Complete Genome Sequence of *Mycoplasma wenyonii* Strain Massachusetts

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*Mycoplasma wenyonii* is a hemotropic mycoplasma that causes acute and chronic infections in cattle. Here, we announce the first complete genome sequence of this organism. The genome is a single circular chromosome with 650,228 bp and G+C% of 33.9. Analyses of *M. wenyonii* genome will provide insights into its biology.

*Mycoplasma wenyonii* (Eperythrozoon wenyonii) is an uncultivable, cell wall-less bacterium that attaches to the erythrocytes of cattle (13). This bacterium and other hemotropic mycoplasmas form a new phylogenetic cluster within the *pneumonieae* group of *Mycoplasmas* (class Mollicutes) and are also referred as hemoplasmas (14, 15). Anemia, bacteremia, edema (scrotal, hind, and limb), lymphadenopathy, transient fever, anorexia, weight loss, infertility, and decreased milk production have been associated with *M. wenyonii* infections (6, 10, 12, 19, 20); however, clinical signs need to be further investigated due to the lack of specific diagnostic methods and presence of coinfections or other concurrent diseases (1, 8, 9, 20). Nonetheless, *M. wenyonii* appears to have low morbidity and animals can become chronic carriers (16, 19, 21). The prevalence of *M. wenyonii* infection has been reported worldwide and ranges from 6% to 78%, depending on the geographic area, type of population studied, and diagnostic test used (5, 8, 10, 11, 21). The complete genome of *M. wenyonii* was sequenced, assembled, and annotated in order to better understand its pathogenicity, metabolism, and evolution.

Genomic DNA was obtained from white blood cell-depleted EDTA blood sample of a 2-year-old female Holstein cow from a farm where several animals were presenting with fever and udder-teat and hind-limb edema. Dot-like and ring structures attached to the erythrocytes and free on the plasma were observed on the blood smear of this animal. DNA extraction was performed using Quick-gDNA MidiPrep (Zymo Research Corporation, Irvine, CA) according to the manufacturer’s recommendations. The whole genome was sequenced using Illumina HiScanSQ (Illumina, Inc., San Diego, CA) at the Purdue University Genomics Core Facility. After assembly, six remaining gaps were closed using conventional PCR followed by Sanger sequencing in both directions. First-pass annotation was achieved using the NCBI annotation pipeline.

The complete genome of *M. wenyonii* is a single circular chromosome with a size of 650,228 bp and G+C content of 33.9% and appears to use the opal stop codon (UGA) for tryptophan. The small genome size and low G+C content are typical characteristics of *Mycoplasma*. The general genomic features of the *M. wenyonii* genome are compatible with those of the hemoplasmas sequenced to date (2–4, 7, 17, 18): the 16S, 23S, and 5S rRNA genes are represented as single copies; however, like that of *Mycoplasma suis*, the 16S rRNA gene is separated from the 5S-23S rRNA in a different operon (7). tRNA-Sec was identified along with other 31 tRNAs covering all amino acids. Also, as seen with other hemoplasmas, a large proportion (57%) of the genome is dedicated to duplicated genes organized in paralog families.

A total of 718 protein-coding sequences (CDS) were predicted and putative functions were automatically assigned by the NCBI annotation pipeline. Most (52.6%) of the CDS are represented by hypothetical proteins, which is due to the large repertoire of paralog genes, indicating that *M. wenyonii* might use recombination and/or phase variation as a mechanism of antigenic variation to evade the host’s immune system. Manual genome annotation and analyses will provide more detailed information about this bacterium.

**Nucleotide sequence accession number.** The *M. wenyonii* strain Massachusetts genome sequence was deposited in the GenBank database under accession number CP003703.

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**REFERENCES**


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