Complete Genome Sequence of *Mycoplasma capricolum* subsp. *capripneumoniae* Strain 9231-Abomsa

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*Mycoplasma capricolum* subsp. *capripneumoniae* is the etiological agent of contagious caprine pleuropneumonia. We report here the complete and annotated genome sequence of *M. capricolum* subsp. *capripneumoniae* strain 9231-Abomsa.

The complete genome consists of a single circular chromosome of 1,017,293 bp, with an overall G+C content of 23.66%. It contains 746 coding sequences (CDSs), 248 pseudogenes, and 43 RNAs. A single CDS coded for the putative transposase OrfA of an insertion sequence similar to IS1296. Two putative prophage proteins were detected. No confirmed clustered regularly interspaced short palindromic repeat (CRISPR) units or integrative conjugative elements were identified. The gap that remains unresolved in the genome sequence of Chinese strain *M. capricolum* subsp. *capripneumoniae* M1601 corresponds to a region containing a cluster of variable lipoprotein genes in the 9231-Abomsa genome sequence. The two rRNA operons presented a high number of interoperon polymorphisms distributed along the entire operon sequences, including the 23S rRNA gene. This feature, already observed in the 16S rRNA gene, has been used for molecular epidemiology studies (4).

Complete circular annotated genomes are now available for all *Mycoplasma* species belonging to the *Mycoplasma mycoides* cluster (5). This provides the foundation for future studies on genome organization plasticity and comprehensive comparative genomics both intra- and interspecifically.

**Nucleotide sequence accession number**. This whole-genome sequence has been deposited in DDBJ/ENA/GenBank under the accession no. LM995445.

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**REFERENCES**


