



Whole-Genome Sequencing of a *Brucella melitensis* Strain (BMWS93) Isolated from a Bank Clerk and Exhibiting Complete Resistance to Rifampin

Zhi-guo Liu,^{a,b} Xiao-an Cao,^d Miao Wang,^c Dong-ri Piao,^a Hong-yan Zhao,^a Bu-yun Cui,^a Hai Jiang,^a Zhen-jun Li^a

^aState Key Laboratory for Infectious Disease Control and Prevention, National Institute for Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, China

^bInner Mongolia Autonomous Region Comprehensive Center for Disease Control and Prevention, Huhhot, China

^cUlanqab Center for Endemic Disease Control and Prevention, Jining, China

^dState Key Laboratory of Veterinary Etiological Biology, Lanzhou Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Lanzhou, China

ABSTRACT Human brucellosis has become the most severe public health problem in the Ulanqab region of Inner Mongolia, China. *Brucella melitensis* BMWS93 was obtained from a blood sample taken from a bank clerk in the Ulanqab region of Inner Mongolia, China, and antimicrobial susceptibility testing *in vitro* showed no zone of inhibition, which confirmed resistance to rifampin. Therefore, whole-genome sequencing of this isolate was performed to better understand the mechanism of this resistance.

Brucella melitensis is a Gram-negative facultative intracellular pathogen that causes abortion in goats and sheep and Malta fever in humans (1). The disease causes severe morbidity in humans and results in serious economic losses in livestock due to abortion and infertility (2). *B. melitensis* bv. 3 was the predominant biovar in Ulanqab (3). We added 5 ml blood from the bank clerk into brucella agar slope medium at 37°C under microaerobic conditions. BMWS93 was identified as *B. melitensis* bv. 3 and exhibited complete resistance to rifampin *in vitro* (4). Subsequently, *rpoB* gene sequencing demonstrated that *rpoB* gene mutations were not present in this isolate. Here, we report the whole-genome sequence of *B. melitensis* strain BMWS93 from the Ulanqab region of Inner Mongolia, China.

Genomic DNA of BMWS93 was extracted using a QIAamp DNA minikit, according to the manufacturer's instructions. After extraction, sequencing was conducted on a Pacific Biosciences RS II platform utilizing single-molecule real-time (SMRT) technology and a SMRTbell version 1.0 template prep kit for library preparation to determine the complete genomic sequence of *B. melitensis* BMWS93. The average read length was 6,625 bp, and the low-quality reads were filtered out using Trimmomatic version 0.38 (5). The filtered reads were assembled using SMRT Portal (6, 7) to generate scaffolds. The annotation was performed using GeneMarkS (8), RepeatMasker (9), Tandem Repeats Finder (TRF) (10), tRNAscan-SE (11), RNAmmer (12), and PAST (13).

The genome size of BMWS93 is 3.30 Mb distributed over two circular chromosomes of 2.12 and 1.19 Mb, with 57.25% G+C content. Circular chromosomes 1 and 2 consist of 2,126,063 and 1,186,194 bases, respectively. The whole genome contains 3,321 coding genes. There are four types of repeat sequences and three kinds of tandem repeat sequences in the genome of this strain. The relative numbers of long terminal repeats, DNA transposons, long scattered repeat sequences, and short scattered repeat sequences are 15, 10, 4, and 8, respectively. There are 83 tandem repeat sequences, 66 minisatellite sequences, and 1 microsatellite sequence. There are 3 bacterial rRNA types (5S, 16S, and 23S), 2 small RNAs (sRNAs), and 55 tRNA operons. In addition, there were

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Address correspondence to Zhen-jun Li, lizhenjun@icdc.cn.

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11 genomic islands, 2 prophages, and 2 efflux transporter systems in the genome in this strain. Moreover, efflux transporter systems may contribute to this *B. melitensis* isolate's resistance to rifampin (14). A comprehensive bioinformatics analysis could help to better understand the evolution, host specificity, and pathogenicity of *B. melitensis*.

Data availability. The whole-genome sequence of *B. melitensis* strain BMWS93 was deposited at DDBJ/EMBL/GenBank under the accession numbers [CP034103](#) and [CP034104](#) for chromosomes 1 and 2, respectively. The version described in this paper can be found under NCBI BioProject number [PRJNA505925](#) and NCBI BioSample number [SAMN10439570](#). The raw reads of sequenced genomic DNA of *B. melitensis* BMWS93 were deposited in the SRA under accession number [SRR9311569](#).

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