



Complete Genome Sequence of *Mycoplasma bovirhinis* Strain HAZ141_2 from Bovine Nasal Discharge in Japan

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ABSTRACT *Mycoplasma bovirhinis*, a mycoplasmal species involved in bovine respiratory diseases, is also a commensal microorganism that inhabits the bovine respiratory and reproductive organs. We present the complete 948,039-bp genome sequence of *M. bovirhinis* strain HAZ141_2, which was isolated from bovine nasal discharge in Japan.

Mycoplasma bovirhinis is a commensal microorganism that inhabits the bovine respiratory and reproductive organs and can become a secondary cause of the calf pneumonia complex at the same time (1, 2). Mycoplasmal calf pneumonia has been increasing in prevalence throughout the world along with the dissemination of large-scale livestock management and high stocking density, and the economic loss caused by this condition is considerable (3). Although the whole-genome sequences of many mycoplasma species that cause calf pneumonia have already been reported, i.e., *M. bovis genitalium* (4), *M. bovis* (5), and *M. dispar* (GenBank accession no. CP007229), that of *M. bovirhinis* has not yet been reported. Hence, we present here the whole-genome sequence of strain HAZ141_2, which was isolated in 2008 from the nasal discharge of a coughing calf in Japan.

The total genomic DNA from *M. bovirhinis* strain HAZ141_2 was prepared and subjected to 454 titanium sequencing at Iwate University, Morioka, Japan. The resulting reads were assembled *de novo* using GS De Novo Assembler software v2.7 (Roche), yielding 109 contigs with 108.5× coverage. An analysis of the contig ends together with PCR amplification and amplicon cloning showed that the 948,039-bp genome had a closed-ring structure. After performing an initial automated annotation using Microbial Genome Annotation Pipeline v2.20 at the DNA Data Bank of Japan (<http://migap.ddbj.nig.ac.jp/mgap/jsp/index.jsp>) (6–8), we carried out manual curation, followed by verification of potential pseudogenes by PCR and Sanger sequencing. We confirmed 629 open reading frames, 37 pseudogenes, 31 tRNAs, three sets of 16S rRNA and 23S rRNA, and two sets of 5S rRNA in this genome sequence. The guanine-cytosine content was 28.24%.

The amino acid sequences of most genes containing rRNA genes in *M. bovirhinis* HAZ141_2 exhibited high similarity to those of the genes encoded by *M. canis* (accession no. CP014281). Furthermore, a large chromosome insertion (from MBVR141_0922 to MBVR141_1042, 53.5 kb) was confirmed in this strain.

With respect to the genes of proteins involved in the production of reactive oxygen species (ROS), which have been suggested to be important mycoplasmal etiologic agents (9), the genes of proteins involved in the membrane-located ATP-binding cassette transporter system, i.e., glycerol ABC transporter ATP-binding protein (MBVR141_0395) and glycerol ABC transporter permease (MBVR141_0397,

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MBVR141_0665, MBVR141_0666), have been confirmed in this genome. Moreover, the genes of proteins involved in glycerol transporter (MBVR141_0783, MBVR141_0897), glycerol kinase (MBVR141_0898), and glycerol-3-phosphate dehydrogenase (MBVR141_0899) have also been confirmed in this genome, so the present strain seems to be able to produce ROS (9).

In this genome, some genes of proteins involved in the synthesis of capsular polysaccharides (galactan), which have been suggested to be important mycoplasmal etiologic agents, were absent (i.e., phosphomannomutase, UTP-glucose-1-phosphate uridylyltransferase, UDP-glucose 4-epimerase, UDP-galactopyranose mutase, and BcsA glycosyltransferases), so the present strain seems not to produce galactan (10).

The genomic sequence of *M. bovirhinis* will provide a foundation for future research on this species. Ultimately, it is hoped that the present study will contribute to the reduction of mycoplasmal bovine diseases.

Accession number(s). This complete genome sequence has been deposited at DDBJ/EMBL/GenBank under accession no. [AP018135](https://doi.org/10.1128/genomeA.01554-16).

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