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# Whole Genome Sequences of Four *Brucella* Strains▽

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***Brucella melitensis* and *Brucella suis* are intracellular pathogens of livestock and humans. Here we report four genome sequences, those of the virulent strain *B. melitensis* M28-12 and vaccine strains *B. melitensis* M5 and M111 and *B. suis* S2, which show different virulences and pathogenicities, which will help to design a more effective brucellosis vaccine.**

*Brucella melitensis* and *Brucella suis* are Gram-negative, facultative, intracellular pathogens that cause brucellosis, a disease that leads to abortion in livestock, resulting in reproductive failure and severe economic losses. It also causes undulant fever in humans that can be treated only through a prolonged course of antibiotics due to its nature of intracellular infection (2, 7). *Brucella* spp. are potential agricultural, civilian, and military bioterrorism agents (3); for example, *Brucella suis* was the first pathogenic organism weaponized by the U.S. military during the 1950s (14).

*B. melitensis* M28-12 is a virulent strain that was isolated from sheep in China and grown through 12 passages *in vivo* in a guinea pig at the China Institute of Veterinary Drug Control (IVDC). *B. melitensis* M5 and M111 and *B. suis* S2 are three vaccine strains currently being used in China. The strain M5 was attenuated from M28. M111 and S2 were isolated by the IVDC. Strain S2 has been through many passages *in vitro*, more than 100 generations during the last 2 decades, and is the most widely used animal vaccine against brucellosis in China.

Here we present the draft genome sequences of these four *Brucella* strains, with different virulences and pathogenicities, by the whole-genome shotgun strategy using the Illumina Genome Analyzer. For each of the genomes, the coverage was more than 140-fold, and the paired-end reads were assembled by SOAPdenovo (11), which yielded an average of 30 scaffolds.

The annotation was done using Glimmer 3.02 (4), tRNAscan-SE 1.21 (12), RNAmmer 1.2 (9), and Tandem Repeats Finder 4.04 (1). In addition, the contigs were analyzed using the KEGG (8), Pfam (6), COGs (15), and NCBI NR protein databases for genome annotation.

The draft genome sequences of four *Brucella* strains have similar sizes, approximately 3.29 Mb, and contain 3,228 (S2) to 3,622 (M111) predicted genes, with an overall G+C content of 57.2%. About 86% of the nucleotide sequences are predicted to be coding sequences, among which single copies of 5S, 16S, and 23S rRNA genes are confirmed and a set of 48 copies of tRNA genes were determined as well. The number of repeated regions for each of the genomes varies from 81 (S2) to 90 (M111).

Comparative genomic analyses were performed using the genome sequences of *B. melitensis* 16 M (5) and *B. suis* 1330 (13) as references. We found a total of 1,370 single-nucleotide polymorphisms (SNPs) for M5, M28-12, and M111 by using Burrows-Wheeler Aligner (10). There are 89 SNPs between the vaccine strains M5 and M111 and virulent strain M28-12 and 61 SNPs between *B. suis* 1330 and S2, which may contribute to the attenuation of vaccine strains. Future studies of these genomic polymorphisms will help to identify molecular factors that could influence the brucellosis vaccines' clinical aspects, including safety, immunogenicity, and protective efficacy, that can be used for novel and more effective vaccine design.

**Nucleotide sequence accession numbers.** The whole-genome shotgun sequences have been deposited at DDBJ/EMBL/GenBank under the accession numbers AFEZ00000000, AFFA00000000, AFFB00000000, and AFFC00000000 for *B. melitensis* M5, M28-12, and M111 and *B. suis* S2, respectively.

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