

# Complete Genome Sequence of the Hydrogenotrophic, Methanogenic Archaeon *Methanoculleus bourgensis* Strain MS2<sup>T</sup>, Isolated from a Sewage Sludge Digester

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***Methanoculleus bourgensis*, of the order *Methanomicrobiales*, is a dominant methanogenic archaeon in many biogas-producing reactor systems fed with renewable primary products. It is capable of synthesizing methane via the hydrogenotrophic pathway utilizing hydrogen and carbon dioxide or formate as the substrates. Here we report the complete and finished genome sequence of *M. bourgensis* strain MS2<sup>T</sup>, isolated from a sewage sludge digester.**

The worldwide shortage and rising price of fossil energy, together with climate and environmental protection aims, have led to enhanced development and utilization of alternative energy resources. In this context, the production of biogas from microbial degradation of organic matter is of great importance, since biogas represents a clean and environmentally compatible energy source (7, 8). Methanogenic subcommunities within biogas-producing consortia are crucial in the anaerobic degradation process for synthesis of methane. Previous studies revealed that members of the genus *Methanoculleus* frequently dominate methanogenic subcommunities in different anaerobic digester systems (7, 9, 13, 19, 20). *Methanoculleus marisnigri* strain JR1, from a marine sediment, is the only member of the genus *Methanoculleus* that has been sequenced so far (1). Moreover, *Methanoculleus bourgensis* was identified in production-scale biogas plants fed with maize silage and manure (4, 7, 10). Other studies reported that *M. bourgensis* seems to be well adapted in biogas communities encountering high salt and ammonium concentrations (5, 16, 17).

*Methanoculleus bourgensis* strain MS2<sup>T</sup> was first isolated from a digester fermenting tannery by-products inoculated with digested sewage sludge from Bourg, France (12). This strain is a hydrogenotrophic methanogen utilizing hydrogen and carbon dioxide or formate as the substrates for methane synthesis. Acetate is required for growth (2). To analyze the adaptability of *M. bourgensis* MS2<sup>T</sup> to the conditions prevailing in biogas reactors, its genome was completely sequenced.

*M. bourgensis* MS2<sup>T</sup> was purchased from the DSMZ (German Collection of Microorganisms and Cell Cultures, Braunschweig, Germany) and grown in modified DSMZ medium 287. Genomic DNA was isolated (14) and sequenced on the Genome Sequencer (GS) Junior system (Roche). A whole-genome shotgun and a paired-end sequencing run yielded 122,030 reads accounting for 57,786,764 bases of total sequence information. Thus, a 21-fold coverage was achieved for the 2.8-Mb *M. bourgensis* MS2<sup>T</sup> genome. After assembling the sequence reads using the GS De Novo assembler software (version 2.6), the order of contigs was determined and gap closure was performed (18). The finished genome has a size of 2,789,773 bp, featuring a GC content of 60.64%. Annotation of the genome was accomplished within the GenDB platform (11), resulting in 2,619 coding sequences, with a mean gene length of 877 bp, 45 tRNA genes, and one *rrn* operon.

Comparative analysis (3, 6, 15) and interpretation of the genome sequence revealed that *M. bourgensis* MS2<sup>T</sup> possesses a central 15,345-kb methanogenesis gene region encoding different enzymes involved in methane synthesis. Additional methanogenesis genes are scattered across the genome. Genes encoding high-affinity hydrogenases most likely involved in the utilization of hydrogen produced by syntrophic acetate or fatty acid-oxidizing microorganisms were identified. *M. bourgensis* MS2<sup>T</sup> possesses genes required for growth on acetate. Moreover, *M. bourgensis* MS2<sup>T</sup> has the genetic potential to produce osmolytes that could be crucial for the adaptation of the strain to the conditions prevailing in biogas reactors. The *M. bourgensis* MS2<sup>T</sup> genome will serve as a reference for comparative analyses comprising other methanogenic *Archaea* from biogas communities and guide studies on the adaptability of related organisms to the conditions in biogas reactor environments.

**Nucleotide sequence accession number.** The *M. bourgensis* MS2<sup>T</sup> genome sequence was deposited at EBI under the accession number [HE964772](https://www.ebi.ac.uk/ena/submitter/HE964772).

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We dedicate this article to Emma Maus, born on 9 August 2012.

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