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GENOME ANNOUNCEMENTS

Whole-Genome Sequences of Two *Borrelia afzelii* and Two *Borrelia garinii* Lyme Disease Agent Isolates

Sherwood R. Casjens,[1]* Emmanuel F. Mongodin,[2] Wei-Gang Qiu,[3] John J. Dunn,[4] Benjamin J. Luft,[5] Claire M. Fraser-Liggett,[2] and Steve E. Schutzer[6]*

Department of Pathology, Division of Microbiology and Immunology, University of Utah Medical School, Salt Lake City, Utah 84112[1]; Institute for Genome Sciences, University of Maryland, School of Medicine, Department of Microbiology and Immunology, Baltimore, Maryland 21201[2]; Department of Biological Sciences, Hunter College of the City University of New York, 695 Park Avenue, New York, New York 10065[3]; Biology Department, Brookhaven National Laboratory, Upton, New York 11793[4]; Department of Medicine, Health Science Center, Stony Brook University, Stony Brook, New York 11794[5]; Department of Medicine, University of Medicine and Dentistry of New Jersey—New Jersey Medical School, Newark, New Jersey 07103[6]

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Human Lyme disease is commonly caused by several species of spirochetes in the *Borrelia* genus. In Eurasia these species are largely *Borrelia afzelii*, *B. garinii*, *B. burgdorferi*, and *B. bavariensis* sp. nov. Whole-genome sequencing is an excellent tool for investigating and understanding the influence of bacterial diversity on the pathogenesis and etiology of Lyme disease. We report here the whole-genome sequences of four isolates from two of the *Borrelia* species that cause human Lyme disease, *B. afzelii* isolates ACA-1 and PKo and *B. garinii* isolates PBr and Far04.

Human Lyme disease is the most prevalent tick-borne disease in North America, Europe, and far-eastern Asia (11). The bacteria that cause Lyme disease belong to a clade of at least 15 species called *Borrelia burgdorferi* sensu lato or the Lyme disease agent bacterial group. Among these species, *B. burgdorferi* causes human Lyme disease in North America, while in Europe and Asia, *B. afzelii*, *B. garinii*, and *B. bavariensis* sp. nov. are also frequent causes of this disease (9). To date, whole-genome sequences have been reported from 14 *B. burgdorferi* sensu stricto isolates (2, 5, 13) and one unnamed sensu lato species (3), and the chromosome and incomplete plasmid sequences have been reported for one *B. afzelii* and one *B. bavariensis* sp. nov. isolate (6, 7).

To further our understanding of the genetic variation among the *Borrelia* species that cause Lyme disease, we performed whole-genome sequencing to about 8-fold coverage (10) on three human isolates and one bird isolate from Europe: *B. afzelii* isolates PKo (human erythema migrans; Germany) (12) and ACA-1 (human acrodermatitis chronica atrophicans; Sweden) (1) and *B. garinii* isolates PBr (human cerebrospinal fluid; Germany) (12) and Far04 (puffin blood; Faroe Islands, Denmark) (8). Low-passage-number isolates were sequenced to minimize plasmid loss during culture growth. Constraints on funds required that the sequences of the ACA-1, PBr, and Far04 chromosomes remain in draft status, but all the plasmid sequences were closed. The ACA-1, PBr, and Far04 genome annotations were performed using the JCVI Prokaryotic Annotation Pipeline (http://www.jcvi.org/cms/research/projects/annotation-service/overview/), and the genome of strain PKo was annotated using the SOM-IGS annotation engine pipeline (http://ae.igs.umaryland.edu/cgi/ae_pipeline_outline.cgi).

These four genome sequences include 5,151,042 total bp, with an average of 1,287,760 bp/genome. Like other *Borrelia* species, these isolates were found to carry numerous plasmids, both linear and circular, ranging from 7 plasmids in Far04 to 17 in PKo. We note that an average of only 3.25 members of the cp32 family of plasmids were present in these isolates, while *B. burgdorferi* sensu stricto isolates average about 7 members/isolate (3). Plasmids cp26, cp32, and lp54 are universally present in these isolates (with the exception of Far04, which has no cp32 plasmid), as they are in *B. burgdorferi* sensu stricto isolates, and the overall gene contents of these plasmids are rather similar to those of the plasmids of *B. burgdorferi*. In addition, plasmids with predicted lp17 compatibility (4) are present in all four genomes; however, their gene contents as well as the contents of most of the other linear plasmid types vary considerably, due to apparent interplasmid DNA rearrangements (our unpublished data).

* Corresponding author. Mailing address for Sherwood R. Casjens: Department of Pathology, Room 2200 EEJMRB, 15 North Medical Drive East, University of Utah Medical School, Salt Lake City, UT 84112. Phone: (801) 581-5980. Fax: (801) 585-2417. E-mail: sherwood.casjens@path.utah.edu. Mailing address for Steven E. Schutzer: Department of Medicine, University of Medicine and Dentistry of New Jersey-New Jersey Medical School, Newark, NJ 07103. E-mail: schutzer@umdnj.edu.

TABLE 1. *B. afzelii* and *B. garinii* sequence accession numbers

Element[a]	Accession no. for[b]:				Total
	Borrelia afzelii		*Borrelia garinii*		
	PKo (68149)	ACA-1 (19641)	PBr (28625)	Far04 (29573)	
Chromosome	CP002933	ABCU02000001-2[c]	ABJV02000001-5[c]	ABPZ02000001-33[c]	
lp17	CP002942	CP001239	CP001309	CP001315	
lp25			CP001301	CP001317	
lp28-1		CP001238	CP001310	CP001316	
lp28-2	CP002943	CP001244			
lp28-3	CP002944	CP001241	CP001307		
lp28-4	CP002945	CP001249	CP001304		
lp28-7	CP002946	CP001242	CP001311		
lp28-8	CP002947				
lp36			CP001302	CP001314	
lp38	CP002949	CP001246			
lp54	CP002950	CP001247	CP001308	CP001318	
cp26	CP002934	CP001250	CP001305	CP001319	
cp32-1	CP002937	CP001243			
cp32-3	CP002938	CP001237			
cp32-4		CP001240			
cp32-5	CP002939	CP001248	CP001303		
cp32-7	CP002940				
cp32-9	CP002941				
cp32-10	CP002948[d]	CP001245[d]	CP001306	CP001320[d]	
cp32-11	CP002935				
cp32-12	CP002936				
No. of:					
cp32s	7	4	2	0	13
Other circles	1	1	1	1	4
Linear plasmids	9	9	8	6	32
Total plasmids	17	14	11	7	49
Total bp sequenced	1,404,232	1,353,779	1,265,591	1,127,440	5,151,042

[a] Plasmids are named according to their type PFam32 partition and replication protein (4).
[b] Numbers in parentheses are genome project ID numbers.
[c] Draft sequence; contigs not joined.
[d] "lp32-10" plasmid; these plasmids are apparently linear but encode a cp32-10 type PFam32 protein. Their gene content is quite different from that of canonical cp32 plasmids (our unpublished data).

These genome sequences contribute to a solid foundation for understanding *B. burgdorferi* sensu lato diversity and evolution, as well as the development of species- and group-specific diagnostics and vaccines.

Nucleotide sequence accession numbers. These sequences have been deposited in the GenBank database, and their accession numbers are listed in Table 1.

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