**GENOME ANNOUNCEMENT**

**Genome Sequence of Borrelia garinii Strain NMJW1, Isolated from China**

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We announce the draft genome sequence of Borrelia garinii strain NMJW1, isolated from Ixodes persulcatus in northeastern China. The 902,789-bp linear chromosome (28.4% GC content) contains 813 open reading frames, 33 tRNAs, and 4 complete rRNAs.

**Borrelia burgdorferi** sensu lato is known to include 15 genospecies, of which B. burgdorferi sensu stricto, B. afzelii, B. garinii, B. spielmanii, and B. valaisiana are associated with human Lyme disease (3, 10–14). To date, whole-genome sequences of B. burgdorferi from China have not been reported. Here, we report the complete linear chromosome of Borrelia garinii strain NMJW1, isolated from Ixodes persulcatus in the Inner Mongolia Autonomous Region in northeastern China. B. garinii NMJW1, grown in Barbour-Stoenner-Kelly H medium (Sigma, St. Louis, MO) supplemented with 6% rabbit serum at 30°C (2, 15), was sequenced with a combined strategy involving the Roche 454 GS FLX sequencer and Solexa. Using strain B. garinii PBI as a reference, an average 157.52-fold genomic coverage was obtained over 383,310 reads, which were assembled using the Newbler 2.6 assembler (Roche), generating 36 interscaffold and intrascaffold gaps. We resequenced by Solexa sequencing technology to close these gaps and then used SOAPdenovo, version 1.05 (7), to assemble the 9,906,046 pair-end Illumina sequencing reads (3-kb and 500-bp inserts) with 1,097.27-fold genome coverage which were generated by using the Illumina HiSeq2000 system (9). Based on this assembly, the interscaffold and intrascaffold gaps were closed by local assembly. Gene prediction was performed using Glimmer1 (4). The rRNA genes were searched for with tRNAscan-SE2 (8). The rRNA genes were searched for with Rfam3 (6). Protein BLAST4 was run, using the translated coding sequences as a query against the reference sequence (1).

The linear B. garinii NMJW1 chromosome includes 902,789 bp in total (28.4% GC content) and carries 33 tRNAs, 4 complete rRNAs, and 813 open reading frames (ORFs), of which 75% do not code for a hypothetical protein. This strain is highly similar to the B. garinii Bgvr strain (isolated from Russian) and the B. garinii PBI strain (isolated from Germany). The core-gene analysis between B. garinii NMJW1 and B. garinii Bgvr (832 genes) (5) showed that 796 ORFs are conserved, and strain NMJW1 was 97.91% similar to strain Bgvr. In-depth comparative analysis among different species will be the focus of our work.

Comparative analysis of B. garinii NMJW1 with the different Borrelia species and in-depth study of strain NMJW1 can provide major insights into the evolution of Borrelia and explain its taxonomic relationships in China, and new knowledge will be gained from analyzing the genome which will help identify new surface proteins to possibly help prevent, diagnose, and treat Lyme disease.

**Nucleotide sequence accession number.** The complete genome sequence of B. garinii NMJW1 was deposited in GenBank under the accession number CP003866.

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**REFERENCES**


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