Complete Genome Sequence of *Brucella melitensis* 133, an Isolate of Biovar 1 of Sequence Type 32

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Brucellosis is highly epidemic in China. Of the six classical species, *Brucella melitensis* and biovar 1 are the most represented species and biovar that cause human brucellosis in China. Here, we report the genome sequence of *Brucella melitensis* strain 133, a strain of biovar 1 of sequence type 32.

Brucellosis is a zoonotic disease that is epidemic worldwide. It is classified as a reemerging infectious disease because of its increasing incidence in recent years. *Brucella* is the etiological pathogen of brucellosis. Four out of the six classical species are pathogenic for humans: *B. abortus*, *B. melitensis*, *B. suis*, and rarely, *B. canis*. Brucellosis is epidemic in China, and human cases have been reported in all 32 provinces (3, 7). Since the 1950s, systematic surveys on the endemic distributions and epidemiological characteristics of brucellosis have been carried out in China (3). Human brucellosis was highly endemic from the mid-1950s well into the 1970s, and then the incidence decreased until the mid-1990s, after which it increased sharply. Therefore, brucellosis in China can be divided into three periods, of high incidence (1950 to 1960s), decline (1970 to 1980s), and reemergence (1990 to 2000s). The prevalent species and biovars of *Brucella* also changed greatly during the three incidence periods (3). *Brucella melitensis* and biovar 1 are the most prevalent during high-incidence periods. Multilocus sequence typing (MLST) is a DNA sequence-based typing method used with many different bacterial species to differentiate strains and identify clonal lineages (6). Genotyping of isolates by multilocus sequence typing has shown a number of prevalent sequence types of *B. melitensis* in China (2). Here, we report the genome sequence of *B. melitensis* strain 133, a strain of biovar 1 of the prevalent sequence type, sequence type 32 (ST32).

The genomic DNA of strain 133 was sequenced with an Illumina HiSeq 2000 sequencer using a paired-end protocol. All low-quality bases were trimmed from the sequence reads, and the remaining reads were assembled with the CChbio genomics workbench, version 5.5, by the de novo assembly method. A total of 173 contigs covering a total of 3,265,383 bp was generated. Seventy of the contigs were >10 kb, and 142 were >1 kb in length. The average length of all the contigs was 18.87 kb.

After assembly, the genome sequence was annotated with different tools. Open reading frames (ORFs) were predicted by using the RAST (rapid annotation using subsystem technology) server (1). rRNAs and tRNAs were identified by using RNAmmer (4) and tRNAscan-SE 1.21 (5). The total genome has a G+C content of 57.26% and is composed of 3,285 coding sequences, including 3,236 protein-coding sequences, 45 tRNAs, 1 copy of 5S RNA, 2 copies of large-subunit rRNA, and 1 copy of small-subunit rRNA. The genome sequence was compared with that of *B. melitensis* 16M. Sequencing reads were mapped to the 16M genome sequence, and SNPs (single-nucleic acid polymorphisms) were predicted. The genome sequence of strain 133 is valuable for genome comparisons of *Brucella* strains from different species and biovars, from both China and other countries. Further detailed analysis will be included in a future publication, with results of a full comparison with other strains.

**Nucleotide sequence accession numbers.** The draft genome sequence of *B. melitensis* strain 133 is available in GenBank under accession number AMPA00000000. The version described in this paper is the first version, AMPA01000000.

**REFERENCES**


