In recent years, growing evidence from culture-independent studies has suggested that methanogens associated with the human gut are far more diverse than was thought (1–4) and partly belong to a Thermoplasmatales-related lineage (2). The methanogenic nature of this lineage was confirmed by the description of Methanomassiliicoccus luminyensis strain B10, isolated from human feces (5). Another methanogen of this Thermoplasmatales-related lineage, “Candidatus Methanomethylophilus alvus” Mx1201, was also cultured from human feces and was found to be closely related to “Methanomethylophilus alvus” (6). This ar-
chaeon is distantly related to “Ca. Methanomassiliicoccus intestinalis” (7).

A highly enriched culture of “Candidatus Methanomassiliicoccus intestinalis” Issoire-Mx1 was obtained by the same procedure followed for “Ca. Methanomethylophilus alvus” (6). This ar-
chaeon is distantly related to “Ca. Methanomethylophilus alvus” and is closely related to “M. luminyensis”, with 87% and 98% of 16S rRNA gene sequence identity, respectively. The affiliation of M. luminyensis and “Ca. Methanomassiliicoccus intestinalis” to a large cluster of sequences retrieved from paddy soils and freshwater and marine sediments suggests their recent adaptation to gut environments.

A 3-kb mate-paired library was constructed and sequenced from a quarter plate of a 454 GS FLX Titanium run (Macrogen, Republic of Korea). A total of 283,279 reads corresponding to 125.5 Mb were obtained. The reads were assembled with Newbler (v2.3), first in 28 contigs (average depth coverage of 42.7-fold) and then in a unique scaffold. The gaps between the contigs were manually curated.

“Ca. Methanomassiliicoccus intestinalis” has a circular genome of 1,931,561 bp, with a G+C content of 41.3%. Despite its close phylogenetic relationship with M. luminyensis, the genome of “Ca. Methanomassiliicoccus intestinalis” is 27% smaller and its G+C content is 20% lower than that of M. luminyensis. This suggests a fast genomic reshuffle in one of the two genomes, which may be due to differential adaptation to the gut environment. The “Ca. Methanomassiliicoccus intestinalis” genome contains 46 tRNA genes, a single copy of the 16S and 23S rRNA genes, and 2 noncontiguous copies of 5S rRNA genes that were distant from the 23S and 16S rRNA genes. A total of 1,820 protein-coding sequences were predicted. A clustered regularly interspaced short palindromic repeat (CRISPR) region containing 110 spacers was identified using CRISPRfinder (10), in close association with cas genes. The genome of “Ca. Methanomassiliicoccus intestinalis” contains one mcr operon (mcrBDGA) and a mcrC gene distantly located from it. Genes involved in methylotrophic methanogenesis from methanol (mtaABC) and methylamine compounds (mtnABC, mtbABC, and mtBC) are also present. The latter are on an 18.7-kb region also containing the genes involved in pyrrolysine biosynthesis. The sequence of “Ca. Methanomassiliicoccus intestinalis” offers a great opportunity to determine the metabolic properties and phenotypic features of this poorly characterized order of methanogens related to Thermoplasmatales, and it will further help to identify the genomic adaptations of methanogens to gut environments.

**Nucleotide sequence accession number.** The draft genome sequence of “Candidatus Methanomassiliicoccus intestinalis” Issoire-Mx1 has been deposited in GenBank under the accession no. CP005934.

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