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.

*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* and *B. garinii* genome sequences have been reported for 26 isolates and 1 strain, respectively. The whole-genome sequences contribute to a solid foundation for understanding 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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**REFERENCES**

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