Draft Genome Sequences of Obligate Methylotrophs
*Methylovorus* sp. Strain MM2 and *Methylobacillus* sp. Strain MM3, Isolated from Grassland Soil

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**ABSTRACT** Methylotrophs of the family *Methylophilaceae* were isolated from grassland soil. Here, we report the draft genome sequences of two obligate methylotrophs, *Methylovorus* sp. strain MM2 and *Methylobacillus* sp. strain MM3. These genome sequences provide further insights into the genetic and metabolic diversity of the *Methylophilaceae*.

The family *Methylophilaceae* is composed of four genera containing facultative and obligate methanol-utilizing methylotrophs (1–4). Members of the *Methylophilaceae* have been isolated from a range of locations, including terrestrial and marine environments (5–10). Here, we report the draft genome sequences of two obligate methylotrophs, *Methylovorus* sp. strain MM2 and *Methylobacillus* sp. strain MM3. The obligate nature of these methylotrophs was confirmed through growth experiments. The strains were isolated from soil collected at a 5-cm depth from grassland in Bawburgh, Norfolk, United Kingdom (52.6276 N, 1.1784 E).

Genome sequencing was performed by MicrobesNG using the Illumina MiSeq platform, producing 2 × 250-bp paired-end reads. Trimmed sequences were assembled using SPAdes version 3.7.1, and genome annotation was performed using the RAST annotation server (http://rast.nmpdr.org) (11, 12). Coverage of the genomes was calculated using BWA, SAMtools, and BEDTools genomecov (13–15). The *Methylovorus* sp. MM2 genome is composed of 27 contigs and includes 2,291 coding sequences (CDSs), 16S rRNA gene copy, and 46 tRNAs. The genome size is 2.42 Mb, with 46% G+C content. The genome of *Methylobacillus* sp. MM3, with 2.95 Mb and 57% G+C content, is composed of 64 contigs and includes 2,897 CDSs and 3 copies of 16S rRNA genes. Both genomes had 30-fold coverage.

Both genomes contain pyrroloquinoline quinone methanol dehydrogenases. *Methylobacillus* sp. MM3 possesses three separate gene clusters for the alternative methanol dehydrogenase XoxF (16, 17) and no copies of the canonical methanol dehydrogenase-encoding genes mxaFI. *Methylovorus* sp. MM2 possesses three copies of xoxF and one set of the genes mxaFI. All genes encoding the N-methylglutamate pathway for methylamine utilization (mgdABC, gmaS, and mgsABC) (18, 19) are present only in the genome of *Methylobacillus* sp. MM3, in addition to genes that encode dimethylamine dehydrogenase and trimethylamine dehydrogenase enzymes (dmd and tmd) (20, 21). The genes for an assimilatory nitrate reductase (nasAB) and the complete denitrification pathway (narGHI, nirK, nirS, norB, and nosZ) are present in the genome of *Methylobacillus* sp. MM3, while *Methylovorus* sp. MM2 possesses only an assimilatory nitrate reductase (nasAB) and a dissimilatory nitrite reductase (nirBD).

**Data availability.** These whole-genome shotgun projects have been deposited at DDBJ/ENA/GenBank under accession numbers LXTQ00000000 for *Methylobacillus* sp.
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REFERENCES


MM3 and LXUF00000000 for Methylovorus sp. MM2. The versions described in this paper are the first versions. The strains are available from the authors upon request.