

Short Research Communication

# Draft Genome Sequences of Two *Brucella abortus* Strains Isolated from Cattle and Pig

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## Abstract

We report the draft genome sequences of two *Brucella abortus* strains LMN1 and LMN2 isolated from cattle and pig. The LMN1 and LMN2 have the genome size of 3,395,952 bp and 3,334,792 bp, respectively. In addition to the conserved genes of *Brucella*, few novel regions showing similarity to the phages were identified in both strains.

Key words: genome sequence, *Brucella abortus*

*Brucella* species are small, non-motile, facultative, intracellular, Gram negative, coccobacilli (1). Members of *Brucella* cause a zoonotic disease brucellosis which is endemic in many areas throughout the world, causing chronic infections with common outcomes being abortion and sterility in infected animals (2). *Brucella* species are designated based on their host preferences. Cattle are the preferred host of *Brucella abortus* and the economic importance attributed to bovine brucellosis (1). *B. abortus* induces spontaneous abortion in cattle and causes economic and industrial loss. *Brucella* infection was treated with a combination of antibiotics. Though, in its chronic phase, eradication is difficult since *Brucella* spp. are intracellular pathogens, which puts them out of reach of humoral immunity and several antibiotics (3). Hence, whole genome sequencing and genome analysis will help in unravelling the mystery behind brucellosis. Here, we present the draft genome sequence of two strains (LMN1 and LMN2) and its annotation.

We isolated two *B. abortus* strains designated LMN1 and LMN2 from cattle and pig. Genomic DNA

of both the strains was isolated using DNeasy kit (Qiagen, Hilden, Germany). The 16S rRNA sequence of these strains showed 100% similarity with all *Brucella* species. Therefore, species identification was performed by multi locus sequence analysis (MLSA) with 9 loci as previously described (4). The genome was sequenced using an Ion Torrent personal genome machine (Life Technologies, Carlsbad, CA). *De novo* assembly was performed using MIRA (Mimicking Intelligent Read Assembly) version 3.9.18 (5). The genome sequences were annotated using the RAST (Rapid Annotations using Subsystems Technology) server (6) and NCBI Prokaryotic Genomes Annotation Pipeline ([http://www.ncbi.nlm.nih.gov/genome/annotation\\_prok/process/](http://www.ncbi.nlm.nih.gov/genome/annotation_prok/process/)). The genome sequence and assembly information of each strain is summarized in **Table 1**. In total, 3,431 genes were predicted in *B. abortus* LMN1, of which 3,373 were protein-coding genes (encoding 2,603 functional and 770 hypothetical proteins), whereas *B. abortus* LMN2 contains 3,358 genes, of which 3,301 were predicted protein-coding sequences (encoding 2,582 functional

and 719 hypothetical proteins). The rRNAs and tRNAs genes were predicted using RNAmmer (7) and tRNAscan-SE 1.21 (8) respectively. *B. abortus* LMN1 contains 58 RNA genes (52 tRNAs and 6 rRNAs genes) and *B. abortus* LMN2 has 57 RNA genes (52 tRNAs and 5 rRNAs genes).

In *B. abortus* LMN1, ~60 kb of novel region was identified, which encodes 57 genes (13 functional proteins and 44 hypothetical proteins). This region showed 73% identity with *Roseobacter* phage. Similarly, in *B. abortus* LMN2 ~9.5 kb of novel region was identified, which encodes 5 genes (3 conserved mega phage proteins and 2 hypothetical proteins) showed 67% identity with *Sinorhizobium meliloti* phage. In addition, a *Brucella* phage (~59 Kb) was observed in both

*B. abortus* LMN1 (contig 15) and *B. abortus* LMN2 (contig 20). This region showed 91% similarity with *Brucella* phage genome. Further comparative genome analysis between these strains and other *Brucella* strains will help in understanding host adaptation and bacterial microevolution.

## Nucleotide sequence accession numbers

The draft genome sequences of the *Brucella abortus* strains LMN1 and LMN2 have been deposited in DDBJ/EMBL/GenBank under the accession numbers JPHM00000000 and JPHL00000000, respectively. The versions described in this paper are JPHM01000000 and JPHL01000000.

**Table 1** Sequencing and assembly statistics for the two strains of *Brucella abortus*

Strain	Total sequenced bases (Mb)	Total reads	Fold coverage	Average read length (bp)	Total consensus (bp)	No. of contigs	Largest contig (bp)	GC content (%)	Accession number at NCBI
<i>B. abortus</i> LMN1	388.2	1,907,540	117X	196	3,395,952	24	971,337	57.2	JPHM00000000
<i>B. abortus</i> LMN2	279.68	1,209,634	75X	200	3,334,792	25	685,937	57.2	JPHL00000000

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## Competing Interests

The authors have declared that no competing interest exists.

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