Complete Genome Sequence of *Brucella abortus* A13334, a New Strain Isolated from the Fetal Gastric Fluid of Dairy Cattle

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Brucella abortus **is a major pathogen that infects livestock and humans. A new strain of** *B. abortus* **(A13334) was isolated from the fetal gastric fluid of a dairy cow, with the aim of using it to compare genetic properties, analyze virulence factor, and survey the epidemiological relationship to other** *Brucella* **species. Here, we report the complete and annotated genome sequence of** *B. abortus* **A13334.**

Brucellosis, caused by a group of Gram-negative bacteria of the genus *Brucella*, is one of the major reproductive disorders afflicting goats, cattle, swine, dogs, and sheep (2, 8). *Brucella abortus* causes brucellosis in dairy cattle (1, 6). Of the *Brucella* spp., *B. arbortus* is second only to *B. melitensis* in that it could be transmitted to humans. However, whole-genome sequences are available only for three known strains, namely, *B. abortus* Rb51, *B. abortus* 9-941, and *B. abortus* 2308.

B. abortus A13334 is a newly isolated strain derived from the fetal gastric fluid of an infected dairy cow in Gyeonggi, Yangpyeong, Republic of Korea. The complete genome sequence of *B. abortus* A13334 was determined using a combination of shotgun and mate-paired sequencing on a Genome Sequencer FLX platform (7). Draft assemblies were based on 458,456 total reads. We generated 85,443 paired-end reads using the Newbler assembler (Roche) and produced 28 large contigs (N_{50} contig size was approximately 251.4 kb), which were then assembled into 6 scaffolds (N_{50} scaffold size was approximately 777.5 kb). The complete genome sequence was generated by assembling the 6 scaffolds in comparison with chromosomes I and II (ChrI and ChrII) of the nearly contiguous strain *B. abortus* S19 (GenBank accession no. NC010742.1 [ChrI] and NC010740.1 [ChrII]) using the phrap assembler (4, 5). Glimmer 3 was used to identify proteins of known function (3). The annotations and classifications were determined using gene ontology analyses.

The genome of *B. abortus* A13334 is 3.3 megabases and is composed of 2 chromosomes of 2,119,726 (ChrI) and 1,162,259 (ChrII) base pairs in length, with each chromosome having a G+C content of approximately 57%. The genome has 3,338 predicted coding sequences, of which 2,182 are in ChrI and 1,153 are in ChrII. Approximately 85% to 87% of the nucleotides in both chromosomes are predicted to encode proteins. The genome contains 55 tRNA genes (41 in ChrI and 14 in ChrII) and 9 rRNA genes (6 in ChrI and 3 in ChrII).

As brucellosis causes reproductive failure, the whole-genome sequence of *B. abortus* A13334, isolated directly from the fetuses of infected animals, may provide deeper insight into the virulence of *Brucella* than the previously sequenced virulent strains. *B. abortus* A13334 evidently has more coding sequences (approximately 152 more in ChrI and 98 more in ChrII) than *B. abortus* 9-941. The comparison of the coding regions of strain A13334 with those of the virulent strain 9-941 and the vaccine strain Rb51 revealed that this newly sequenced strain had 48 unique genes. The percentages

of coding sequence similarity of vaccine strain Rb51 with the virulent strains 9-941 and A13334 are 83% and 98%, respectively. Our genomic data, in conjunction with the genome sequences of other virulent and vaccine strains, may contribute to the generation of a "road map" that will ultimately facilitate the understanding of the mechanisms involved in brucellosis.

Nucleotide sequence accession numbers. The complete genome sequence of *B. abortus* strain A13334 was deposited in GenBank under the accession no. CP003176.1 for ChrI and CP003177.1 for ChrII. More detailed annotations are available in the GenBank database.

ACKNOWLEDGMENT

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