Geographic Differences in Genetic Locus Linkages for *Borrelia burgdorferi*

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Borrelia burdorferi genotype in the northeastern United States is associated with Lyme borreliosis severity. Analysis of DNA sequences of the outer surface protein C gene and *rrs-rrlA* intergenic spacer from extracts of *Ixodes* spp. ticks in 3 US regions showed linkage disequilibrium between the 2 loci within a region but not consistently between regions.

Most bacterial pathogens comprise a variety of strains in various proportions. For *Borrelia burgdorferi*, an agent of Lyme borreliosis, strains differ in their reservoir host preferences (*1*), propensities to disseminate in humans (*2*,*3*), and prevalences in ticks by geographic area (*4*,*5*). Strain identification of *B. burgdorferi* now is predominantly based on DNA sequences of either of 2 genetic loci: 1) the plasmid-borne, highly polymorphic outer surface protein (*ospC*) gene, which encodes outer surface protein C (*6*,*7*), or 2) the intergenic spacer (IGS) between the *rrs* and *rrlA* rDNA, here called IGS1. Other loci for genotyping are the plasmid-borne *ospA* gene (*7*) and the rrfA-rrlB rDNA intergenic spacer, here called IGS2 (*8*). The apparent clonality of *B. burgdorferi* was justification for inferring strain identity from a single locus (*9*,*10*), but the extent of genomewide genetic exchange in this species may have been underestimated (*6*).

Given reports of an association between disease severity and *B. burgdorferi* genotype (*2*,*3*), prediction of a strain's virulence potential from its genotype has clinical, diagnostic, and epidemiologic relevance. But is a single locus sufficient for this assessment?

The Study

To investigate this issue, we determined sequences of *ospC* and IGS1 loci, and in selected cases the *ospA* and IGS2 loci, in 1,522 DNA extracts from *B. burgdorferi*–infected *Ixodes scapularis* nymphs collected from the northeastern, mid-Atlantic, and north-central United States during the summers of 2004, 2005, 2006, and 2007, as described (*4*,*11*). We also included results from 214 infected *I. pacificus* nymphs collected in Mendocino County, California (*5*); 20 infected *I. pacificus* adults from Contra Costa County, California (J. Bunikis and A.G. Barbour, unpub. data); and 10 *B. burgdorferi* genomes (strains B31, ZS7, 156a, 64b, 72a, 118a, WI91-23, 94a, 29805, and CA-11.2a), for which sequences are publicly available (www.ncbi.nlm.nih.gov). Multilocus sequence typing (MLST), based on 8 chromosomal housekeeping genes, had been carried out for several strains represented in the extracts (Table) (*4*,*12*). The corresponding MLST types of the 10 genome sequences were assigned by reference to a *B. burgdorferi* MLST database (http://borrelia.mlst.net) (*12*). For this study, we also determined the MLST type of strain CA8.

The methods for 1) DNA extraction from ticks (*11*), 2) PCR amplification of *ospC*, *ospA*, and IGS1 (*7*), 3) amplification of IGS2 (*8*), and 4) amplification of 8 chromosomal loci for MLST (*12*) have been described. Sequences for both strands were determined from either PCR products or cloned fragments with custom primers (*7*). We followed the basic nomenclature of Wang et al. (*13*) until, after exhausting the alphabet, we assigned both a letter and, arbitrarily, the number 3 (e.g., C3) when a new nucleotide sequence differed by >8% from known *ospC* alleles. We distinguished *ospC* variants with <1% sequence difference by adding a lowercase letter, e.g., Da and Db. Except for *ospC* D3 and Oa, novel polymorphisms were confirmed in at least 1 other sample. To simplify IGS1 nomenclature, we numbered types sequentially, beginning with the original 9 types (*7*); *ospA* alleles (*7*) and IGS2 loci were likewise sequentially numbered. The online Appendix Table (www.cdc.gov/EID/content/16/7/1147-appT.htm) provides accession numbers for all sequences, as well as original and revised names for IGS1 sequences.

For 741 *Ixodes* ticks from northeastern and north-central United States or from northern California, 1 *ospC* allele was identified and sequenced. In the remaining samples, we found a mixture of strains or evidence of ≥2 *ospC* and/or ≥2 IGS sequences (*9*). In 678 (91%) of the 741 samples with a single *ospC*, the allele could be matched with particular IGS1 (Table). We identified 9 unique *ospC* sequences: Fc, Ob, Ub, A3, B3, C3, D3, E3, and F3, all from the north-central United States. Alleles H3 and I3 of California were recently reported by Girard et al. (*5*). Of 32 codon-aligned *ospC* sequences, 6 pairs and 1 trio (Fa, Fb, and Fc) differed in sequence by <1% (Figure, panel A). Nine novel IGS1 sequences, numbered 24–31 and 33, were discovered in samples from which *ospC* alleles were determined.

When we confined analysis to samples from northeastern states, we confirmed linkage disequilibrium between *ospC* and IGS1 loci (*7*,*10*,*14*). However, when results from north-central states and California were included, a different picture emerged (Table, Figure, panel B). Most of the

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ospC alleles showed concordance with the chromosomal loci; monophyletic MLST showed either the same *ospC* allele or a minor variant of it. However, in several instances, the *ospC* alleles were linked to different IGS1 sequences, different *ospA* sequences, and/or different MLST with internal nodes in common. We observed this linkage for *ospC* alleles A, G, Hb, and N. In the case of *ospC* Hb, the shared internal node was deep.

Table. Linkages between *ospC* alleles and other loci in *Borrelia burgdorferi* strains*

ospC	IGS1	Geographic region*	Representative cultured isolate or tick sample†	IGS1-*ospC* associations‡	*ospA*	IGS2	MLST§
A	1	1, 2	**B31**	45/52	1	1	1
A	11	2	*2206617*	4/4	22	1	55
A	10	3	CA4, CA6	14/18	23	1	2
Ba	3	1	**64b**, B373	39/41	3	1	7,58,59
Ba	6	2	51405UT	7/9	14	1	30
Bb	16	4	**ZS7**	–	28	–	20
C	24	1	JD1, BL515	10/10	8	5	11
Da	5	1	*516113*	13/14	5	4	38
Db	5	2	*424404*	13/15	18	7	51
Db	19	3	**CA11.2A**	16/16	27	4	70
E	9	1, 2	N40, B348	17/19	9	1	19
Fa	17	1, 2, 3	B156	61/64	3	4	8
Fb	18	2	MI407	14/19	8	6	–
Fc	18	2	*1469205*	7/8	13	6	56
G	26	1	**72a**, MR616	10/11	9	4	14
G	22	2, 3	*1468503*	9/10	21	4	48,49
Ha/Hb	12	1	B509/**156a**	13/13	2	2	4
Hb	12	2	519014UT	56/65	11	2	32
Hb	13	3	CA92-0953	20/20	23	2	6
Ia	7	1	B500, B331	12/16	7	4	15,16
Ia	7	2	**WI91-23**	5/5	11	4	71
Ib	7	3	CA92-1096	–	30	4	17
J	20	1, 2	**118a**	3/5	8	4	34
K	2	1	297	67/68	2	2	3
K	14	2	*149901*	7/10	31	2	–
L	14	2	47703UT	23/25	8	2	29
M	6	1	**29805**	4/4	2	3	12
M	6	2, 3	CA92-1337	16/16	17	3	13
N	4	1	MR661, *500203*	41/41	4	10	9,36
N	23	2	*51108*	8/10	2	1	43
Oa	27	1	*501427*	1/1	–	–	54
Ob	6	2	*2207807*	6/7	2	–	–
T	28	1	23509	16/16	8	4	37
T	29	2	1476702	10/11	20	4	46
Ua	8	1	**94a**, B485	19/19	8	4	18
Ua	8	2	*48802*	4/4	16	4	47
Ua	17	2	*2207116*	4/4	12	10	–
Ub	30	2	*426905*	3/3	8	9	–
A3	14	2	*2206613*	6/6	19	2	–
B3	23	1, 2	*2250201*	3/3	17	1	57
C3	17	2	*50202*	6/9	15	5	–
D3	31	2	*2150902*	1/1	–	–	–
E3	20	2	*2127701*	4/4	8	8	52
E3	21	3	HRT25	12/12	24	–	–
E3	5	3	LMR28	12/12	25	–	–
F3	5	2	*1456802*	8/12	8	4	–
H3	25	3	CA8	37/40	26	4	(72)
I3	17	3	CA11, CA12	5/5	27	4	–

*Regions: 1, northeastern United States; 2, north-central United States; 3, northern California; 4, western Europe; *osp*, outer surface protein; IGS, intergenic spacer; MLST, multilocus sequence typing; –, MLST not determined.
†Tick samples (*4*) are indicated by *italics*; strains with genome sequences are indicated in **boldface**.
‡Number of tick extracts with the listed IGS1 locus (numerator)/number of extracts with the listed *ospC* allele (denominator).
§MLST from (*4*,*12*) or this study (in parentheses).

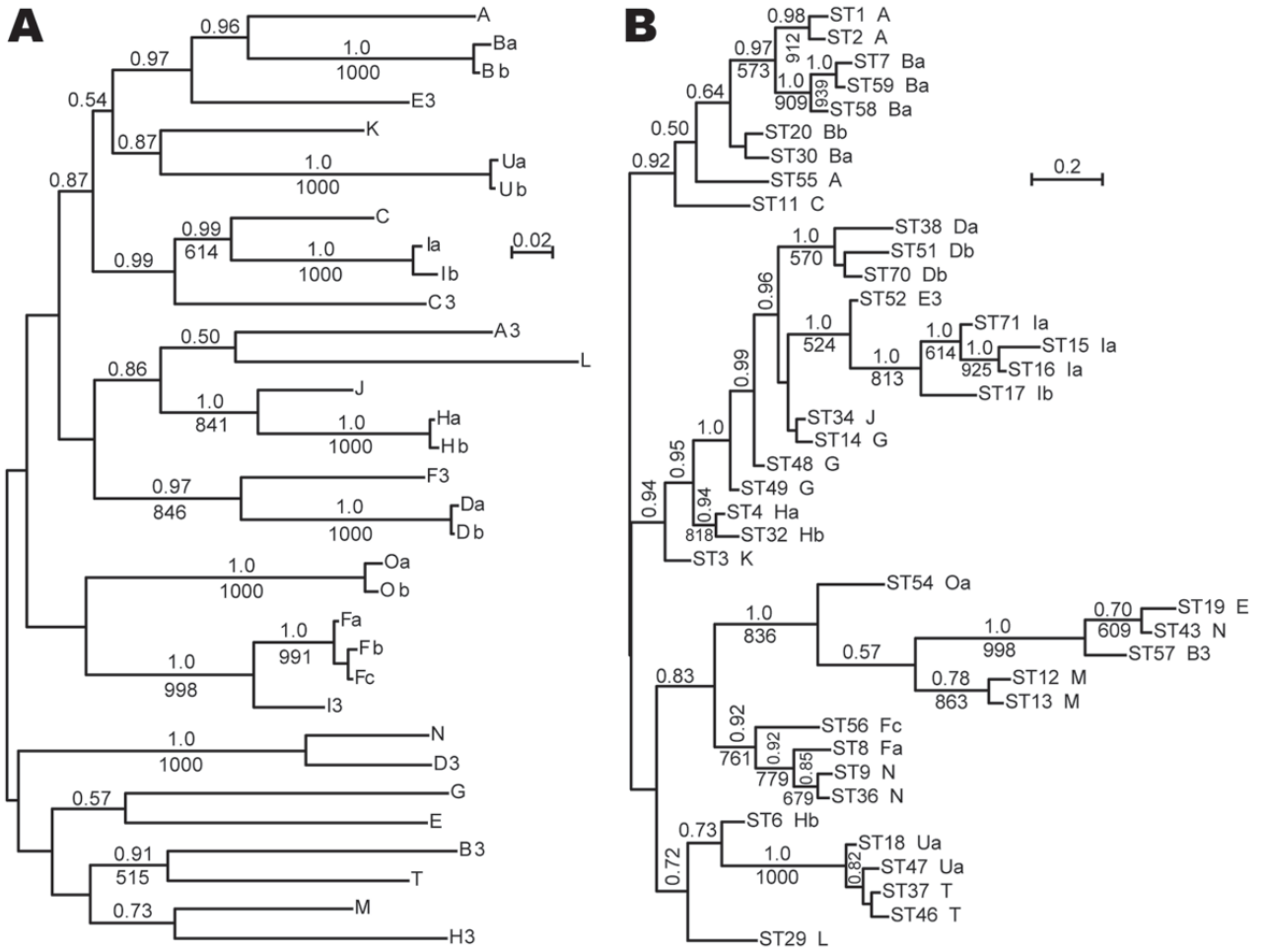

Figure. A) Bayesian and maximum-likelihood phylogenetic inference of outer surface protein C (*ospC*) gene sequences and B) concatenated multilocus sequence typing (MLST) sequences of *Borrelia burgdorferi*. Sequences were aligned by codon. Labels at the tips refer to *ospC* alleles (A) or MLST (ST) and linked *ospC* alleles (B; Table). Consensus phylograms were the output of the MrBayes version 3.1.2 algorithm (http://mrbayes.csit.fsu.edu). There were 500,000 generations with the first 1,000 discarded. Nodes with posterior probabilities of >0.5 are indicated by values above the branches. Below the branches are integer values for nodes with support of >500 of 1,000 bootstrap iterations of the maximum-likelihood method, as carried out with the PhyML 3.0 algorithm (www.atgc-montpellier.fr/phyml). For both data sets and both algorithms, the models were general time reversible with empirical estimations of the proportions of invariant sites and gamma shape parameters. Scale bars indicate genetic distance. GenBank accession numbers for sequences are given in the online Appendix Table (www.cdc.gov/EID/content/16/7/1147-appT.htm).

We applied the Simpson index of diversity, as implemented by Hunter and Gaston (*15*), to the data in the Table to compare the discriminatory power (DP) of genotyping on the basis of a combination of *ospC* and IGS1 sequences with genotyping by 8-locus MLST (*12*). For double-locus typing, there were 43 types were found for 678 strains; DP value was 0.96. For MLST in this data set, 36 types were shown for 554 strains; DP was 0.95. In the study of Hoen et al. in which selection was made for geographic isolation, 37 types were distributed among 78 strains; DP was 0.97 (*4*).

Conclusions

Dependence on a single locus for typing may falsely identify different lineages as the same, especially when the samples come from different regions. Other loci may be as informative as *ospC* or IGS1, but the abundance of extant sequences for these loci justifies their continued use. Uncertainties about the linkage of *ospC* and IGS1 usually can be resolved by sequencing the *ospA* allele (Table). IGS2 provided little additional information in this study.

One interpretation of these findings is that lateral gene transfer of all or nearly all of an *ospC* gene has occurred between different genetic lineages. We previously had not detected recombination at the IGS1 locus on the chromo-

some (*7*), but there may be recombination at other chromosomal loci, as well as plasmid loci (*6*). Besides extending the understanding of the geographic structuring of the *B. burgdorferi* population, the results indicate that the *ospC* allele does not fully represent the complexity of *B. burgdorferi* lineages; thus, inferring phenotypes on the basis of this single locus should be made with caution.

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