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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Brucella canis* Strain 118, a Strain Isolated from Canine

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***Brucella canis* infects several species of animals, and canine is the preferred host. Genome sequences of strains from different hosts are valuable for comparative analysis of host adaptation and microevolution. Here, we report the genome sequence of *Brucella canis* strain 118, a strain isolated from canine.**

Brucellosis is an important infectious zoonosis epidemic in many countries. *Brucella* is the etiological pathogen of brucellosis (8). According to host preferences, *Brucella* is divided into six classical species, four of which are pathogenic for humans. *Brucella canis* is the causative agent of canine brucellosis, which causes contagious abortion, orchiepididymitis, and uveitis (6, 7). Dogs infected with *B. canis* appear to be relatively healthy, but persistent bacteremia without fever or symptoms is common (7). Symptomatic human infections are rarely reported because of the low virulence of *B. canis* (9). Different from other *Brucella* species that are highly pathogenic for humans and yield smooth colonies, *B. canis* colonies are naturally rough, making diagnosis of *B. canis* brucellosis difficult. Pathogenic bacteria have the capability to adapt to different environments and hosts through two main mechanisms, expression regulation and genetic changes. Adaptation to different hosts usually results in genetic polymorphisms in the genome; therefore, it will be valuable to decode genome sequences of strains from different hosts, especially the natural hosts of *B. canis* (1, 3). Here, we announce the genome sequence of *Brucella canis* strain 118, a strain isolated from canine.

The genomic DNA of *Brucella canis* strain 118 was isolated and sequenced with a HighSeq 2000 sequencer with a paired-end protocol. The generated sequencing reads were filtered to remove low-quality ones, and the remaining reads were then assembled with CLC Bio Genomics Workbench version 5.5 by the *de novo* assembly method. A total of 154 contigs were generated, 77 of which are >10 kb and 136 of which are >1 kb. The average length of the contigs is 21 kb, and the total length is 3,234,827 bp. The GC% content for the contigs was 57.27%. The final approximate coverage for these contigs was about 170×.

The genome sequence was then annotated with several annotation tools. Open reading frames (ORFs) were predicted by the RAST server (2). The rRNA sequence was predicted by using RNAmmer (4), and tRNAs were identified with tRNAscan-SE 1.21 (5). A total of 3,194 ORFs were predicted, including 3,146 protein coding sequences, 44 tRNAs, one copy of 5S RNA, two copies of large-subunit rRNA, and one copy of small-subunit rRNA. The filtered reads were mapped to the genome sequence of *B. canis* 23365, and small deletions, small insertions, and single-nucleotide variants (SNV) were predicted. A total of 27 small deletions, 3 insertions, and 399 polymorphism sites were identified. This implied that the field strain of *B. canis* isolated from its natural host, canine, is different from the laboratory strain. This difference might result from host adaptation or immune stress from hosts. It will be interesting to compare the genome sequences of *B. canis* isolates from different hosts. Further detailed analysis of the genetic polymorphisms will contribute to understanding their roles in host adaptation and microevolution of *B. canis*.

Nucleotide sequence accession numbers. The draft genome sequence of *B. canis* strain 118 is available in GenBank under accession number AMOZ00000000. The version described in this paper is the first version, AMOZ01000000.

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