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Genome Sequence of *Borrelia garinii* Strain SZ, Isolated in China

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We announce the genome sequence of *Borrelia garinii* strain SZ, isolated from *Dermacentor* ticks collected in northeastern China. *B. garinii* strain SZ carries numerous plasmids, both 10 circular and 9 linear plasmids. The 902,487-bp linear chromosome (28.2% GC content) contains 820 open reading frames, 33 tRNAs, and 4 complete rRNAs. The plasmid cp32-10 contains one clustered regularly interspaced short palindromic repeat (CRISPR) with four repeats.

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Borrelia burgdorferi is the agent of Lyme disease, which is caused by infection with the tick-borne spirochete *Borrelia burgdorferi sensu lato* complex. The species complex currently consists of 20 proposed and confirmed species (http://www.ncbi.nlm.nih.gov/Taxonomy), of which *B. burgdorferi sensu stricto*, *B. afzelii*, *B. garinii*, *B. lusitaniae, B. spielmanii*, *B. valaisiana*, and *B. bissettii* are associated with human Lyme disease (1–3). During recent years, there has been an extraordinary accumulation of knowledge on the genomics of these organisms. To date, whole-genome sequences have been reported for 26 *B. burgdorferi* isolates, including 14 *B. burgdorferi sensu stricto*, 3 *B. afzelii*, and 5 *B. garinii* isolates and 1 *B. bissettii*, 1 *B. valaisiana*, 1 *B. spielmanii*, and 1 *B. bavariensis* sp. nov. isolate (4–9). Since the epidemiological investigation of Lyme disease in 1986, more than 100 *Borrelia* strains have been isolated from 30 provinces of China (10, 11). The whole-genome sequences of *B. afzelii* HLJ01 and *B. garinii* NMJW1 have been reported (7, 8). The whole-genome sequences of other Chinese isolates have not yet been reported.

To further understanding of the genomic information and genetic polymorphisms of *B. burgdorferi* isolates in China, we announce here the whole-genome sequence of *B. garinii* SZ, which was isolated from *Dermacentor* ticks collected in the Heilongjiang Province of China (12) and triggers multisystem pathological damage in mice (13). DNA from a low-passage-number culture was sequenced to minimize plasmid loss, and sequencing proceeded to about 8-fold coverage by use of Illumina HiSeq 2000 technology. Solexa sequencing technology was used to close gaps and exclude scaffolded regions in the sequences, and then CLC Workbench 6.0 was used to *de novo* assemble the 7,068,070 paired-end Illumina sequencing reads. Based on this assembly, the interscaffold and intrascaffold gaps were closed by local assembly. Gene prediction was performed using Glimmer3.02. tRNAScan-SE1.23 was used to search for tRNA genes and RNAmmer1.2 to search for rRNA genes. Protein BLAST was run, using the translated coding sequences as a query against the reference sequence. Clustered regularly interspaced short palindromic repeat (CRISPR) analysis was run by CRT1.2.

Like other *Borrelia* species, this isolate was found to carry numerous plasmids, both linear and circular. The linear *B. garinii* SZ chromosome includes 902,487 bp in total (28.2% GC content) and carries 33 tRNAs and 4 complete rRNAs. On the chromosome are 820 open reading frames (ORFs), of which 35% code for hypothetical proteins. This strain is highly similar to *B. garinii* NMJW1 and *B. garinii* Bgvir. Plasmids cp26, cp32, lp17, lp28, lp36, lp38, lp54, and lp56 are universally present in *B. garinii* SZ, as they are in *B. burgdorferi* isolates, and the overall gene contents of these plasmids are rather similar to those of the plasmids of *B. burgdorferi*. However, *B. garinii* SZ contains more cp32 plasmids than other *B. garinii* isolates; their gene contents vary considerably. The plasmid cp32-10 contains one CRISPR with four repeats (our unpublished data). In-depth comparative analysis among different species is now the focus of our work.

This genome sequence contributes to a solid foundation for understanding *B. burgdorferi sensu lato* diversity and providing clues for the pathogenesis of Lyme disease.

Nucleotide sequence accession number. The *B. garinii* strain SZ genome sequence has been deposited in the NCBI database with the accession number CP007564.

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