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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a dPPP, dissimilatory pentose-phosphate pathway; EDD, Entner-Doudoroff pathway; EMP, Embden-Meyerhof-Parnas pathway; FDH, formate dehydrogenase; H,F, folate-linked C4 transfer; H,MPT, methanopterin-linked C4 transfer; Mxa, PQQ-linked methanol dehydrogenases; pMMO, membrane-bound methane monoxygenase; 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 (pmoCAB), the PQQ-dependent methanol dehydrogenases (mxaF1 and multiple copies of xoxF), genes for tetrahydrodiaminoethane (H4MPT)- and tetrahydrofolate (H4F)-dependent C4-transfer pathways, genes of the ribulose monophosphate pathway, including its phosphoketolase variant (10), and genes encoding a complete tricarboxylic acid (TCA) cycle and a partial serine cycle (10) (Table 1). The genes encoding ammonia and nitrogen fixation.

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/age/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