



Complete Genome Sequence of *Mycoplasma gallopavonis* Type Strain WR1

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ABSTRACT Here, we report the complete genome sequence of *Mycoplasma gallopavonis* type strain WR1 (= ATCC 33551 = NCTC 10186), which is a common microorganism in eastern wild turkeys and is considered a nonpathogenic commensal in turkeys.

Mycoplasma is a genus within the class *Mollicutes*. *Mycoplasma* cells lack a cell wall around their cell membranes, and they are the smallest known self-replicating prokaryotes. They are small in genome and cell size and thus deficient in genes controlling biosynthetic pathways, and they are reliant on their host for the provision of many essential nutrients (1).

Mycoplasma gallopavonis was first described in 1982 as a *Mycoplasma* serovar of avian origin (2). *M. gallopavonis* can often be isolated from free-ranging eastern wild turkeys (*Meleagris gallopavo silvestris*), and it has not been considered a pathogenic avian *Mycoplasma* species (3, 4). To date, very little is known about the role of *M. gallopavonis* in poultry, such as whether the bacterium can act as a primary pathogen or an opportunistic secondary pathogen. The lack of published genome sequences has limited the molecular characterization of *M. gallopavonis* and the elucidation of its significance for animal health.

Mycoplasma gallopavonis type strain WR1, also known as ATCC 33551 and NCTC 10186, was received from a culture stock from Denmark in 1984. DNA for whole-genome sequencing was prepared from colonies grown on nutrient broth agar culture plates, using a High Pure PCR template preparation kit (Roche Diagnostics GmbH, Mannheim, Germany). The sequencing library was generated using the Nextera XT DNA library prep kit (Illumina, Inc., San Diego, CA). From an Illumina MiSeq run with an average read length of 300 bp and an expected insert size of 350 bp, 408,000 paired-end reads were generated, with a Phred score averaging >38 (mean sequencing depth of >200 reads, with a standard deviation of 60 bp). Further processing included quality trimming and assembly (included in SPAdes 3.12.1. in Bayes Hammer mode [-careful]) (5). Analysis of the data was performed with QUAST v4.3 and Bandage 0.8.1, using standard settings (6, 7). Filtering of the sample was performed by removing contigs with coverage less than 25× and a size below 850 bases. The assembly was finalized by a removal of contaminations with Kraken (8). The genome assembly was represented by 91 contigs with an N_{50} contig length of 15,045 bp, in which the largest contig had 39,296 bp. Annotation was performed with Prokka (9), using the code for *Entomoplasmatales* and *Mycoplasmatales* (10). Annotation features include 603 coding sequence(s) (CDS), 4 rRNAs, 31 tRNAs, and 1 transfer-messenger RNA (tmRNA), for a total sequence length of 795,497 bp. The GC content was calculated to be 28.14%. Analysis with Rapid Annotations using Subsystems Technology (RAST) and SEED (also in standard settings [9], using the code for *Mycoplasmatales*) (11, 12) revealed the closest neighbors, *M. synoviae* 53, *M. mobile* 163K, and *M. pulmonis* UAB CTIP, and thus might be important to differentiate mycoplasmas in a diagnostic context.

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Data availability. The whole-genome sequence of *Mycoplasma gallopavonis* type strain WR1, also known as ATCC 33551 and NCTC 10186, was submitted under GenBank accession number [OXGN000000000](https://www.ncbi.nlm.nih.gov/nuclseq/OXGN000000000), BioProject accession number [PRJNA488011](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA488011), and BioSample accession number [SAMN09935187](https://www.ncbi.nlm.nih.gov/biosample/SAMN09935187). Primary data were deposited in the NCBI primary data archive, SRA, with the reference number [SRP159222](https://www.ncbi.nlm.nih.gov/sra/SRP159222). The version described in this paper is the first version.

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REFERENCES

- Razin S, Barile MF, Harasawa R, Amikam D, Glaser G. 1983. Characterization of the mycoplasma genome. *Yale J Biol Med* 56:357–366.
- Jordan FTW, Erno H, Cottew GS, Hinz KH, Stipkovits L. 1982. Characterization and taxonomic description of five mycoplasma serovars (serotypes) of avian origin and their elevation to species rank and further evaluation of the taxonomic status of *Mycoplasma synoviae*. *Int J Syst Bacteriol* 32:108–115. <https://doi.org/10.1099/00207713-32-1-108>.
- MacDonald AM, Jardine CM, Rejman E, Barta JR, Bowman J, Cai HY, Susta L, Nemeth NM. 2018. High prevalence of *Mycoplasma* and *Eimeria* species in free-ranging eastern wild turkeys (*Meleagris gallopavo silvestris*) in Ontario, Canada. *J Wildl Dis* <https://doi.org/10.7589/2017-11-273>.
- Luttrell MP, Eleazer TH, Kleven SH. 1992. *Mycoplasma gallopavonis* in eastern wild turkeys. *J Wildl Dis* 28:288–291. <https://doi.org/10.7589/0090-3558-28.2.288>.
- 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. <https://doi.org/10.1089/cmb.2012.0021>.
- Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. *Bioinformatics* 29:1072–1075. <https://doi.org/10.1093/bioinformatics/btt086>.
- Wick RR, Schultz MB, Zobel J, Holt KE. 2015. Bandage: interactive visualization of *de novo* genome assemblies. *Bioinformatics* 31:3350–3352. <https://doi.org/10.1093/bioinformatics/btv383>.
- Wood DE, Salzberg SL. 2014. Kraken: ultrafast metagenomic sequence classification using exact alignments. *Genome Biol* 15:R46. <https://doi.org/10.1186/gb-2014-15-3-r46>.
- Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30:2068–2069. <https://doi.org/10.1093/bioinformatics/btu153>.
- Bove JM. 1993. Molecular features of mollicutes. *Clin Infect Dis* 17: S10–S31. https://doi.org/10.1093/clinids/17.Supplement_1.S10.
- Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <https://doi.org/10.1186/1471-2164-9-75>.
- Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). *Nucleic Acids Res* 42:D206–D214. <https://doi.org/10.1093/nar/gkt1226>.