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Draft Genome Sequences of *Methanobrevibacter curvatus* DSM11111, *Methanobrevibacter cuticularis* DSM11139, *Methanobrevibacter filiformis* DSM11501, and *Methanobrevibacter oralis* DSM7256

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Here, the draft genome sequences of four different *Methanobrevibacter* species are presented. Three of the *Methanobrevibacter* species (*M. curvatus, M. cuticularis*, and *M. filiformis*) have been isolated from the termite hindgut, while *M. oralis* was isolated from human subgingival plaque.

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Methanobacteriales, in particular members of the genera *Methanobrevibacter*, have been shown to be some of the most abundant methanogenic archaea in various intestinal environments, including the human gut (1), the termite hindgut (2), and the ovine and bovine rumen (3). Recent studies have indicated that *Methanobrevibacter* species may not only be contributing to greenhouse gas emissions from farm animals (4, 5), but may also have effects on human physiology and health (6, 7). It is therefore of great interest to gain a better understanding of how different *Methanobrevibacter* species have adapted to specific host environments at the molecular level. Genome sequences of *Methanobrevibacter* species have been obtained so far for strains from the human intestinal tract and the rumen (8–12), but not from any insect guts or the human oral cavity. *Methanobrevibacter oralis* DSM7256, isolated from the human subgingival plaque (13), is also the first sequenced representative of all human oral methanogens.

Genomic DNA was ordered by the DSMZ (Braunschweig) or was isolated using the MasterPure complete DNA purification kit (Epicentre, Madison, WI, USA). The extracted DNA was used to generate Illumina-shotgun libraries according to the manufacturer's protocol (Illumina, San Diego, CA, USA). Sequencing was conducted using a MiSeq and MiSeq reagent kit v3 (2 × 300 bp paired end) as recommended by the manufacturer (Illumina). Sequencing resulted in 1,934,710 (*M. filiformis*), 1,983,778 (*M. oralis*), 3,298,762 (*M. curvatus*), and 3,533,158 paired end reads (*M. cuticularis*), respectively. Trimmomatic 0.32 (14) was used to filter low-quality reads and for clipping of adapter contaminations. The assembly was performed with the SPAdes genome assembler software 3.6.2 (15). Coverages were determined using QualiMap version 2.1 (15, 16) and automatic annotation was performed using the software tool PROKKA (17). General genome features are listed in Table 1.

Sequencing the genomes of the four different *Methanobrevibacter* genomes provides reference sequences for comparative analyses with other *Methanobrevibacter* genomes and may reveal adaptive traits of *Methanobrevibacter* species to different environments. Some characteristic features and differences between *Methanobrevibacter* species are already apparent from formal description of the type strains, e.g., presence of catalase activity in the three *Methanobrevibacter* species from the termite hindgut (18, 19). The genome sequences allow the identification of the potential molecular basis of this enzyme activity: A monofunctional heme-depended catalase similar to the enzyme purified from *M. arboriphilus* (20). The gene encoding this enzyme is present in each of the genomes of the three *Methanobrevibacter* species isolated from the termite hindgut, but appears to be absent from the genome of *M. oralis*.

Nucleotide sequence accession numbers. These whole-genome shotgun projects have been deposited at DDBJ/EMBL/

TABLE 1 Genome features and GenBank accession numbers of sequenced strains

Strain	Genome size (bp)	G+C content (%)	No. of scaffolds (>500 bp)	No. of CDSs[a]	No. of rRNAs	No. of tRNAs	Accession no.
M. filiformis DSM 11501	2,606,143	26.99	295	1,933	3	29	LWMT00000000
M. oralis DSM 7256	2,140,433	27.71	136	1,994	5	24	LWMU00000000
M. curvatus DSM 11111	2,414,608	25.72	232	1,969	4	31	LWMV00000000
M. cuticularis DSM 11139	2,608,702	26.79	169	2,061	3	30	LWMW00000000

[a] CDSs, coding sequences.

GenBank under the accession numbers listed in Table 1. The versions described here are the first versions.

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REFERENCES

1. **Dridi B, Henry M, El Khéchine A, Raoult D, Drancourt M**. 2009. High prevalence of *Methanobrevibacter smithii* and *Methanosphaera stadtmanae* detected in the human gut using an improved DNA detection protocol. PLoS One **4:**e7063. http://dx.doi.org/10.1371/journal.pone.0007063.
2. **Ohkuma M, Noda S, Kudo T**. 1999. Phylogenetic relationships of symbiotic methanogens in diverse termites. FEMS Microbiol Lett **171:** 147–153. http://dx.doi.org/10.1111/j.1574-6968.1999.tb13425.x.
3. **Janssen PH, Kirs M**. 2008. Structure of the archaeal community of the rumen. Appl Environ Microbiol **74:**3619–3625. http://dx.doi.org/10.1128/AEM.02812-07.
4. **Seedorf H, Kittelmann S, Henderson G, Janssen PH**. 2014. Rim-DB: a taxonomic framework for community structure analysis of methanogenic archaea from the rumen and other intestinal environments. PeerJ **2:**e494. http://dx.doi.org/10.7717/peerj.494.
5. **Shi W, Moon CD, Leahy SC, Kang D, Froula J, Kittelmann S, Fan C, Deutsch S, Gagic D, Seedorf H, Kelly WJ, Atua R, Sang C, Soni P, Li D, Pinares-Patiño CS, McEwan JC, Janssen PH, Chen F, Visel A, Wang Z, Attwood GT, Rubin EM**. 2014. Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. Genome Res **24:**1517–1525. http://dx.doi.org/10.1101/gr.168245.113.
6. **Lepp PW, Brinig MM, Ouverney CC, Palm K, Armitage GC, Relman DA**. 2004. Methanogenic *Archaea* and human periodontal disease. Proc Natl Acad Sci USA **101:**6176–6181. http://dx.doi.org/10.1073/pnas.0308766101.
7. **Million M, Maraninchi M, Henry M, Armougom F, Richet H, Carrieri P, Valero R, Raccah D, Vialettes B, Raoult D**. 2012. Obesity-associated gut microbiota is enriched in *Lactobacillus reuteri* and depleted in *Bifidobacterium animalis* and *Methanobrevibacter smithii*. Int J Obes **36:** 817–825. http://dx.doi.org/10.1038/ijo.2011.153.
8. **Leahy SC, Kelly WJ, Altermann E, Ronimus RS, Yeoman CJ, Pacheco DM, Li D, Kong Z, McTavish S, Sang C, Lambie SC, Janssen PH, Dey D, Attwood GT**. 2010. The genome sequence of the rumen methanogen *Methanobrevibacter ruminantium* reveals new possibilities for controlling ruminant methane emissions. PLoS One **5:**e8926. http://dx.doi.org/10.1371/journal.pone.0008926.
9. **Hansen EE, Lozupone CA, Rey FE, Wu M, Guruge JL, Narra A, Goodfellow J, Zaneveld JR, McDonald DT, Goodrich JA, Heath AC, Knight R, Gordon JI**. 2011. Pan-genome of the dominant human gut-associated archaeon, *Methanobrevibacter smithii*, studied in twins. Proc Natl Acad Sci USA **108:**4599–4606. http://dx.doi.org/10.1073/pnas.1000071108.
10. **Leahy SC, Kelly WJ, Li D, Li Y, Altermann E, Lambie SC, Cox F, Attwood GT**. 2013. The complete genome sequence of *Methanobrevibacter* sp. AbM4. Stand Genomic Sci **8:**215–227. http://dx.doi.org/10.4056/sigs.3977691.
11. **Lee J-H, Rhee M-S, Kumar S, Lee G-H, Chang D-H, Kim D-S, Choi S-H, Lee D-W, Yoon M-H, Kim B-C**. 2013. Genome sequence of *Methanobrevibacter* sp. strain JH1, isolated from rumen of Korean native cattle. Genome Announc **1**(1):e00002-13. http://dx.doi.org/10.1128/genomeA.00002-13.
12. **Kelly WJ, Li D, Lambie SC, Cox F, Attwood GT, Altermann E, Leahy SC**. 2016. Draft genome sequence of the rumen methanogen *Methanobrevibacter olleyae* YLM1. Genome Announc **4**(2):e00232-00216. http://dx.doi.org/10.1128/genomeA.00232-16.
13. **Ferrari A, Brusa T, Rutili A, Canzi E, Biavati B**. 1994. Isolation and characterization of *Methanobrevibacter oralis* sp. nov. Curr Microbiol **29:** 7–12. http://dx.doi.org/10.1007/BF01570184.
14. **Bolger AM, Lohse M, Usadel B**. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics **30:**2114–2120. http://dx.doi.org/10.1093/bioinformatics/btu170.
15. **Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA**. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol **19:**455–477. http://dx.doi.org/10.1089/cmb.2012.0021.
16. **García-Alcalde F, Okonechnikov K, Carbonell J, Cruz LM, Götz S, Tarazona S, Dopazo J, Meyer TF, Conesa A**. 2012. Qualimap: evaluating next-generation sequencing alignment data. Bioinformatics **28:** 2678–2679. http://dx.doi.org/10.1093/bioinformatics/bts503.
17. **Seemann T**. 2014. Prokka: rapid prokaryotic genome annotation. Bioinformatics **30:**2068–2069. http://dx.doi.org/10.1093/bioinformatics/btu153.
18. **Leadbetter JR, Breznak JA**. 1996. Physiological ecology of *Methanobrevibacter cuticularis* sp. nov. and *Methanobrevibacter curvatus* sp. nov., isolated from the hindgut of the termite *Reticulitermes flavipes*. Appl Environ Microbiol **62:**3620–3631.
19. **Leadbetter JR, Crosby LD, Breznak JA**. 1998. *Methanobrevibacter filiformis* sp. nov., a filamentous methanogen from termite hindguts. Arch Microbiol **169:**287–292. http://dx.doi.org/10.1007/s002030050574.
20. **Shima S, Sordel-Klippert M, Brioukhanov A, Netrusov A, Linder D, Thauer RK**. 2001. Characterization of a heme-dependent catalase from *Methanobrevibacter arboriphilus*. Appl Environ Microbiol **67:**3041–3045. http://dx.doi.org/10.1128/AEM.67.7.3041-3045.2001.