In northwestern California, USA, the western black-legged tick, _Ixodes pacificus_, is a known vector of _Borrelia burgdorferi_, the spirochete that causes Lyme disease. _Borrelia miyamotoi_, which is more closely related to spirochetes that cause relapsing fever, has also been detected in 2 locations in California (1,2) and has recently been implicated as a human pathogen in the northeastern United States (3,4). Other studies may have unintentionally included _B. miyamotoi_ infections among measures of _B. burgdorferi_ if the diagnostics were for spirochetes (such as, direct fluorescent antibody tests or dark-field microscopy) or genetically targeted for _Borrelia_ spp. (5).

To investigate _Borrelia_ spp. ecology in California, we collected adult _I. pacificus_ ticks by dragging a 1-sq m white flannel blanket along vegetation and/or leaf litter in 12 recreational areas in the San Francisco Bay area during January-May 2012 (Table). Habitat varied from chaparral and grassland to coastal live oak woodland. Ticks were pooled for examination by quantitative PCR (qPCR) for the presence of _Borrelia_ spp. We interpreted the prevalence of _Borrelia_ spp. from positive pools as the minimum infection prevalence (that is, assuming 1 positive tick/positive pool). DNA was extracted from ticks by using the DNeasy Blood and Tissue Kit (QIAGEN, Valencia, CA, USA) according to the manufacturer's protocols and then stored at -20 deg C [-4 deg F] until use. DNA was analyzed by qPCR, with use of primer and fluorescent hybridization probes previously developed to differentiate _Borrelia_ spp. spirochetes (5).

To identify the _Borrelia_ spp. genotype, we attempted to sequence the 16S-23S (rrs-rrlA) intergenic spacer of each sample positive by qPCR (8). The nested PCR product was further purified by using the QIAquick Kit (QIAGEN) and then sequenced (Environmental Genetics and Genomics Laboratory, Northern Arizona University, Flagstaff, AZ, USA; <http://www.enggen.nau.edu/dna.html>) by using capillary Sanger sequencing on an ABI 3730 sequencer (Life Technologies, Grand Island, NY, USA). BLAST (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) was used to compare each sequence to other _Borrelia_ spp. sequences available from GenBank.
>From a total of 1180 adult ticks, we found 43 samples positive for _Borrelia_ spp., resulting in a minimum infection prevalence of 3.6 percent (Table). We obtained intergenic spacer sequence data for 27 of the positive samples; 6 samples were _B. burgdorferi_ sensu stricto, 7 were _B. burgdorferi_ sensu lato (both on the basis of alignments of 816 bp), and 14 were _B. miyamotoi_ (on the basis of alignments of 503 bp). The _B. miyamotoi_ sequences for our samples from California and those for isolates from the eastern United States (9) and Japan (8) formed a monophyletic clade that was oriented as a sister clade to the 3 _Borrelia_ spp. that cause tick-borne relapsing fever in the United States (_B. hermsii_, _B. turicatae_, and _B. parkeri_).

We found borreliae-infected adult _I. pacificus_ ticks at all 12 sites from which tick sample sizes exceeded 30. When the presence of _B. burgdorferi_ sensu stricto or _B. burgdorferi_ sensu lato was detected (4/12 sites each), prevalence was 0.6-2.2 percent and 0.7-2.5 percent, respectively.

_B. miyamotoi_ was detected at 7/12 sites, and prevalence ranged from 0.7 percent to 7.5 percent. A previous survey of _B. burgdorferi_ in nearby Santa Cruz County recreational areas reported an infection prevalence of approximately 6 percent among adult _I. pacificus_ ticks (6); the study did not, however, differentiate between _Borrelia_ spp. and therefore may have included _B. miyamotoi_ among its prevalence measures (5).

In our study, _B. burgdorferi_ was found more frequently in woodland habitats, but it was also detected in a grassland-chaparral habitat several hundred meters from the nearest woodland. We did not detect _Borrelia bissettii_, a species recently implicated as a human pathogen in Mendocino County, California (10). The high level of habitat variation in northwestern California presents a varied risk for _Borrelia_-associated tick-borne disease in humans because of diverse variations in vertebrate reservoir ecology, tick abundance, and human exposure to ticks. This variation emphasizes the need to understand the local epidemiology and ecology of a disease.

In adult _I. pacificus_ ticks in the San Francisco Bay area, _B. miyamotoi_ is as abundant as its congener _B. burgdorferi_. Human disease caused by _B. miyamotoi_ infection has not been reported in California, and transmission efficiency of _B. miyamotoi_ by _I. pacificus_ ticks is unknown. However, it is possible that _B. miyamotoi_ infections in ticks and humans have not been accurately diagnosed. We advocate for increased scrutiny of the eco-epidemiology of _B. miyamotoi_ in human, tick, and possible vertebrate host populations in northwestern California.

[The tables and references are available at the source URL above.]

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It is apparent that human infection with _B. miyamotoi_ can present as a non-specific acute febrile illness with fever as high as 39.5 deg C (103.1 deg F), headache, and myalgias or as a relapsing fever-like illness. It also has the potential to be misdiagnosed as Lyme disease, although _B. miyamotoi_ usually does not cause the bull's eye shaped rash that characterizes Lyme disease, or be misdiagnosed as human granulocytic anaplasmosis, two other tick-borne diseases. The infection has also presented in an elderly, immunocompromised woman with confusion and an unsteady gait.

_B. miyamotoi_ can be detected by PCR in the blood of infected patients, or the diagnosis could be made with a specific serologic test, for example, one that uses _Borrelia miyamotoi_ GlpQ protein (an antigen that is nonreactive to _Borrelia burgdorferi_ antibody), but these tests may not be widely available. The 2 step serology for Lyme disease is usually negative in _B. miyamotoi_ infections. Because of its non-specific clinical presentation and lack of readily available diagnostic laboratory tests, the true extent of _B. miyamotoi_ infection may be underappreciated.