**Genome Sequence of Duck Pathogen *Mycoplasma anatis* Strain 1340**

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*Mycoplasma anatis*, a member of the class *Mollicutes*, is a causative agent of a contagious infectious disease of domestic ducklings, wild birds, and eggs. Increasing reports show that coinfection of *M. anatis* with *Escherichia coli* results in substantial economic impacts on the duck farms in China. Here, we announce the first genome sequence of *M. anatis*.

*Mycoplasma anatis* was identified to be pathogenic to domestic and wild ducklings and eggs and could be isolated from the respiratory tracts, sinuses, and cloaca of waterfowl (11). *M. anatis* infection can cause clinical disease of the respiratory disease, reduced hatchability, conjunctivitis, rhinitis, sinusitis, tenosynovitis, arthritis, and growth retardation (11). Recently *M. anatis* infection frequently occurs in conjunction with *Escherichia coli*, resulting in large mortalities and great economic loss for duck farms in China (6, 13).

We sequenced the genome of *M. anatis* type strain 1340, a virulent strain that was isolated from aerocysts and sinuses by Roberts in 1964 (10). The genome sequence was performed by the Genome Sequencer FLX Titanium platform in Shanghai, China (8). Putative protein-coding sequences were determined by combining the prediction results of the Glimmer 3.02, Genemark, and Z-Curve programs (2). Tandem repeats, tRNA genes, and rRNA genes were detected by the tandem repeats finder, tRNAscan, and RNAmmer, respectively (1, 5, 7). Each gene was functionally classified by searching translated open reading frames (ORFs) against sequences in the COG (12) and KEGG (4) databases.

*M. anatis* strain 1340 was found to be a 928,687-bp chromosome with a G+C content of 26.64%, and 88.74% of coding sequences assembled into 44 contigs. A total of 778 protein-coding genes are predicted, with an average length of 1,059 bp. The genome includes 62 tandem repeats, 14 pseudogenes, 4 rRNA loci, and 33 tRNA genes. Analysis of protein secretion revealed the presence of a truncated Sec-SRP protein secretion system, consisting of SecD, SecY, SecA, YidC, FtsH, and Ffh. Pathway analyses indicated that *M. anatis* strain 1340 has an incomplete or missing arginine and proline metabolism as well as tricarboxylic acid cycle. A predicted set of genes encoding phosphotransferase systems (PTS) were identified in the genome of *M. anatis* 1340, supporting its utilization of various sugars, including glucose, d-glucosamine, cellobiose, and fructose. *M. anatis* strain 1340 encodes a hypothetical protein (GIG_00240) homologous with SdrD of *Staphylococcus pseudointermedius* and *Staphylococcus aureus*, which contributed to the ability to adhere to squamous nasal epithelial cells (3). Interestingly, this protein contained two tandem repeat sequences, ACAACCATCTAACAA in 5.3 copies and CCAA ACAACCGTGAAACCAACATCAAC in 3.3 copies, which might be involved in phase switching or antigenic variation (15). Additionally, genes encoding two LcID family outer membrane proteins (GIG_0075 and GIG_01785), with 30% identity to each other, were identified in *M. anatis* strain 1340. The LcID protein has been shown to contribute to the modification of phase-variable phosphorylcholine, which is strongly implicated as a virulence factor and may aid the ability of bacteria to adhere to epithelial cells (9, 14).

This is the first genome sequence of the *M. anatis* species, which will provide the basis for a better understanding of the pathogenicity-determining mechanisms and genetic background for future studies.

**Nucleotide sequence accession number.** The genome sequence of *Mycoplasma anatis* strain 1340 was deposited at DDBJ/EMBL/GenBank and assigned accession number AFVJ00000000.

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**REFERENCES**


