Complete Genome Sequence of *Mycoplasma meleagridis*, a Possible Emerging Pathogen in Chickens

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*Mycoplasma meleagridis* strain B2096 8B was isolated from domestic chickens in South Africa. The 845,307-bp full genome was sequenced, assembled, and annotated.

*Mycoplasma*, a genus within the class *Mollicutes*, is the smallest known self-replicating prokaryote. As a consequence of the evolutionary reduction in genome and cell size, mycoplasmas are deficient in genes controlling biosynthetic pathways and are reliant on their host to provide many essential nutrients (1). *Mycoplasma meleagridis* is widespread in turkey flocks across the world, causing deterioration in growth and feathering, airsacculitis, osteodystrophy, and a reduction in hatchability (2).

*M. meleagridis* has always been considered a turkey-specific pathogen (2), but a natural infection of domestic chickens with *M. meleagridis* was recently reported in Tunisia. Laying hens developed typical clinical signs of mycoplasmosis, such as respiratory symptoms and egg production losses, and the etiological agent was identified as *M. meleagridis* by a growth inhibition assay with specific antisera and *M. meleagridis*-specific PCR and DNA sequence analysis (3). *M. meleagridis* strain B2096 8B was isolated in September 2014 from the Gauteng Province of South Africa from 62-week-old laying hens with typical mycoplasma symptoms. Similar isolates were identified in chickens from as far back as 2005.

DNA extraction from the organism cultured in mycoplasma broth was performed, as previously described (4). The genomic DNA library was sequenced using Illumina MiSeq technology for 600 cycles, generating approximately 1 GB of data (Inqaba Biotec [Pty] Ltd., Pretoria, South Africa). The genome was assembled de novo from 6,229,108 reads, with an average length of 133.03 nucleotides (nt) and approximately 700× coverage in the CLC Genomics Workbench version 7.5.2. Contigs were aligned in the CLC Genome Finishing Tool version 1.4, visually inspected, and systematically joined after each realignment. The assembled genome was annotated in the NCBI Prokaryotic Genome Annotation Pipeline, and the functions of open reading frames (ORFs) were predicted on the BASys Web server (5).

The assembled circular genome of *Mycoplasma meleagridis* strain B2096 8B was 845,307 bp in length, with a G+C content of 28.38%. This G+C content is similar to a value of 28.6% calculated by cesium-chloride density gradient analysis for *Mycoplasma meleagridis* strain 529 (6), but the genome size of strain B2096 8B was larger, at 5.1 × 10^8 Da compared to 4.2 × 10^8 ± 0.5 × 10^8 Da calculated for strain 529. Proteins were identified with functions in energy production and conversion (1.6%), cell division and chromosome partitioning (0.5%), amino acid transport and metabolism (3%), nucleotide transport and metabolism (1%), carbohydrate transport and metabolism (4.3%), coenzyme metabolism (1.2%), lipid metabolism (0.3%), translation, ribosomal structure, and biogenesis (7.7%), transcription (1.4%), DNA replication, recombination, and repair (4.2%), cell envelope biogenesis/outer membrane (0.1%), posttranslational modification, protein turnover, and chaperones (1.3%), inorganic ion transport and metabolism (0.9%), and proteins with a general function prediction only (4.6%). The functions of 65% of the open reading frames (ORFs) identified in *M. meleagridis* are unknown. The complete genome of *M. meleagridis* will assist in future studies aimed at unravelling the complex etiology of *M. meleagridis* in multifactorial disease not only in turkeys but also in chickens.

**Nucleotide sequence accession number.** The complete sequence of *M. meleagridis* strain B2096 8B was deposited in GenBank under the accession no. CP011021.

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