JB Journals.ASM.org

GENOME ANNOUNCEMENT

Complete Genome Sequence of *Brucella suis* VBI22, Isolated from Bovine Milk

Hongseok Tae,[a] Shamira Shallom,[a] Robert Settlage,[a] Gregory N. Hawkins,[b] L. Garry Adams,[c] and Harold R. Garner[a]

Virginia Bioinformatics Institute, Virginia Tech, Blacksburg, Virginia, USA[a]; Texas Animal Health Commission, State-Federal Diagnostic Laboratory, Austin, Texas, USA[b]; and Department of Veterinary Pathobiology, College of Veterinary Medicine, Texas A&M University, College Station, Texas, USA[c]

***Brucella suis* is the causative agent of swine brucellosis and is known to be able to infect several different hosts, including cattle, dogs, and horses, without causing disease symptoms. Here we report the complete genome sequence of *Brucella suis* VBI22, which was isolated from raw milk from an infected cow.**

Brucella is a category B priority pathogenic bacterium causing zoonotic disease in domestic animals (4). The genus is further classified into several species based on host preference and phenotypic characteristics. *Brucella suis* causes swine brucellosis, resulting in reproductive losses, but it is also known to be able to infect several other hosts, including cattle, dogs, and horses, without causing significant disease symptoms in these secondary host animals (1). Currently, the complete genome sequences of two strains of *Brucella suis*,*Brucella suis* 1330 (7) and *Brucella suis* ATCC 23445 (http://www.ncbi.nlm.nih.gov/bioproject/59015), are publically available. Here, we report the complete genome sequence of the *Brucella suis* VBI22 strain isolated from raw milk from an infected cow in Texas.

Genomic DNA was sequenced via the Illumina GAIIx sequencer following the standard Illumina 76-cycle paired-end protocols generating 24,600,000 sequence read pairs (49,200,000 reads) per sample. All low-quality bases (<0.99 of quality score) were trimmed from the sequence reads, and contig sequences were assembled using two *de novo* assemblers, AByss (6) and CLCbio genomics workbench. The contig sequences were aligned to a consensus sequence generated from the reads mapped by BWA (5) to the *Brucella suis* 1330 reference sequence (7). The aligned sequences were revised iteratively by a novel iterative mapping-assembly method (H. Tae, R. Settlage, S. Shallom, I. Sethi, G. N. Hawkins, L. G. Adams, and H. R. Garner, submitted for publication). The final output of this assembly is composed of two chromosomes containing 2,108,637 and 1,207,451 bases each.

After assembly, we annotated the genome of this assembly by comparing the nucleotide sequences of annotated genes encoding proteins, tRNAs, and rRNAs found within all published *Brucella* references using BLAST. If the length of a BLAST hit was consistent with the length of the corresponding gene, the gene was used as a reference for the annotation. We gave higher priority to genes of *Brucella suis* 1330 when choosing among several potential annotations. If the lengths of the BLAST hit and the gene of *Brucella suis* 1330 were different, genes of other species having the lowest number of mismatches to the assembled genome sequence were used for annotation. When a frameshift was identified at a gene position, the annotation from the RAST annotation server (2) was used for the position. This process resulted in annotations of 3,270 protein-encoding genes, 55 tRNA genes, and 9 rRNA genes.

The *Brucella* genome contains an IS*711* transposon element that is often used in fingerprinting *Brucella* species samples (3). While *Brucella suis* 1330 and *Brucella suis* ATCC 23445 contain 7 and 13 *IS711* copies, respectively, *Brucella suis* VBI22 has 8 copies. All 7 IS*711* loci in the *Brucella suis* 1330 genome are observed in the genomes of the ATCC 23445 and VBI22 strains. *Brucella suis* VBI22 has an additional IS*711* locus right after the stop codon of the BSVBI22_A1627 gene, which has not yet been previously observed in any sequenced *Brucella* species.

Nucleotide sequence accession numbers. The genome sequence of *B. suis* VBI22 is available in GenBank under accession numbers CP003128 and CP003129.

ACKNOWLEDGMENTS

This work was supported by the Virginia Bioinformatics Institute director's fund and the U.S. Department of Homeland Security through the National Center of Excellence for Foreign Animal and Zoonotic Disease Defense at Texas A&M University (subaward 570636 from DHS 2007-ST-061-000002).

Genomic DNAs from *Brucella* field isolates were kindly provided by Texas Animal Health Commission (TAHC) and Texas A&M University. The Core Laboratory Facility and the Data Analysis Core at Virginia Bioinformatics Institute kindly sequenced the genomic DNAs and assembled contigs, respectively.

REFERENCES

1. **Alton GG.** 1990. *Brucella suis*, p 411–422. *In* Animal brucellosis. CRC Press, Boca Raton, FL.
2. **Aziz RK, et al.** 2008. The RAST Server: rapid annotations using subsystems technology. BMC Genomics **9**:75.
3. **Bricker BJ, Halling SM.** 1994. Differentiation of *Brucella abortus* bv. 1, 2, and 4, *Brucella melitensis*, *Brucella ovis*, and *Brucella suis* bv. 1 by PCR. J. Clin. Microbiol. **32**:2660–2666.
4. **Glynn MK, Lynn TV.** 2008. Brucellosis. J. Am. Vet. Med. Assoc. **223**:900–908.
5. **Li H, Durbin R.** 2009. Fast and accurate short read alignment with Burrows-Wheeler transform. Bioinformatics **25**:1754–1760.
6. **Simpson JT, et al.** 2009. ABySS: a parallel assembler for short read sequence data. Genome Res. **19**:1117–1123.
7. **Tae H, et al.** 2011. Revised genome sequence of *Brucella suis* 1330. J. Bacteriol. **193**:6410.

Received 21 November 2011 **Accepted** 30 November 2011

Address correspondence to Harold R. Garner, garner@vbi.vt.edu.

doi:10.1128/JB.06556-11