

Genome Sequence of *Taylorella equigenitalis* MCE9, the Causative Agent of Contagious Equine Metritis[▽]

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***Taylorella equigenitalis* is the causative agent of contagious equine metritis (CEM), a sexually transmitted infection of horses. We herein report the genome sequence of *T. equigenitalis* strain MCE9, isolated in 2005 from the urethral fossa of a 4-year-old stallion in France.**

Taylorella equigenitalis is a slow-growing microaerophilic Gram-negative coccobacillus, classified in the family *Alcaligenaceae* (10). It is the causative agent of contagious equine metritis (CEM), a sexually transmitted infection of horses first reported in 1977 (3, 11), and currently has been detected in many countries and various horse breeds. CEM is characterized in infected mares by abundant mucopurulent vaginal discharge and a variable degree of vaginitis, endometritis, and cervicitis that usually result in temporary infertility or early abortion. However, mares may also be asymptomatic (9). Although no clinical signs have been observed in stallions, the infection is most frequently transmitted by carrier stallions, which are the main vector for the infection (4). We report herein the genome sequence of *T. equigenitalis* MCE9, which was isolated in 2005 from the urethral fossa of a 4-year-old stallion from a stud farm in the Haute-Savoie (France). The strain is currently maintained by the French National Reference Laboratory for CEM (Anses, Dozulé Laboratory for Equine Diseases, Dozulé, France).

Whole-genome sequencing was performed by combining the GS FLX (8) and Solexa (2) paired-end sequencing technologies (carried out by Beckman Coulter Genomics, Danvers, MA). Genomic libraries containing 3-kb inserts were constructed, and 410,100 reads (including 50.5% of paired-end reads) were produced using the GS FLX system, giving 71-fold coverage of the genome, and then assembled into five large contigs in one potential large scaffold using the Newbler software program (454 Life Sciences, Branford, CT). A total of 1.5 million reads with an average length of 92 bp were generated using an Illumina Solexa Genome Analyzer II instrument and mapped to the contigs using the Consed graphical software tool (5) in order to correct eventual error generated by the 454 technology. The order and orientation of the five large contigs were confirmed by PCR and assembled into a single sequence. Annotation resulted from merging the results obtained from the RAST (Rapid Annotation using Subsystem Technology)

server (1), tRNAscan-SE-1.21 (7), and RNAmmer-1.2 (6), followed by manual curation.

The *T. equigenitalis* MCE9 genome is 1,695,860 bp long with an overall G+C content of 37.42%. There was no evidence of plasmids. There were 1,556 protein-coding genes, with an average length of 1,007 bp. Of these, 1,231 (≈79%) were assigned a predicted function. There are 38 tRNA genes for all amino acids and three copies of the 16S-23S-5S rRNA operon, three putative transposase genes, and four putative phage-related genes.

This is the first genome sequence of the *Taylorella* genus (which also contains the donkey-related *Taylorella asinigenitalis* species), and its availability will provide a better-defined genetic background for future studies of the organism's metabolism and pathobiology.

Nucleotide sequence accession number. The genome sequence of *Taylorella equigenitalis* is available at GenBank through accession number CP002456.

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