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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Brucella canis* Strain HSK A52141, Isolated from the Blood of an Infected Dog

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***Brucella canis* infection can be clinically inapparent in dogs, and when infection goes unnoticed, there is a chance for dog-to-human transmission. A new strain of *B. canis* was isolated from the blood of an infected dog in order to analyze the pathogenic mechanism, compare genetic properties, and develop new genetic tools for early diagnosis of canine brucellosis. Herein, we report the complete genome sequence of the strain *B. canis* HSK A52141. This is the second complete genome sequence and biological annotation available for a member of *B. canis*.**

Brucella canis is a major cause of canine brucellosis, leading to infertility in male dogs and abortion in female dogs (8). The clinical symptoms of infection may not be apparent in animals that are reproductively serene. However, the infected animals are capable of transmitting it to humans (5). *B. canis* is a small, Gram-negative bacterium that has either a rough or a mucoid outer membrane (4). Whole-genome sequence information is available for one etiological strain of canine brucellosis, *B. canis* ATCC 23365. Herein, we report the complete genome sequence of a pathogenic strain, *B. canis* HSK A52141, isolated directly from the blood of an infected dog in Hwasung, Geyonggi, Republic of Korea.

The complete genome sequence of *B. canis* HSK A52141 was determined using 454 pyrosequencing technology on a Genome Sequencer FLX platform (6). Draft assemblies were based on 450,358 total reads. The 82,900 paired-end reads generated were assembled into 6 scaffolds with a mean size of 543 kb using the Newbler Assembler (Roche). The complete genome sequence was then obtained by assembling the 6 scaffolds in conjunction with chromosomes I (ChrI) and II (ChrII) of the previously sequenced strain *B. canis* ATCC 23365 (GenBank accession numbers CP000872.1 [ChrI] and CP000873.1 [ChrII]) using the Phrap assembler (2, 3). Glimmer 3 was used to identify proteins of known function (1). The annotations and classifications were performed according to the Gene Ontology analyses.

The genome of *B. canis* HSK A52141 is 3.3 Mb and is composed of 2 chromosomes that are 2,102,716 (ChrI) and 1,170,489 (ChrII) base pairs in length. The G+C content of each chromosome is approximately 57%. The genome has 3,276 predicted open reading frames (ORFs), of which 2,125 are in ChrI and 1,151 are in ChrII. Approximately 85% to 87% of nucleotides in both chromosomes are predicted to code for proteins. The genome contains 55 tRNA (41 in ChrI and 14 in ChrII) and 9 rRNA (6 in ChrI and 3 in ChrII) genes.

The HSK A52141 strain has 69 unique ORFs. Approximately 3,207 ORFs are common between *B. canis* strains ATCC 23365 and HSK A52141. IS*711* transposase, a representative transposase of all *Brucella* species, was found to be completely absent in the strain HSK A52141 (7). In addition, 92% of the ORFs present in HSK A52141 are also present in the bovine brucellosis vaccine strain *Brucella abortus* Rb51, whereas only 82% of ORFs are common between ATCC 23365 and Rb51. The complete genome sequence of this newly sequenced pathogen may provide better insights into the pathogenicity of *B. canis* and may contribute to the development of effective vaccines against bovine and canine brucellosis.

Nucleotide sequence accession numbers. The complete nucleotide sequence of the *B. canis* HSK A52141 strain was deposited in GenBank under accession numbers CP003174.1 and CP003175.1 for ChrI and ChrII, respectively. More-detailed annotations are available in the GenBank database.

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