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GENOME ANNOUNCEMENT

Whole-Genome Sequencing of *Borrelia garinii* BgVir, Isolated from Taiga Ticks (*Ixodes persulcatus*)

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Most Lyme borreliosis cases in Russia result from *Borrelia garinii* NT29 group infection. Borrelias of this group circulate exclusively in *Ixodes persulcatus* ticks, which are seldom found beyond Russia and the far east. Here we report the whole-genome sequence of *Borrelia garinii* BgVir isolated from an *I. persulcatus* female.

Lyme disease, caused by bacteria of the *Borrelia* genus, is the most frequent tick-borne infection in Russia (4). More than a million tick bites of humans were reported in the region last year. About 50% of the ticks investigated were infected with *Borrelia*, primarily of the *B. garinii* NT29 group (1, 2, 7). *Borrelia* bacteria of this group not only present a peculiar clinical picture, common in Russian patients, but are also limited in their inhabitation to Russia and northern China. These are also the only *Borrelia* bacteria that can effectively circulate in *Ixodes persulcatus* (5, 6). Hence, they are often omitted from the most prominent investigations, which usually rely on *Borrelia* strains common in Europe and North America. Here we report the first whole-genome sequence of a *B. garinii* NT29 group (strain BgVir).

BgVir was isolated from an *I. persulcatus* female (2). *Borrelia* cells from the fourth passage on BSK-H media were used to avoid possible plasmid diminution. A rapid fragment library was sequenced on a Roche FLX instrument following the Titanium protocol, resulting in approximately 236 Mb of raw data with a mean read length of 341 nucleotides. A number of subsets of data, differing in coverage and mean read length, were then generated and fed to Newbler v. 2.3 to chase the best contig metrics. A 2× 50-bp mate-paired library with a mean insertion size of 1 kb was additionally sequenced following the ABI SOLiD v.3.5. protocol. To achieve as narrow an insert size distribution as possible, the DNA shearing was followed by additional size selection on an agarose gel. The introduction of different sequencing platforms and library types allowed us to perform scaffolding and error correction in Roche FLX reads, which especially occurred in homopolymer stretches ubiquitous in the *Borrelia* genome. Gap sizes were derived from pairing of SOLiD reads. Local mapping of FLX reads was performed to the ends of each gap, followed by insertion of trimmed unmapped sequences. This operation was repeated until all gaps were closed. Validation and error correction were performed by mapping both the FLX and SOLiD reads on the obtained draft sequence. Full-length sequences of chromosome, linear plasmid lp54, and circular plasmid cp26 were obtained. The rest of the plasmids are represented by 46 scaffolds. The nucleotide sequences were annotated using GeneMark.hmm-PS and Glimmer algorithms.

After alignment was performed, the chromosome nucleotide sequences of *B. garinii* BgVir and *B. garinii* PBi exhibited 98% identity. Most of the single nucleotide polymorphisms (SNPs) detected were synonymous polymorphisms. The most dramatic structural alteration is the insertion into BgVir of the chromosome sequence harboring the KK9_0542 gene locus. The latter is homologous to the inositol monophosphatase gene present in the *B. burgdorferi* B31 genome and absent from the *B. garinii* PBi genome (3).

The most notable feature of the plasmid sequences obtained is the translocation of approximately 5 kb, harboring 8 coding sequences (CDS) of unknown function, to the 5′ end of the lp54 plasmid sequence.

Nucleotide sequence accession numbers. The full annotated sequences of chromosome, linear plasmid lp54, and circular plasmid cp26 are available from GenBank under accession numbers CP003151, CP003202, and CP003201, respectively.

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