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Whole-Genome Sequence of *Mycoplasma bovis* Strain Ningxia-1

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ABSTRACT A genome sequence of the *Mycoplasma bovis* Ningxia-1 strain was tested by Pacific Biosciences (PacBio) single-molecule real-time (SMRT) sequencing technology. The strain was isolated from a lesioned calf lung in 2013 in Pengyang, Ningxia, China. The single circular chromosome of 1,033,629 bp shows differences between complete *Mycoplasma bovis* genome in insertion-like sequences (ISs), integrative conjugative elements (ICEs), lipoproteins (LPs), variable surface lipoproteins (VSPs), pathogenicity islands (PAIs), etc.

Mycoplasma bovis is the main cause of bovine respiratory disease syndrome. At present, the pathogen is prevalent worldwide, which causes huge economic losses to national cattle industries (1). In 2008, *M. bovis* was isolated from beef cattle in Hubei, China (2). Other places in China, such as Xinjiang, Ningxia, Chongqing, Guizhou, and Qingdao, later reported *M. bovis* isolated from beef cattle and dairy cows (3).

The whole-genome sequence of the *M. bovis* Ningxia-1 strain was isolated in 2013 from the lesioned lung of a beef calf, which was tested using single-molecule real-time (SMRT) technology (4), resulting in approximately 1,262-fold final sequence coverage. The genome of *M. bovis* Ningxia-1 contains a single circular chromosome of 1,033,629 bp, with a GC content of 29.33%. A total of 754 open reading frames (ORFs) were identified, totaling 845,928 bp (maximum length, 9,981 bp; minimum length, 114 bp), and occupied 81.84% of the whole genome, with an average length of 1121 bp and a mean GC content of 29.77%. A total of 577 coding sequence (CDS) genes could be classified into clusters of orthologous groups (COG) families, which have 19 functional categories. Seventy-four pseudogenes were predicted by GeneMarkS+ (5). The genome encodes 6 rRNA and 34 tRNA genes, representing all 20 amino acids.

We found 60 insertion-like sequence (IS) elements that comprised three distinct categories (https://www-is.biotoul.fr). A cluster of 8 variable surface protein (VSP)-related ORFs were found in the genome. Sixty-six lipoproteins (LPs) revealed signatures denoting distinct mutation-based mechanisms of phase variation (6). Of three predicted pathogenicity islands (PAIs) (7) with a lower GC content (8), PAI-1 (463,228 to 485,927) encoded one single-stranded DNA-binding protein and one conjugal transfer protein, TraE, and contained a transposase at the 5′ end. PAI-2 (541731 to 556809) presented an IS*4* and IS*30* family transposase at the 3′ end and contained an IS*1634* family transposase gene. A total of two nucleotidyl transferase AbiEii/AbiGii toxin family proteins and abortive phage infection proteins in PAI-3 (968,698 to 977,477) were without an IS element but still denoted a pathogenicity island. These characteristics may contribute to the emergence of bacterial pathogens with new virulence properties (9).

Accession number(s). This whole-genome sequence assembly has been deposited at GenBank under the accession no. CP023663.

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