What the science tells us about Lyme Disease

Lyme disease cases are concentrated in the Northeast and upper Midwest, with 14 states accounting for over 96% of cases reported to the Center for Disease Control (CDC), with about 300,000 people diagnosed each year. (SOURCE)

Borrelia burgdorferi, is the causative agent of Lyme disease (Lyme borreliosis). The long, thin serpentine morphology is the signature feature shared among spirochetes. The spirochetes in the *Borrelia burgdorferi* sensu lato genospecies group, cycle in nature between tick vectors and vertebrate hosts. (SOURCE)

In the United States, the age distribution of Lyme borreliosis is typically bimodal, with peaks among children 5–15 years of age and adults 45–55 years of age. The incidence of Lyme borreliosis is higher among men than among women in those <60 years of age, but the sex ratio is nearly equal or slightly higher in women in older age groups. In some European countries, such as Slovenia and Germany, the incidence of Lyme borreliosis is higher among adult women (55%) than among men (45%). In the northeastern United States and in most of Europe, the peak months of disease onset are June and July, which is owing to the feeding habits of nymphal ticks. (SOURCE)

If Lyme disease is not treated early in the course of infection, chronic illness may result and a variety of symptoms may develop. These symptoms include fatigue, musculoskeletal pain, arthritis, cardiac disease and neurological involvement with peripheral neuropathy, meningitis, encephalitis, cranial neuritis and cognitive dysfunction. One viewpoint claims that persistent Lyme disease symptoms are related to ongoing spirochetal infection despite antibiotic therapy. The opposing viewpoint claims that persistent Lyme disease symptoms may be due to spirochetal “debris” without active infection. In this pilot study we demonstrated persistent infection despite antibiotic therapy in 12 North American patients with ongoing symptoms of Lyme disease. Cultures were positive in all 12 patients in our study, indicating that the *Borrelia* spirochetes were replicating and therefore alive. (SOURCE)
Parasites from the genus *Babesia* are responsible for causing an emerging zoonotic disease called babesiosis. *Babesia microti* and *Babesia divergens* are the most frequent etiological agents

associated with human babesiosis in North America and Europe, respectively. Transmission occurs mainly through the bite of a *Babesia*-infected tick and, less commonly, by blood transfusion. (SOURCE)

Persistent infection is a characteristic feature of babesiosis, a worldwide, emerging tick-borne disease caused by members of the genus *Babesia.* Persistence of *Babesia* infection in reservoir hosts increases the probability of survival and transmission of these pathogens. Laboratory tools to detect *Babesia* in red blood cells include microscopic detection using peripheral blood smears, nucleic acid detection (polymerase chain reaction and transcription mediated amplification), antigen detection, and antibody detection. *Babesia microti*, the major cause of human babesiosis, can asymptomatically infect immunocompetent individuals for up to two years. (SOURCE)

Babesia microti and *Borrelia burgdorferi* cause two of the most prominent tick-borne diseases in the U.S.A., human babesiosis and Lyme disease, respectively.

Babesia microti is transmitted by species of *Ixodes,* the same ticks that transmit the Lyme disease-causing spirochete, *Borrelia burgdorferi. B. microti* can also be transmitted through transfusion of blood products and is the most common transfusion-transmitted infection in the U.S.A.

Ixodes ticks are commonly infected with both *B. microti* and *B. burgdorferi*, and are competent vectors for transmitting them together into hosts.
Few studies have examined the effects of coinfections on humans and those have had somewhat contradictory results.

One study linked coinfection with *B. microti* to a greater number of symptoms of overall disease in patients, while another report indicated that *B. burgdorferi* infection either did not affect babesiosis symptoms or decreased its severity.
Mouse models of infection that manifest pathological effects similar to those observed in human babesiosis and Lyme disease offer a unique opportunity to thoroughly investigate the effects of coinfection on the host.

Lyme disease has been studied using the susceptible C3H mouse infection model, which can also be used to examine *B. microti* infection to understand pathological mechanisms of human diseases, both during a single infection and during coinfections.

We observed that high *B. microti* parasitaemia leads to low haemoglobin levels in infected mice, reflecting the anemia observed in human babesiosis. Similar to humans, *B. microti* coinfection appears to enhance the severity of Lyme disease-like symptoms in mice.

Coinfected mice have lower peak *B. microti* parasitaemia compared to mice infected with *B. microti* alone, which may reflect attenuation of babesiosis symptoms reported in some human coinfections.

These findings suggest that *B. burgdorferi* coinfection attenuates parasite growth while *B. microti* presence exacerbates Lyme disease-like symptoms in mice. (SOURCE)

The Gram-negative bacterial genus *Bartonella* currently comprises roughly fifteen different species, which cause Bartonellosis in humans. It is known to be transmitted by a vector, primarily fleas and also animal bites, scratches, or needle sticks. However, the clinical implications of many of these human infections are poorly understood, and it is possible that some of the species are non-pathogenic, at least in immunocompetent people. *B. henselae* or “Cat scratch disease” is reported in approximately twenty thousand cases per year in the United States.

The DNA of various *Bartonella* species can also be amplified by polymerase chain reaction (PCR) in blood, spinal fluid, and tissue; given the cross-reactivity of the *Bartonella* antibody tests, PCR may be the most reliable and useful test for *Bartonella* infection. (SOURCE)

ORIGNAL ARTICLE

Regional prevalences of *Borrelia burgdorferi*, *Borrelia bissettiae*, and *Bartonella henselae* in *Ixodes affinis, Ixodes pacificus* and *Ixodes scapularis* in the USA

Abstract

The objective of this work was to determine the prevalence of *Borrelia* and *Bartonella* species in *Ixodes* spp. ticks collected from 16 USA states. Genus PCR amplification and sequence analysis of *Bartonella* and *Borrelia*16SsRNA-23SsRNA intergenic regions were performed on DNA extracted from 929 questing adult ticks (671 *Ixodes scapularis*, 155 *Ixodes affinis*, and 103 *Ixodes pacificus*). Overall, 129/929 (13.9%) *Ixodes* ticks were PCR positive for *Borrelia burgdorferi* sensu stricto, 48/929 for *B. bissettiae*whereas 23/929 (2.5%) were PCR positive for a *Bartonella henselae*. Borrelia bissettiae or *B. burgdorferi* s.s. and *B. henselae* co-infections were found in *I. affinis* from North Carolina at a rate of 4.5%; in a single *I. scapularis*from Minnesota, but not in *I. pacificus*. For both bacterial genera, PCR positive rates were highly variable depending on geographic location and tick species, with *Ixodes affinis* (n = 155) collected from North Carolina, being the tick species with the highest prevalence's for both *Borrelia* spp. (63.2%) and *B. henselae* (10.3%). Based on the results of this and other published studies, improved understanding of the enzootic cycle, transmission dynamics, and vector competence of *Ixodes* species (especially *I. affinis*) for transmission of *Borrelia* spp. and *B. henselae*should be a public health research priority. (SOURCE)

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SOURCE REFERENCES LYME DISEASE

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