Genome Sequence of *Borrelia afzelii* Strain HLJ01, Isolated from a Patient in China

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We report here the genome sequence of *Borrelia afzelii* strain HLJ01, isolated from a patient with Lyme disease in China. It is the first report of the whole genome of a *B. burgdorferi* sensu lato isolate from a human in China.

Human Lyme disease is caused by a number of *Borrelia burgdorferi* sensu lato species. Among these species, *B. burgdorferi*, *B. afzelii*, and *B. garinii* are known causes of Lyme disease in North America and Eurasia (16). Recently, *B. lusitaniae*, *B. spielmanii*, *B. valaisiana*, and *B. bavariensis* sp. nov. have also been isolated from Lyme disease patients (4, 6, 7, 9, 10, 17). To date, genome sequences have been completed for 14 *B. burgdorferi* sensu stricto isolates, as well as for two each *B. afzelii*, two *B. garinii*, one each *B. bisettii*, *B. valaisiana*, and *B. spielmanii*, and one *B. bavariensis* sp. nov. isolate (4, 11, 12). However, a whole-genome sequence of *B. burgdorferi* sensu lato from humans in China has not been reported.

Here, we report the whole genome of a *B. afzelii* isolate (named *B. afzelii* HLJ01) from blood plasma of a Lyme disease patient in Heilongjiang Province, China. The patient was a man of about 40 with a skin lesion, an 8- by 20-cm erythema migrans (EM), on the left trunk. The blood of the patient was extracted for laboratory tests and culture in complete BSK-H medium (Sigma, St. Louis, MO) at 30°C (3, 18). The bacterial whole DNA was sequenced using pyrosequencing technology on an Ion Torrent personal genome machine (PGM) (Life Technologies). An average 260-fold genomic coverage was obtained over 1,256,911 reads, which were assembled using the Newbler 2.5.3 assembler (Roche), generating 142 contigs. Ordering, using the *B. afzelii* Pko genome as a reference (12), left 118 plasmid contigs in draft status, whereas 24 chromosome contigs were closed by reference sequencing. The Glimmer program was used to predict open reading frames (ORFs) (8). The tRNAs were predicted using the tRNAscan-SE program, and rRNAs were predicted using RNAmmer (14, 15). The functional annotation of predicted genes was performed using RAST and xBASE (2, 5, 13). BLAST analysis was used to find orthology in *B. afzelii* HLJ01 (1).

The 905,471-bp linear *B. afzelii* HLJ01 chromosome carries 1,061 ORFs, 32 tRNAs, and three complete rRNAs. The hypothetical protein BafPko_0210 is absent from the *B. afzelii* HLJ01 strain, and a surface-located membrane protein in *B. afzelii* HLJ01. Most of the other genes proved to be orthologous between *B. afzelii* HLJ01 and *B. afzelii* Pko. The exact number of plasmids varies among *Borrelia* species. Here, we completed 4 plasmid sequences which were found by analysis of the contigs using BLAST. All of the plasmids were shown to be orthologous with the plasmids of *B. afzelii* Pko.

The in-depth analysis of these genome sequences will be the

focus of our work and will be useful for attaining a complete understanding of *B. burgdorferi* sensu lato diversity. As the Lyme disease caused by *B. afzelii* is prevalent in China and Europe, these foundational sequencing efforts can contribute to the prevention, diagnosis, and treatment of Lyme disease in Eurasia.

Nucleotide sequence accession number. The complete genome sequence of the *B. afzelii* HLJ01 strain was deposited in GenBank under the accession number CP003882.

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