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Complete Genome Sequence of the Chloromethane-Degrading *Hyphomicrobium* sp. Strain MC1

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***Hyphomicrobium* sp. strain MC1 is an aerobic methylophilic originally isolated from industrial sewage. This prosthecae bacterium was the first strain reported to grow with chloromethane as the sole carbon and energy source. Its genome, consisting of a single 4.76-Mb chromosome, is the first for a chloromethane-degrading bacterium to be formally reported.**

Strains of the genus *Hyphomicrobium* originally attracted interest for their distinctive prosthecae and atypical complex growth cycle (9). Strains of this genus are ubiquitous but were detected in wastewater treatment plants in particular, and often under denitrifying conditions (3, 8). Following the description of strain MC1 (6), several chloromethane-degrading *Hyphomicrobium* strains were isolated from various aquatic and soil environments, and most recently also from the surfaces of plant leaves (11). Strain MC1 features the consecutive *cmuBCA* gene arrangement; these genes encode chloromethane dehalogenase, which has been found in all aerobic chloromethane-degrading bacteria characterized so far with the exception of *Methylobacterium extorquens* CM4, from which chloromethane dehalogenase was purified (13) and in which regulation of chloromethane dehalogenase expression was investigated (14).

The assembled genome sequence of *Hyphomicrobium* sp. strain MC1 was obtained using a mix of sequencing technologies. A mate-paired 454 library with an 8-kb insert size was constructed (version Titanium), and 559,691 reads (173,407,941 bp; approximately 36× coverage) were assembled using Newbler (version 2.3, release 091027_1459). Assembly validation was made via Consed (www.phrap.org), and 129 PCRs between contigs were performed and sequenced for gap closure. For quality assessment, a total of 25,299,825 Illumina 36-bp reads were mapped onto the whole genome sequence using SOAP (http://soap.genomics.org.cn) (2), allowing us to correct potential base errors and confirming the final closed circular 4,757,528-bp assembly. Sequence annotation and comparative genome analysis are under way using the MicroScope platform at Genoscope (15).

Based on the 16S rRNA sequence of its single rRNA operon, strain MC1 appears to be most closely related to *Hyphomicrobium facile* subspecies type strains. Of its 4,679

predicted open reading frames (ORFs), 947 (20%) have close homologs (>80% amino acid identity over >80% of protein length, almost all of them in synteny) in *Hyphomicrobium denitrificans* ATCC 51888, whose genome sequence has been determined (NC_014313) (4).

Genes encoding enzymes and proteins for oxidation of methanol (*mx*) and methylamine (*mgs* and *mgd* [5, 7] but not *mau* genes) were identified, together with proteins and enzymes involved in pyrroloquinoline quinone synthesis and tetrahydrofolate- and tetrahydromethanopterin-linked pathways. Genes for complete serine and ethylmalonyl coenzyme A pathways (1) for carbon assimilation were identified. The genome of strain MC1 also encodes a complete glycolysis pathway and a closed tricarboxylic acid cycle, but no genes for the glyoxylate shunt (isocitrate lyase and malate synthase) were detected. Six terminal oxidases of different types were identified. Unlike in *H. denitrificans* ATCC 51888, genes for N₂ fixation, a complete uptake hydrogenase gene cluster, and gene systems for both assimilative (*nas*) and dissimilative (*nar*) reduction of nitrate, ammonia and nitrate/nitrite transport, a putative nitrate-inducible formate dehydrogenase, an alkane sulfonate oxidation and transport system, and an acetone carboxylase (*acxRABC*) cluster (12) were detected. In contrast, the dichloromethane dehalogenation genes (*dcmRABC*) (10) allowing *H. denitrificans* ATCC 51888 to grow on DCM were not found in strain MC1.

Hyphomicrobium sp. strain MC1 thus emerges as a promising model for investigating the degradation of halogenated pollutants in the context of methylophilic metabolism using genomic information (16) and for studies of morphological and metabolic features supporting bacterial growth under nutrient-scarce conditions.

Nucleic acid sequence accession number. The *Hyphomicrobium* sp. strain MC1 genome sequence was deposited in GenBank/EMBL under accession number FQ859181.

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