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

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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.

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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 Ehrlicia 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 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. B. miyamotoi positive | No. B. burgdorferi s.l. positive |
|--------------|-----------------|---------------------------|---------------------------------|
| Amblyomma americanum | 1,167 | 0 | 0 |
| A. cajennense | 1 | 0 | 0 |
| A. maculatum | 8 | 0 | 0 |
| Dermacentor andersoni | 60 | 0 | 0 |
| D. occidentalis | 91 | 0 | 0 |
| D. variabilis | 1,060 | 0 | 0 |
| Haemaphysalis leporispalustris | 2 | 0 | 0 |
| H. longicornis | 7 | 0 | 0 |
| Ixodes affinis | 2 | 0 | 0 |
| I. angustus | 55 | 0 | 0 |
| I. cookei | 123 | 0 | 0 |
| I. dentatus | 48 | 0 | 7 |
| I. marxi | 26 | 0 | 0 |
| I. muris | 9 | 0 | 2 |
| I. pacificus | 1,497 | 14 | 25 |
| I. scapularis | 34,621 | 594 | 11,287 |
| I. spinipalpis | 63 | 0 | 3 |
| Rhicophorus sanguineus | 15 | 0 | 0 |
| Total | 38,855 | 608 | 11,324 |
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 Invet Mammal. 2006;43:120–3. https://doi.org/10.1093/jmedent/43.1.120
6. Jiang BC, 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.2018.2523
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

Wohlfahrtiimonas chitiniclastica

**Monomicrobial Bacteremia in a Homeless Man**

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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/µL (reference range 4.5–11.0 K/µL), 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, aspartate aminotransferase level of 436 U/L (reference range 0.5–2.2 mmol/L), 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...
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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.
Appendix Figure 2. Alignment of *Borrelia miyamotoi* fla gene segment.