



First published October 2010, doi: 10.1128/JB.01158-10

J. Bacteriol. February 2011 vol. 193 no. 4 1018-1020

Whole-Genome Sequences of Thirteen Isolates of *Borrelia burgdorferi*[†]

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ABSTRACT

Borrelia burgdorferi is a causative agent of Lyme disease in North America and Eurasia. The first complete genome sequence of *B. burgdorferi* strain 31, available for more than a decade, has assisted research on the pathogenesis of Lyme disease. Because a single genome sequence is not sufficient to understand the relationship between genotypic and geographic variation and disease phenotype, we determined the whole-genome sequences of 13 additional *B. burgdorferi* isolates that span the range of natural variation. These sequences should allow improved understanding of pathogenesis and provide a foundation for novel detection, diagnosis, and prevention strategies.

FOOTNOTES

Received 28 September 2010.

Accepted 6 October 2010.

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Published ahead of print on 8 October 2010.

Supplemental material for this article may be found at <http://jb.asm.org/>.

American Society for Microbiology

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