Members of the genus Methanobrevibacter are the dominant methanogens found in the digestive tract of ruminant livestock, and two different clades (M. gottschalkii and M. ruminantium) of closely related species constitute the bulk of the population (1–3). The M. ruminantium clade contains two described species, M. ruminantium (4) and M. olleyae (5). Here, we report the draft genome sequence of the hydrogenotrophic methanogen M. olleyae YLM1, which was isolated from the rumen of a lamb (6).

The genome sequence of M. olleyae YLM1 was determined using pyrosequencing of 3-kb mate-paired libraries on a 454 GS FLX platform with titanium chemistry (Macrogen, South Korea) and combined with reads from an Illumina HiSeq 2000 platform (BGI, China), where a 2-kb mate-paired library was constructed with paired-end sequencing of 90-bp reads. Pyrosequencing reads were assembled using the Newbler assembler version 2.0 (Roche FLX platform with titanium chemistry, Macrogen, South Korea) and combined with reads from an Illumina HiSeq 2000 platform. Pyrosequencing reads (454 Life Sciences, USA) and Illumina reads using the SPAdes genome assembler version 3.0 (7). This resulted in 10 contigs in a single scaffold. Gap closure was managed using the Staden package (8), and gaps were closed using standard PCR techniques with Sanger sequencing, resulting in a single contig. One remaining gap, which is predicted to contain several tRNA genes, was unable to be closed. Protein-encoding genes were identified by Glimmer (9) and a GAMOLA/ARTEMIS (10, 11) software suite was used to manage genome annotation. Assignment of protein function to open reading frames was performed manually using results from BLASTp and the COG (Clusters of Orthologous Groups), Pfam, and TIGRFAM databases (12–14).

The draft genome sequence of M. olleyae YLM1 consists of a single 2,201,192-bp contig with a GC content of 26.9%, and 1,834 predicted protein-coding genes representing 75.7% of the genome. The YLM1 genome encodes 64 large adhesin-like proteins predicted to grow at differing hydrogen concentrations. Similar to M1, the YLM1 genome encodes 64 large adhesin-like proteins predicted to have a role in mediating interactions with other members of the rumen microbial community (15). Genomic information from M. olleyae YLM1 will complement genome sequences from other rumen methanogens (16).

**Nucleotide sequence accession number.** This whole-genome sequencing project has been deposited at DDBJ/EMBL/GenBank under the accession number CP014265.

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