

## *Borrelia miyamotoi* in Human-Biting Ticks, United States, 2013–2019

Guang Xu, Chu-Yuan Luo, Fumiko Ribbe, Patrick Pearson, Michel Ledizet, Stephen M. Rich

Author affiliations: University of Massachusetts–Amherst, Amherst, Massachusetts USA (G. Xu, C.-Y. Luo, F. Ribbe, P. Pearson, S.M. Rich); L2 Diagnostics, New Haven, Connecticut, USA (M. Ledizet)

During 2013–2019, *Borrelia miyamotoi* infection was detected in 19 US states. Infection rate was 0.5%–3.2%; of *B. miyamotoi*-positive ticks, 59.09% had concurrent infections. *B. miyamotoi* is homogeneous with 1 genotype from *Ixodes scapularis* ticks in northeastern and midwestern states and 1 from *I. pacificus* in western states.

DOI: <https://doi.org/10.3201/eid2712.204646>

*Borrelia miyamotoi*, a relapsing fever group spirochete (1), was first isolated from *Ixodes persulcatus* ticks in Japan in 1995 (2) and later detected in *Ixodes* ticks in the United States and Europe (3–5). Although *B. miyamotoi* bacteria have been mainly detected in *I. ricinus* species complex ticks that transmit *B. burgdorferi* worldwide, the vector specificity needs further study because investigators have found *B. miyamotoi* in multiple tick species (6). *B. miyamotoi* has 3 geographically distinct genotypes: Asian, European, and American. In the United States, *B. miyamotoi* bacteria have been found in field-collected *I. scapularis* ticks in the northeastern and northern midwestern regions, where the average infection rate is 1.9% (7). However, an expanded geographic study of the prevalence of

*B. miyamotoi* in human-biting ticks, its genotypes, and concurrent infections with other tickborne pathogens is warranted.

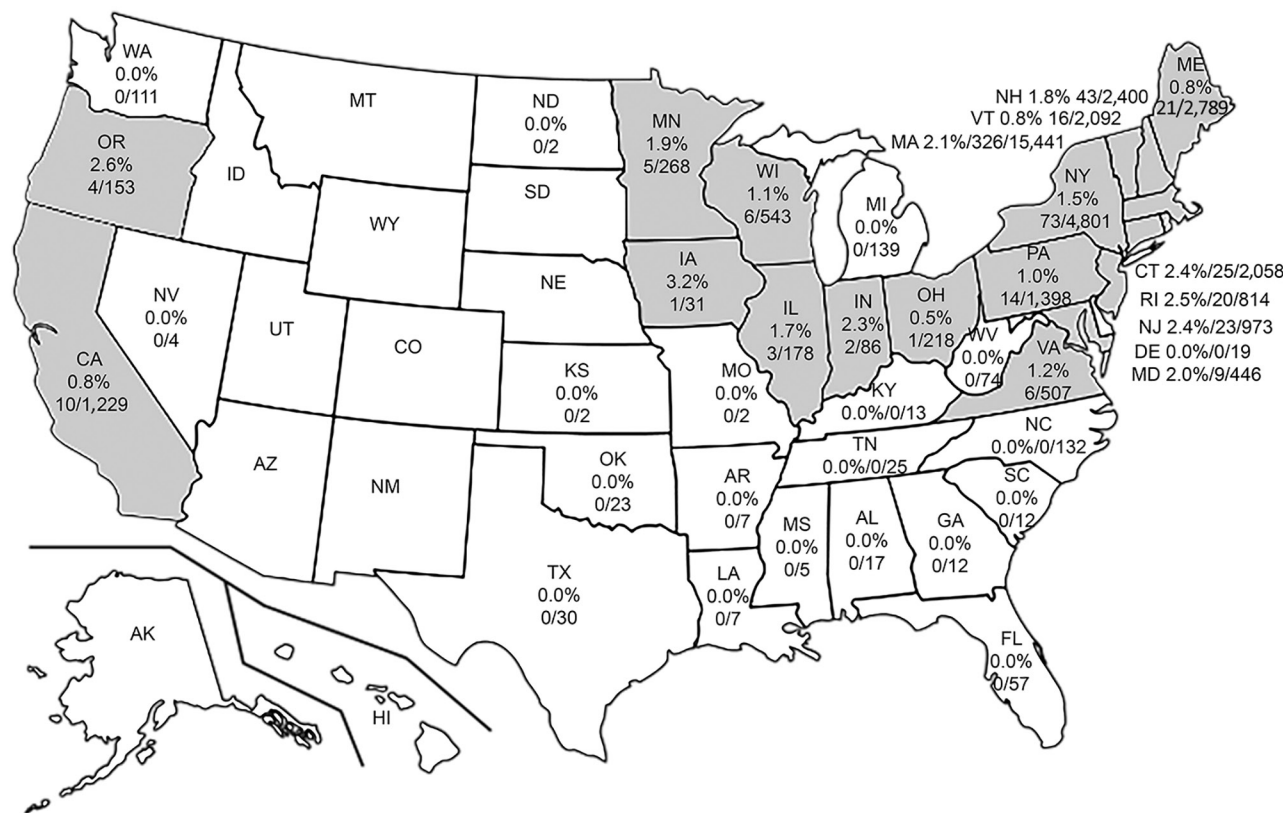
Human-biting ticks were submitted to the public tick testing program at the University of Massachusetts (Amherst, Massachusetts, USA) during May 2013–December 2019. We extracted DNA from individual ticks using the Epicenter Master Complete DNA and RNA Purification Kits (Lucigen, <https://www.lucigen.com>). We performed a species-specific quantitative PCR (qPCR) for differentiation of *I. scapularis* and *I. pacificus* ticks (8). To detect *Borrelia* bacteria, we first applied a genus-specific detection assay, followed by specific qPCR assays for *B. burgdorferi* sensu lato and *B. miyamotoi*. We detected the tickborne pathogens *Anaplasma phagocytophilum*, *Babesia microti*, *B. mayonii*, and *Ehrlichia muris*-like agent (EMLA) by a multiplex qPCR assay targeting different genes. We used a qPCR assay targeting tick 16S mtDNA gene as an internal control (8). We sequenced 3 partial gene fragments, 16S rDNA (16S) (9), flagellin (*fla*) (6), and glycerophosphodiester phosphodiesterase (*glpQ*) (6), for *B. miyamotoi* samples that were positive by qPCR.

We received and tested 39,198 ticks found on humans for *B. miyamotoi* during May 2013–December 2019. Of those, 38,855 (99.12%) ticks originated from the continental United States, comprising 18 tick species (Table). Although *Ixodes* ticks are the main vectors for *B. miyamotoi*, we did not detect *B. miyamotoi* DNA in *I. affinis*, *I. angustus*, *I. cookei*, *I. dentatus*, *I. marxi*, *I. muris*, or *I. spinipalpis* ticks. We detected *B. miyamotoi* in *I. pacificus* (14/1,497, 0.94%) and *I. scapularis* (594/34,621, 1.72%) ticks.

*B. miyamotoi* was found in 19 states; infection rates were 0.5%–3.2% (Figure). In the western

**Table.** Human-biting tick species positive for *Borrelia miyamotoi* and *B. burgdorferi* sensu lato, United States, 2013–2019

Tick species	Total no. tested	No. <i>B. miyamotoi</i> positive	No. <i>B. burgdorferi</i> s.l. positive
<i>Amblyomma americanum</i>	1,167	0	0
<i>A. cajennense</i>	1	0	0
<i>A. maculatum</i>	8	0	0
<i>Dermacentor andersoni</i>	60	0	0
<i>D. occidentalis</i>	91	0	0
<i>D. variabilis</i>	1,060	0	0
<i>Haemaphysalis leporispalustris</i>	2	0	0
<i>H. longicornis</i>	7	0	0
<i>Ixodes affinis</i>	2	0	0
<i>I. angustus</i>	55	0	0
<i>I. cookei</i>	123	0	0
<i>I. dentatus</i>	48	0	7
<i>I. marxi</i>	26	0	0
<i>I. muris</i>	9	0	2
<i>I. pacificus</i>	1,497	14	25
<i>I. scapularis</i>	34,621	594	11,287
<i>I. spinipalpis</i>	63	0	3
<i>Rhipicephalus sanguineus</i>	15	0	0
Total	38,855	608	11,324



**Figure.** *Borrelia miyamotoi* positivity rates in human-biting *Ixodes scapularis* and *I. pacificus* ticks, United States, 2013–2019. Gray shading indicates states in which *B. miyamotoi* was detected in human-biting ticks.

United States, *B. miyamotoi* was found in *I. pacificus* ticks in Oregon and California (14/1,497, 0.94%). Although *I. scapularis* ticks are distributed across the eastern United States, no *B. miyamotoi*-positive ticks were detected south of Virginia. *B. miyamotoi*-positive ticks were concentrated in the Northeast and upper Midwest (594 of 34,621, 1.72%) (Figure). Lyme disease remains the principal public health concern; the causative agent, *B. burgdorferi* (11,287/34,621; 32.60%, 95% CI 32.1%–33.1%), was 19 times more prevalent than *B. miyamotoi* (594/34,621, 1.72%) in *I. scapularis* ticks.

On average, prevalence of *B. miyamotoi* infection in *I. scapularis* ticks (1.72%, 95% CI 1.58%–1.86%) was higher than in *I. pacificus* ticks (0.94%, 95% CI 0.51%–1.56%). The prevalence of *B. miyamotoi* in *I. pacificus* ticks was 1.00% (95% CI 0.53%–1.7%) in adults (13/1,300), 0.53% (95% CI 0.01%–2.9%) in nymphs (1/190), and 0.00% (95% CI 0%–40.1%) in larvae (0/7). The prevalence of *B. miyamotoi* in *I. scapularis* ticks was 1.80% (95% CI 1.64%–1.97%) in adults (456/25,376), 1.54% (95% CI 1.29%–1.83%) in nymphs (133/8,615), and 0.79% (95% CI 0.26%–1.84%) in larvae (5/630).

Of 594 *B. miyamotoi*-positive *I. scapularis* ticks, 351 (59.09%) had concurrent infections. We found 293 (49.33%) *I. scapularis* ticks had a dual infection with *B. miyamotoi*: 220 (37.04%) were also infected with *B. burgdorferi* s.l., 43 (7.24%) with *A. phagocytophilum*, and 30 (5.05%) with *B. microti*. We further found 52 (8.75%) had a triple infection with *B. miyamotoi*: 23 (3.87%) were also infected with *B. burgdorferi* s.l. and *A. phagocytophilum*, 22 (3.70%) with *B. burgdorferi* s.l. and *B. microti*, and 7 (1.18%) with *A. phagocytophilum* and *B. microti*. Six (1.01%) of the *B. miyamotoi*-positive ticks had a quadruple infection with *B. miyamotoi*, *B. burgdorferi* s.l., *A. phagocytophilum*, and *B. microti*. No ticks with *B. mayonii* or EMLA were additionally infected with *B. miyamotoi*.

Multilocus sequence typing of the 16S, *fla*, and *glpQ* genes revealed 2 distinct *B. miyamotoi* genotypes separated by their tick vectors, *I. scapularis* ticks in the Northeast and upper Midwest and *I. pacificus* ticks in the West (Appendix, <https://wwwnc.cdc.gov/EID/article/27/12/20-4646-App1.pdf>). Whereas the 16S gene sequences were identical among all isolates, variable sites were found among *fla* and *glpQ* nucleotide sequences. Among 14 *I. pacificus* tick-borne

*B. miyamotoi* isolates, all *fla* and *glpQ* sequences were identical. A previously reported A/G substitution in *B. miyamotoi fla* sequences from *I. pacificus* ticks (5,9) was outside of our sequenced *fla* fragment (Appendix). The genetic identity between the 2 tick species-specific genotypes was 0.996 for *fla* and 0.986 for *glpQ*. Unlike heterogeneous *B. burgdorferi* populations, *B. miyamotoi* appears to be very homogeneous within its respective tick vectors.

### About the Author

Dr. Xu is a research professor in the department of microbiology, University of Massachusetts–Amherst. His research interests include ticks and tickborne diseases.

### References

1. Krause PJ, Fish D, Narasimhan S, Barbour AG. *Borrelia miyamotoi* infection in nature and in humans. Clin Microbiol Infect. 2015;21:631–9. <https://doi.org/10.1016/j.cmi.2015.02.006>
2. Fukunaga M, Takahashi Y, Tsuruta Y, Matsushita O, Ralph D, McClelland M, et al. Genetic and phenotypic analysis of *Borrelia miyamotoi* sp. nov., isolated from the ixodid tick *Ixodes persulcatus*, the vector for Lyme disease in Japan. Int J Syst Bacteriol. 1995;45:804–10. <https://doi.org/10.1099/00207713-45-4-804>
3. Scoles GA, Papero M, Beati L, Fish D. A relapsing fever group spirochete transmitted by *Ixodes scapularis* ticks. Vector Borne Zoonotic Dis. 2001;1:21–34. <https://doi.org/10.1089/153036601750137624>
4. Bunikis J, Tsao J, Garpmo U, Berglund J, Fish D, Barbour AG. Typing of *Borrelia* relapsing fever group strains. Emerg Infect Dis. 2004;10:1661–4. <https://doi.org/10.3201/eid1009.040236>
5. Mun J, Eisen RJ, Eisen L, Lane RS. Detection of a *Borrelia miyamotoi* sensu lato relapsing-fever group spirochete from *Ixodes pacificus* in California. J Med Entomol. 2006;43:120–3. <https://doi.org/10.1093/jmedent/43.1.120>
6. Jiang BG, Jia N, Jiang JF, Zheng YC, Chu YL, Jiang RR, et al. *Borrelia miyamotoi* infections in humans and ticks, northeastern China. Emerg Infect Dis. 2018;24:236–41. <https://doi.org/10.3201/eid2402.160378>
7. Barbour AG, Bunikis J, Travinsky B, Hoen AG, Diuk-Wasser MA, Fish D, et al. Niche partitioning of *Borrelia burgdorferi* and *Borrelia miyamotoi* in the same tick vector and mammalian reservoir species. Am J Trop Med Hyg. 2009;81:1120–31. <https://doi.org/10.4269/ajtmh.2009.09-0208>
8. Xu G, Pearson P, Dykstra E, Andrews ES, Rich SM. Human-biting *Ixodes* ticks and pathogen prevalence from California, Oregon, and Washington. Vector Borne Zoonotic Dis. 2019;19:106–14. <https://doi.org/10.1089/vbz.2018.2323>
9. Cook VJ, Fedorova N, Macdonald WP, Lane RS, Barbour AG. Unique strain of *Borrelia miyamotoi* in *Ixodes pacificus* ticks, California, USA. Emerg Infect Dis. 2016;22:2205–7. <https://doi.org/10.3201/eid2212.152046>

Address for correspondence: Guang Xu, University of Massachusetts—Microbiology, Fernald Hall Room B1, 270 Stockbridge Rd, University of Massachusetts, Amherst, MA 01003, USA; email: gxu@umass.edu

## Wohlfahrtiimonas chitiniclastica Monomicrobial Bacteremia in a Homeless Man

Omar Harfouch, Paul M. Luethy, Mandee Noval, Jonathan D. Baghdadi

Author affiliation: University of Maryland Medical Center, Baltimore, Maryland, USA

DOI: <https://doi.org/10.3201/eid2712.210327>

We report a case of septic shock attributable to monomicrobial bloodstream infection secondary to *Wohlfahrtiimonas chitiniclastica* infection. This case suggests that *W. chitiniclastica* likely possesses the virulence to cause severe disease. Culture-independent techniques were essential in the identification of this organism, which enabled selection of appropriate therapy.

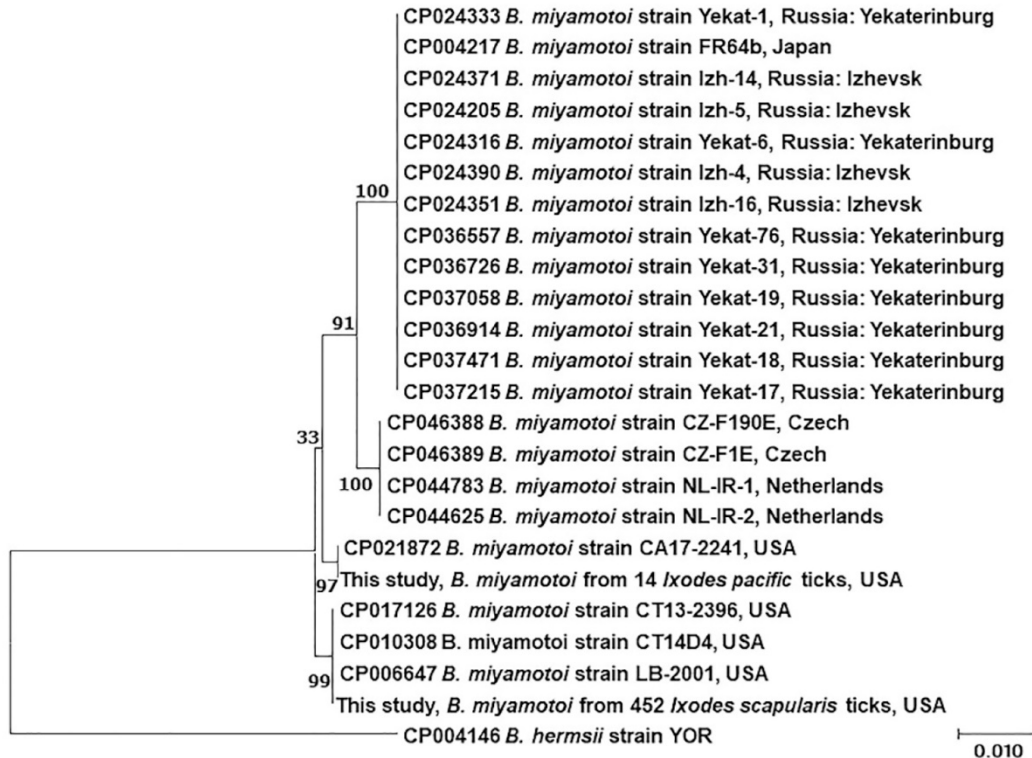
In August 2020, a 63-year-old homeless man with a history of deep vein thrombosis and chronic venous insufficiency was found in his truck, unconscious and covered in feces and maggots. He reportedly had been parked in a single parking spot in rural Maryland, USA, for 3 days. His blood pressure in the field was too low to be quantified, and he was admitted to a community hospital in septic shock. Blood cultures were drawn before establishing intravenous access for administration of vancomycin, piperacillin/tazobactam, and crystalloid. After being stabilized, he was transferred to our hospital, a tertiary care center in Baltimore, Maryland, USA, where surgeons performed superficial surgical debridement of his lower extremities and removed maggots by using a scrub brush with the patient under anesthesia in the operating room. We discarded the maggots, and they were not submitted for identification.

The patient's leukocyte count on arrival was 38.6 K/ $\mu$ L (reference range 4.5–11.0 K/ $\mu$ L), his creatinine 6.86 mg/dL (reference range 0.7–1.5 mg/dL), and his lactic acid 3.5 mmol/L (reference range 0.5–2.2 mmol/L). He had elevated transaminases, an aspartate aminotransferase level of 436 U/L (reference range 17–59 U/L) and alanine transaminase of 174 U/L (reference range 0–49 U/L). A computed tomography scan of the lower extremities showed ulceration of the anterior right lower leg with edema and fat stranding of the subcutaneous tissue without fluid collection or gas. A magnetic resonance imaging of his left foot showed no evidence of osteomyelitis.

On day 2 of hospitalization, transient hemodynamic instability necessitated initiation of

# *Borrelia miyamotoi* in Human-Biting Ticks, United States, 2013–2019

## Appendix

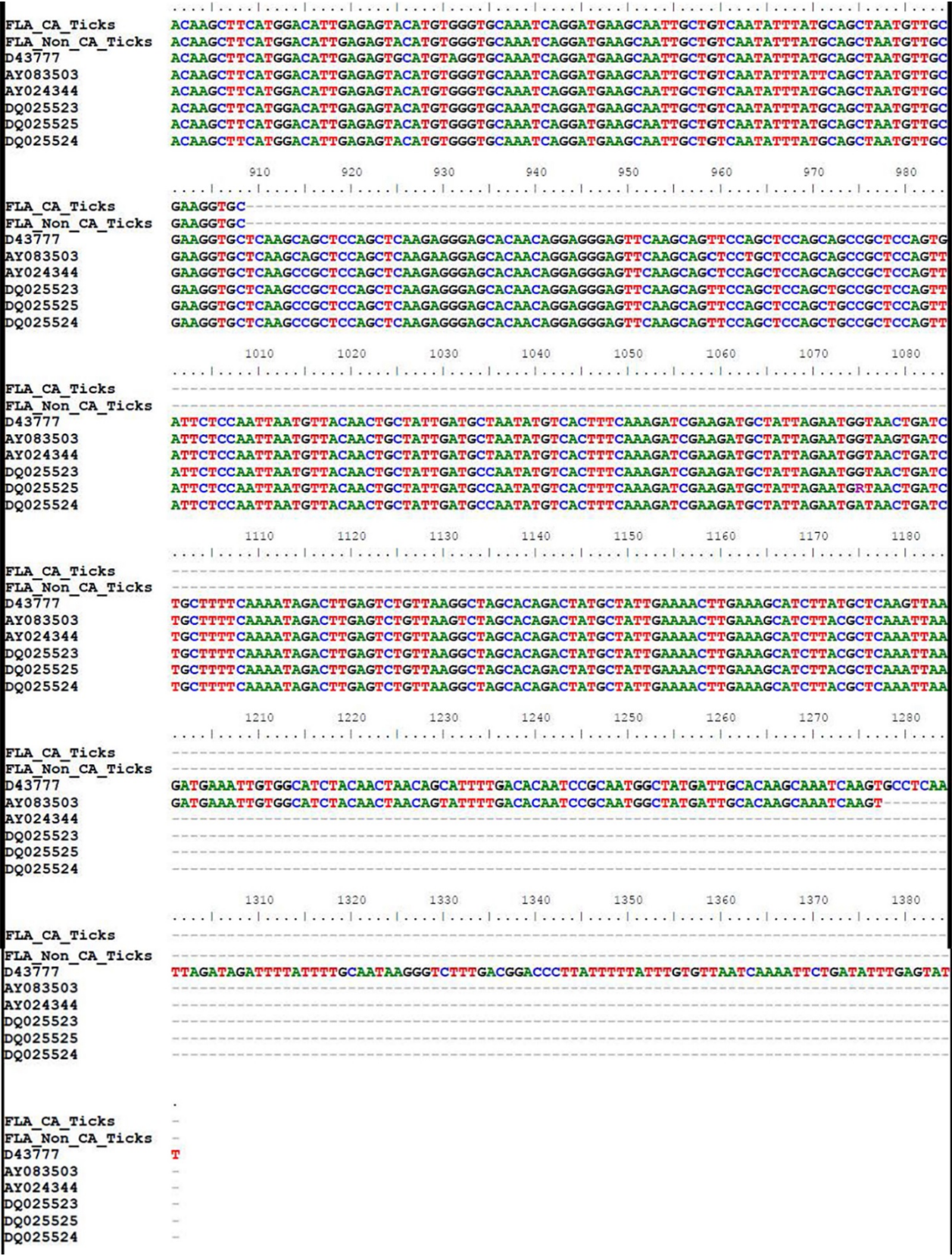


**Appendix Figure 1.** Phylogenetic tree of *Borrelia miyamotoi* 16S rDNA (16S), flagellin (*fla*), and glycerophosphodiester phosphodiesterase (*glpQ*) genes constructed by maximum likelihood method of MEGA software version 10 (<http://www.megasoftware.net>). Of 594 *B. miyamotoi*-positive *Ixodes scapularis* ticks, we successfully sequenced a 1,545bp long fragment of 3 concatenated genes from 452 ticks. We selected Hasegawa-Kishino-Yano with invariable site as the best model based on Bayesian information criterion scores. Numbers on the branches represent bootstrap support with 500 bootstrap replicates. Scale bar represents nucleotide substitutions per site.

```

          10      20      30      40      50      60      70      80
FLA_CA_Ticks
FLA_Non_CA_Ticks
D43777
AY083503
AY024344
DQ025523
DQ025525
DQ025524
          110      120      130      140      150      160      170      180
FLA_CA_Ticks
FLA_Non_CA_Ticks
D43777
AY083503
AY024344
DQ025523
DQ025525
DQ025524
          210      220      230      240      250      260      270      280
FLA_CA_Ticks
FLA_Non_CA_Ticks
D43777
AY083503
AY024344
DQ025523
DQ025525
DQ025524
          310      320      330      340      350      360      370      380
FLA_CA_Ticks
FLA_Non_CA_Ticks
D43777
AY083503
AY024344
DQ025523
DQ025525
DQ025524
          410      420      430      440      450      460      470      480
FLA_CA_Ticks
FLA_Non_CA_Ticks
D43777
AY083503
AY024344
DQ025523
DQ025525
DQ025524
          510      520      530      540      550      560      570      580
FLA_CA_Ticks
FLA_Non_CA_Ticks
D43777
AY083503
AY024344
DQ025523
DQ025525
DQ025524
          610      620      630      640      650      660      670      680
FLA_CA_Ticks
FLA_Non_CA_Ticks
D43777
AY083503
AY024344
DQ025523
DQ025525
DQ025524
          710      720      730      740      750      760      770      780
FLA_CA_Ticks
FLA_Non_CA_Ticks
D43777
AY083503
AY024344
DQ025523
DQ025525
DQ025524

```



Appendix Figure 2. Alignment of *Borrelia miyamotoi* fla gene segment.