

# Draft Genome Sequence of “*Candidatus Methylacidiphilum kamchatkense*” Strain Kam1, a Thermoacidophilic Methanotrophic Verrucomicrobium

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**“*Candidatus Methylacidiphilum kamchatkense*” strain Kam1 is an aerobic methane-oxidizing thermoacidophilic bacterium belonging to the *Verrucomicrobia* phylum. It was recovered from an acidic geothermal site in Uzon Caldera, Kamchatka, Russian Federation. Its genome possesses three complete *pmoCAB* gene clusters encoding particulate methane monooxygenase enzymes and a complete Calvin-Benson-Bassham cycle for carbon assimilation.**

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Methane-oxidizing bacteria are capable of using methane as the sole carbon and energy source and are important sinks for limiting the release of methane to the atmosphere. The use of methanotrophs as biocatalysts for the conversion of natural gas to biofuels, biopolymers, single-cell proteins, and high-value products is a promising approach for biotechnological use of natural gas (1). Large-scale methane fermentation at a commercial scale has already been proven as a technically viable process using a loop reactor system (<http://calysta.com/company>).

“*Candidatus Methylacidiphilum kamchatkense*” strain Kam1, is a rod-shaped and Gram-negative aerobic methane-oxidizing bacterium belonging to the *Verrucomicrobia* phylum, isolated from an acidic hot spring in the Uzon Caldera, in Kamchatka, Russian Federation (2), and was one of the first nonproteobacterial methanotrophs to be described. Two related strains, “*Ca. Methylacidiphilum infernorum*” (strain V4) and “*Ca. Methylacidiphilum fumariolicum*” (strain SolV), have also been recovered from similar geothermal environments (3, 4), and together they form a novel verrucomicrobial subdivision (5). All three isolates are thermoacidophilic, with optimal growth at pH 2 to 3.5 and 55 to 60°C. The draft genome of strain Kam1 was sequenced with 454 technology using a GS-FLX pyrosequencer at GATC Biotech, Germany (<http://www.gatc-biotech.com>). A total of 300,132 reads accounting for 72,788,864 bases were obtained. Assembly into 41 contigs was done with Newbler version 2.9 accessed through the Lifeportal, University of Oslo (<http://www.uio.no/english/services/it/research/hpc/lifeportal>).

The draft genome sequence of “*Ca. Methylacidiphilum kamchatkense*” Kam1 comprises 2,210,643 bp in size, with a GC content of 40.8% and 1,805 protein-coding sequences. A single rRNA operon is present, together with 46 tRNA genes. This is comparable with the genome of the other strains, V4 and SolV, whose complete genomes constitute ~2.3 and 2.5 Mbp, respectively (6, 7). An average nucleotide identity (ANI) analysis using the online ANI calculator (<http://enve-omics.ce.gatech.edu/ani/index>) re-

vealed ANI values of 78 and 93%, respectively, when the Kam1 draft sequence was compared with the complete sequences of strains V4 and SolV. This indicates that Kam1 represents a separate species, as this value is lower than the threshold value of 95%, which corresponds to a genomic DNA:DNA hybridization value of 70% and is a common threshold value for distinction between species (8).

Three operons, each encoding one set of the three subunits of the key enzyme, particulate methane monooxygenase, *pmoCAB1-3*, as well as one truncated *pmoCA* cluster and a solitary *pmoC* gene, have been described before (9). The ribulose monophosphate pathway and the serine pathway were until recently believed to be the main carbon assimilatory routes in aerobic methanotrophs. Like strains V4 and SolV, strain Kam1 lacks complete serine and ribulose monophosphate pathways for assimilation of carbon from formaldehyde, while possessing a complete Calvin-Benson-Bassham cycle, confirming an autotrophic type of carbon assimilation also in this species (10). Genes for the Embden-Meyerhof-Parnas glycolytic pathway, the pentose phosphate pathway, and the tricarboxylic acid cycle are present.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number **JQNX00000000**. The version described in this paper is version JQNX01000000.

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