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Draft Genome Sequence of the Volcano-Inhabiting Thermoacidophilic Methanotroph *Methylacidiphilum fumariolicum* Strain SolV

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The draft genome of *Methylacidiphilum fumariolicum* SolV, a thermoacidophilic methanotroph of the phylum *Verrucomicrobia*, is presented. Annotation revealed pathways for one-carbon, nitrogen, and hydrogen catabolism and respiration together with central metabolic pathways. The genome encodes three orthologues of particulate methane monooxygenases. Sequencing of this genome will help in the understanding of methane cycling in volcanic environments.

Isolation (14) and genome sequencing of strain SolV led to the proposal that *Methylacidiphilum fumariolicum* be one of three proposed species within the genus *Methylacidiphilum* (13), together with *M. infernorum* (strain V4) (4) and *M. kamchatkensis* (strain Kam1) (7). All three strains were isolated from acidic volcanic areas and are well adapted to the harsh volcanic environment (13, 14), being able to thrive at very low methane and oxygen concentrations and pH values as low as 1.

The high-quality draft genome of *M. fumariolicum* SolV (109 contigs) was assembled from Illumina and Roche 454 reads using CLCbio (CLCbio, Aarhus, Denmark) and manual adjustments. The draft genome is 2.36 Mbp in size, with a GC content of 40.9%. Auto-annotation was performed based on comparison to public databases using the MicroScope platform (Genoscope, France) (17), which identified 2,283 protein-encoding gene models. For 623 of these, full-length homologs (>80% identity at the protein level) were present in the complete genome of *M. infernorum* V4 (6), with 619 of them organized in synteny in the two strains. Biosynthetic pathways and tRNAs of all 20 amino acids were present together with a single rRNA operon.

Key genes for the ribulose monophosphate pathway and the serine cycle were absent. However, genes encoding the Calvin-Benson-Bassham cycle enzymes were present, supporting physiological studies (9). The genome encodes all three central pathways: the Embden-Meyerhof-Parnas glycolytic pathway, the pentose phosphate pathway, and the tricarboxylic acid cycle. Genes encoding keto-deoxy-gluconate catabolism of the Entner-Doudoroff pathway were absent. Three particulate methane monooxygenase operons (*pmoCAB*) were predicted, while genes encoding soluble methane monooxygenase were not found. The *mxoA* genes encoding methanol dehydrogenase (2, 3) were absent, but a homologous *xoxFJG* gene cluster and a *pqqABCDEF* operon for the biosynthesis of the cofactor pyrroloquinoline quinone were detected. H₄MPT-linked C₁ transfer genes are not present. The H₄Folate-linked pathway inventory includes *metF*, *fold*, and *ftl* genes. *mtaA*, *fch*, and *purU* were not found. Genes encoding NAD-linked formate dehydrogenase (*fdsABG*) were identified (12). Should the

identified genes encoding acetate kinase and acetyl-coenzyme A synthase prove functional, strain SolV may be able to assimilate C₂ compounds and thus be a facultative methanotroph (15). The presence of a hydrogenase gene cluster points toward possible chemolithotrophic growth or the use of hydrogen to provide reducing equivalents for methane oxidation (5). A complex IV-type heme-copper oxidase gene cluster possibly encodes the terminal cytochrome *c* oxidase.

Strain SolV was able to grow with ammonium, nitrate, or dinitrogen gas as a nitrogen source (8, 14). Coincidentally, genes were predicted for direct ammonium uptake (*amtB*) and assimilation (e.g., glutamine synthase, *glnA*; glutamate synthase, *gltB*; alanine dehydrogenase, *ald*) as well as for urea metabolism. As in most other methanotrophs, however, the urea cycle is incomplete (1). A full complement of genes for dinitrogen fixation, nitrate/nitrite transport, and assimilation was also found. In addition, genes for nitrite reduction (*nirK*) and nitric oxide reduction (*norB norC*) were identified, but the inventory to encode nitrous oxide reduction was missing. A *haoAB* gene cluster encoding hydroxylamine oxidase was identified, suggesting the capability of nitrification and nitrosative stress handling (10, 11, 16).

Nucleotide sequence accession numbers. The nucleotide genome sequence of *M. fumariolicum* SolV has been deposited in the European Nucleotide Archive (ENA) under accession numbers CAHT01000001 to CAHT01000109.

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