



# Complete Genome Sequence of *Mycoplasma pullorum* Isolated from Domestic Chickens

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**ABSTRACT** The 1,007,172-bp complete genome of *Mycoplasma pullorum* strain B359\_6, isolated from domestic chickens, has been sequenced, assembled, and annotated.

**M**ycoplasmas evolved through reductive evolution from Gram-positive bacteria, resulting in the smallest known self-replicating prokaryotes. These prokaryotes are dependent on their hosts for most of their nutrients due to the loss of most of their protein-coding genes (1). *Mycoplasma pullorum* was first characterized in 1982 as an aerobic and anaerobic fermenter of glucose, but it is unable to reduce tetrazolium chloride or hydrolyze arginine or urea, and lacks phosphatase activity (2). *M. pullorum* is predominately isolated from chickens, but has also been found in turkeys, pheasants, and partridges (3–5).

*M. pullorum* strain B359\_6 was isolated in February 2015 from a 72-week-old layer hen showing clinical signs of mycoplasma infection, which included breathing difficulty, rales, and nasal discharge. The organism was cultured in mycoplasma broth, and the DNA was extracted from 200 mL of culture, as previously described (6). Genomic DNA was sequenced on both the Ion Torrent (University of Pretoria) and Illumina MiSeq (Inqaba Biotech [Pty] Ltd., Pretoria) platforms. The Ion Torrent data set comprised 4,048,280 reads with an average length of 176.74 nucleotides (nt) and approximately 700× coverage, and the Illumina MiSeq data set contained 332,818 reads with an average length of 185.12 nt and approximately 60× coverage. The genome was assembled *de novo* in CLC Genomics Workbench version 8.5.1 to create two contig sets. The Ion Torrent data set was also submitted to IonGap (<http://iongap.hpc.iter.es>) for *de novo* assembly to create a third contig set (7). The three contig data sets were then aligned in the CLC Genome Finishing Tool version 1.5.4 and systematically joined by visual inspection. The 16S rRNA gene of strain B359\_6, identified using RNAmmer (<http://www.cbs.dtu.dk/services/RNAmmer>), as well as the 16S rRNA genes from reference sequences retrieved from GenBank, were used to reconstruct the 16S rRNA phylogeny (8). Parsimony, maximum likelihood, and Bayesian inference phylogenetic trees were constructed in PAUP version 4, PhyML version 3.0, and MrBayes version 3.2.6, respectively, and strain B359\_6 was identified as *M. pullorum* (9–12). Strain B359\_6 had 99.80% nucleotide sequence identity to the 16S rRNA gene of *M. pullorum* strain ATCC 33553.

Annotation of the 1,007,172-bp circular genome of the *M. pullorum* strain B359\_6 genome was completed in the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (13). The genome has a G+C content of 29.07% and molecular weight of  $6 \times 10^8$  Da, and contains 763 coding genes, two sets of the 16S and 23S rRNA genes, and 34 tRNAs. This sequence represents the first complete, annotated genome for *M. pullorum*.

**Accession number(s).** The whole-genome sequence for *M. pullorum* strain B359\_6 was submitted to GenBank under accession number [CP017813](https://www.ncbi.nlm.nih.gov/nuclink/CP017813).

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