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Genome Sequence of *Mycoplasma ovipneumoniae* Strain SC01▽

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***Mycoplasma ovipneumoniae* is associated with chronic nonprogressive pneumonia in both sheep and goats. Studies concerning its molecular pathogenesis, genetic analysis, and vaccine development have been hindered due to limited genomic information. Here, we announce the first complete genome sequence of this organism.**

Mycoplasma ovipneumoniae is considered to be a cause of nonprogressive pneumonia of both sheep and goats (1, 4, 7). As well as causing disease in its own right, *M. ovipneumoniae* predisposes animals to invasion by more serious respiratory pathogens, such as *Mannheimia haemolytica*, *Pasteurella*, and parainfluenza 3 virus (3, 5). Although *M. ovipneumoniae* is an important concern in the sheep and goat industry, little genomic information is available. Therefore, we sequenced the complete genome of *M. ovipneumoniae* to facilitate related studies in the future.

M. ovipneumoniae strain SC01 was isolated from the lung of a goat with pneumonia in Sichuan Province, China. Genomic DNA was extracted and sequenced using the Illumina GA. We constructed a 350-bp library and obtained 216.12 Mb of clean reads (97.69% paired-end reads). The reads were assembled using SOAP de novo (6). Gene prediction was performed using Glimmer3.0. rRNAs were analyzed with rRNAmmer. tRNA sequences were predicted by tRNAscan-SE. The genes were annotated through Blast searches in the databases Swiss-Prot and TrEMBL (release 2010-04), COG (version 2.0), KEGG (release 48.2), and NCBI-NR (release 2010-8-7).

The *M. ovipneumoniae* SC01 genome is 1,020,601 bp in length, with a GC content of 28.85%. The genome contains 864 putative coding sequences (CDSs) with an average gene length of 950 bp, and the mean coding percentage is 80.48%. There is only a single 16S-23S rRNA operon, and the 5S rRNA gene is separate from the 16S-23S rRNA operon. A total of 30 tRNA genes were identified. One prominent feature of the SC01 genome is the frequent usage of UUG as initiation codon. The number of UUG initiation codons is as high as 187, and these codons account for 21.6% of all initiation codons, which is the highest percentage among the mycoplasma genome sequences available so far.

M. ovipneumoniae strain SC01 contains several recognizable genes likely to be involved in virulence. Two proteins are highly similar to bacterial toxins, hemolysin A (*hlyA*) and hemolysin C (*hlyC*). They are also present in other mycoplasmas, such as *M. hyopneumoniae*, *M. capricolum*, and *M. conjunctivae* (2), although their contribution to pathogenicity in *Mycoplasma* species is unclear. Niang et al. (7) reported the correlation between ciliostasis induced by *M. ovipneumoniae* and hydrogen peroxide production. We identified three genes, *glpF*, *glpK*, and *glpD*, involved in glycerol import and production of H_2O_2 and reactive oxygen species. *Mycoplasma* infection depends on adherence to host epithelial cells. *M. ovipneumoniae* SC01 possesses at least 8 CDSs encoding proteins homologous to adhesin-like proteins of *M. hyopneumoniae* which is phylogenetically closely related to *M. ovipneumoniae* (8), including three homologues of P102-like protein, two homologues of adhesin like-protein P146, and one homologue to each of P97-like protein, adhesin, and P76 protein.

This is the first complete genome sequence of *M. ovipneumoniae*.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession AFHO00000000. The version described in this paper is the first version, AFHO01000000.

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REFERENCES

1. **Besser, T. E., et al.** 2008. Association of *Mycoplasma ovipneumoniae* infection with population limiting respiratory disease in free-ranging Rocky Mountain bighorn sheep (*Ovis canadensis canadensis*). J. Clin. Microbiol. **46:**423–430.
2. **Calderon-Copete, S. P., et al.** 2009. The *Mycoplasma conjunctivae* genome sequencing, annotation and analysis. BMC Bioinformatics **10**(Suppl. 6)**:**S7.
3. **Dassanayake, R. P., et al.** 2010. *Mycoplasma ovipneumoniae* can predispose bighorn sheep to fatal *Mannheimia haemolytica* pneumonia. Vet. Microbiol. **145:**354–359.
4. **Goltz, J. P., S. Rosendal, B. M. McCraw, and H. L. Ruhnke.** 1986. Experimental studies on the pathogenicity of *Mycoplasma ovipneumoniae* and *M. arginini* for the respiratory tract of goats. Can. J. Vet. Res. **50:**59–67.
5. **Jones, G. E., J. S. Gilmour, and A. G. Rae.** 1982. The effect of *Mycoplasma ovipneumoniae* and *Pasteurella haemolytica* on specific pathogen-free lambs. J. Comp. Pathol. **92:**261–266.
6. **Li, R. Q., et al.** 2009. SOAP2: an improved ultrafast tool for short read alignment. Bioinformatics **25:**1966–1967.
7. **Niang, M., et al.** 1998. Field isolates of *Mycoplasma ovipneumoniae* exhibit distinct cytopathic effects in ovine tracheal organ cultures. J. Vet. Med. Ser. A **45:**29–40.
8. **Pettersson, B., M. Uhlén, and K.-E. Johansson.** 1996. Phylogeny of some mycoplasmas from ruminants based on 16S rRNA sequences and definition of a new cluster within the hominis group. Int. J. Syst. Bacteriol. **46:**1093–1098.

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