Draft Genome Sequence of \textit{Methylomicrobium buryatense} Strain 5G, a Haloalkaline-Tolerant Methanotrophic Bacterium

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Robust growth of the gammaproteobacterium \textit{Methylomicrobium buryatense} strain 5G on methane makes it an attractive system for CH\textsubscript{4}-based biocatalysis. Here we present a draft genome sequence of the strain that will provide a valuable framework for metabolic engineering of the core pathways for the production of valuable chemicals from methane.

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\begin{itemize}
\item Methylomicrobium strain 5G was most similar to \textit{Methylomicrobium alcaliphilum} strain 20Z, revealing that 5G was most similar to \textit{M. alcaliphilum}, sharing approximately 70% of its proteome at 90% protein sequence identity.
\item We identified genes encoding membrane-associated methane monooxygenase, soluble methane monooxygenase and an associated chaperon and a transcriptional activator, pyrroloquinoline quinone (PQQ)-dependent methanol dehydrogenase, an associated \textit{c}-cytochrome, genes for enzyme assembly and PQQ biosynthesis, tetrahydromethanopterin- and tetrahydrofolate-linked \textit{C}\textsubscript{1}-transfer pathways, two formate dehydrogenases, and the ribulose monophosphate pathway. The Embden-Meyerhof-Parnas pathway, the Entner–Doudoroff pathway, and the pentose phosphate pathway (transaldolase variant) are predicted. As with the genomes of other gammaproteobacterial methanotrophs, the genome of \textit{M. buryatense} 5G encodes all genes essential for operation of the citric acid cycle and the serine cycle, except for phosphoenolpyruvate carboxylase, isocitrate lyase, and the ethylmalonyl pathway.
\item Genes for urea uptake and hydrolysis, assimilatory nitrate/nitrite reduction, dissimilatory nitric oxide reduction, and ammonium uptake were identified. A gene homologous to hy-
d Roxylamine oxidoreductase is present (17, 18). The ammonium assimilation inventory includes genes for glutamate and alanine dehydrogenases, glutamate synthase/glutamine synthetase, serine-pyruvate/serine-glyoxylate, and aspartate aminotransferases (19). Genes essential for ectoine biosynthesis were identified.

**Nucleotide sequence accession numbers.** The *Methylomicrobium buryatense* 5G genome sequence was deposited in GenBank/EMBL under the accession numbers AOTL01000000 and KB455575 and KB455576.

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**REFERENCES**