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GENOME ANNOUNCEMENT

Genome Sequence of *Brucella melitensis* S66, an Isolate of Sequence Type 8, Prevalent in China

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***Brucella melitensis* is the most-represented *Brucella* species causing human brucellosis in China. Here we report the complete genome sequence of *B. melitensis* strain S66, a representative strain of sequence type 8 (ST8), which is prevalent in China, making it possible to compare the genome sequences of isolates from different countries.**

Brucellae are Gram-negative, facultatively intracellular bacteria that can infect many species of animals and humans (6). On the basis of differences in pathogenicity, host preference, and phenotypic characteristics, six species were classically recognized within the genus *Brucella*, i.e., *Brucella melitensis*, *B. abortus*, *B. suis*, *B. canis*, *B. ovis*, and *B. neotomae*. Of these six species, the first four are pathogenic for humans and *B. melitensis* is the most pathogenic for humans (7). Brucellosis is epidemic in China, and human cases have been reported in all of the provinces. *B. melitensis* is the most prominent species causing human brucellosis in China, accounting for over 80% of the cases (3). Genotyping of isolates by multilocus sequence typing showed that sequence type 8 (ST8) is the most-represented sequence type of *B. melitensis* in China (2). Here we report the genome sequence of *B. melitensis* S66, a representative isolates of ST8. This strain was isolated from the blood of a patient in Jilin Province, one of the highest-incidence areas in China.

The genomic DNA of S66 was sequenced with an Illumina GA IIx Sequencer with the paired-end protocol. All low-quality bases were trimmed from the sequence reads, and the remaining reads were assembled with Clcbio genomics workbench version 4.03 by the *de novo* assembly method. About 1.3 gigabytes of clear data were obtained. The approximate coverage was about 450×. A total of 73 contigs covering a total of 3,287,279 bp were generated. All of the contigs were >200 bp in length. The number of contigs of >1,000 bp was 68, and the total size was 3,284,467 bp.

After assembly, the genome sequence was annotated. Open reading frames (ORFs) were predicted by using the RAST (rapid annotations using subsystems technology) server (1). The rRNAs and tRNAs were identified by using RNAmmer (4) and tRNAscan-SE 1.21 (5). The total genome has a G+C content of 57.28% and is composed of 3,341 coding sequences (CDSs), including 3,290 potential protein CDSs, 47 tRNAs, one 5S RNA copy, two large-subunit rRNA copies, and one small-subunit rRNA copy. The 3,291 ORFs range from 114 to 10,254 bp, and 2,732 of the ORFs are between 300 and 2,000 bp, with only 2 ORFs of >3,000 bp and 557 ORFs of <300 bp. The initial functional assignment of these potential protein CDSs was performed by using RAST. The S66 genome sequence represents the first sequence of a clinical isolate from China. This makes it possible to compare the sequences of strains from China with those of strains from other countries. A further detailed analysis will be published in the near future, with results of a full comparison with other strains.

Nucleotide sequence accession numbers. The draft genome sequence of *B. melitensis* S66 is available in GenBank under accession number AHWB00000000. The version described in this paper is the first version, AHWB01000000.

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